

CC host cells. The replication of this plasmid in the host cells is also
CC very stable. The host cells used are cells derived from mammals,
CC preferably from a human. The plasmid is useful to provide a large amount
CC of heterologous peptide in recombinant cells. The offspring of an animal
CC carrying the gene can be used as peptide producing animals
XX
SQ Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 665 CAATCTGCTCCTGCA 682
Db 18 CGATCTGCTCCTGCA 1

RESULT 1587
AAZ89776/C
ID AAZ89776 standard; DNA; 18 BP.

XX AAZ89776;

DT 05-MAY-2000 (first entry)

DE Human RIP-1 antisense oligonucleotide ISIS# 23931.

KW RIP-1; RalBP; RLP; antisense inhibitor; anti-inflammatory; cytostatic;
KM anti-infective; diagnose; prevent; treatment; tumour formation; ss.

XX Homo sapiens.

OS US6020198-A.

PN 01-FEB-2000.

PD 25-SEP-1998; 98US-00161443.

PF 25-SEP-1998; 98US-00161443.

PR (ISIS-) ISIS PHARM INC.

PA Bennett CF, Cowsett LM;

PI WPI; 2000-146889/13.

PT Antisense inhibition of human RIP-1 expression, useful for diagnosing,
PT preventing and treating conditions such as inflammation.
XX
XX

PS Example 15; Col 27; 26pp; English.

CC This sequence represents an antisense oligonucleotide which binds to the
CC 3' untranslated region of RIP-1. RIP-1 (also known as RalBP and RLP) is
CC a GTPase activating protein (GAP) thought to be a downstream target of
CC Ral. The invention relates to antisense phosphorothioate oligonucleotides
CC with anti-infective, anti-inflammatory and cytostatic activity. The
CC oligonucleotides are RIP-1 antisense inhibitors and are used in the
CC diagnosis, prevention and treatment of conditions associated with RIP-1
CC expression. Conditions associated with RIP-1 expression include various
CC infections, inflammation and tumour formation
XX
XX

SQ Sequence 18 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 383 CCTCCAAAGTGTGGA 400
Db 18 CTTCCAAAGTGTGGA 1

RESULT 1588

AAZ89747/C
ID AAZ89747 standard; DNA; 18 BP.

XX AAZ89747;

DT 05-MAY-2000 (first entry)

DE Human RIP-1 antisense oligonucleotide ISIS# 23930.

KW RIP-1; RalBP; RLP; antisense inhibitor; anti-inflammatory; cytostatic;
KM anti-infective; diagnose; prevent; treatment; tumour formation; ss.

XX Homo sapiens.

OS US6020198-A.

PN 01-FEB-2000.

PD 25-SEP-1998; 98US-00161443.

PF 25-SEP-1998; 98US-00161443.

PR (ISIS-) ISIS PHARM INC.

PA Bennett CF, Cowsett LM;

PI WPI; 2000-146889/13.

PT Antisense inhibition of human RIP-1 expression, useful for diagnosing,
PT preventing and treating conditions such as inflammation.
XX
XX

PS Claim 3; Col 27; 26pp; English.

CC This sequence represents an antisense oligonucleotide which binds to the
CC 3' untranslated region of RIP-1. RIP-1 (also known as RalBP and RLP) is
CC a GTPase activating protein (GAP) thought to be a downstream target of
CC Ral. The invention relates to antisense phosphorothioate oligonucleotides
CC with anti-infective, anti-inflammatory and cytostatic activity. The
CC oligonucleotides are RIP-1 antisense inhibitors and are used in the
CC diagnosis, prevention and treatment of conditions associated with RIP-1
CC expression. Conditions associated with RIP-1 expression include various
CC infections, inflammation and tumour formation
XX
XX

SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1112 AGCTGTCTCAACTCC 1129
Db 18 AGCTGTCTCAACTTC 1

RESULT 1589
AAZ39625
ID AAZ39625 standard; DNA; 18 BP.

XX AAZ39625;

DT 28-FEB-2000 (first entry)

DE Human CREL mRNA inhibiting antisense oligo ISIS #24109.

KW Human; CREL; transcriptional activator; antisense compound; therapeutic;
KM ss.

XX Synthetic.

OS Homo sapiens.

PN US6001652-A.

PD 14-DEC-1999.

Query	Match	Similarity	Score	DB	Length
Best Local	Similarity	94.4%	Pred. No. 1.5e+03		
Matches	17	Conservative	0	Mismatches	1
				Indels	0
				Gaps	0
QY	385	TCCCAAGCTCGGATT	402		
DB	1	TCCCAAGCTCGGATT	18		
RESULT 1590					
AAH40733/c					
ID	AAH40733	standard	DNA	18	BP.
XX	AAH40733				
AC					
XX					
DT					
XX					
DE	14-AUG-2001	(fixat entry)			
SNP	specific upper PCR primer	SEQ ID 3529.			
XX					
XX	Single nucleotide polymorphism; SNP; single nucleotide primer extension;				
KW	SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;				
KW	lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;				
KW	polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;				
KW	acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;				
KW	inflammation; forensic investigation; paternity analysis; PCR primer; ss.				
OS	Homo sapiens.				
XX					
PN	WO200129262-A2.				
XX					
PD	26-APR-2001.				
XX					
PF	13-OCT-2000; 2000WO-US028436.				
XX					
PR	15-OCT-1999; 99US-0160096P.				
XX					
PA	(ORCHID) ORCHID BIOSCIENCES INC.				
XX					
PI	Picoult-Newburg L, Pohl M;				
XX					
DR	WPI; 2001-290930/30.				
XX					
PT	New genotyping oligonucleotide, useful for detecting the presence,				

absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

Claim 1; Page 68; 83pp; English.

Sequences AAH37205 - AAH4994 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association a pathological phenotype trait suspected of being individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease or which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence

Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

874 CAGCGGTGAGCCACCACG 891
|||||
DB 18 CAGGTGTGAGCCACCACG 1

RESULT 1591
AAH38918/c
ID AAH38918 standard; DNA; 18 BP.
XX
XX
XX AAH38918;
AC
DT 14-AUG-2001 (first entry)
XX
XX
DE SNP specific lower PCR primer SEQ ID 1744.
XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
PN
PD 26-APR-2001.
PP 13-OCT-2000; 2000WO-USO28436.
PF
PK 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA Picoult-Newburg L., Pohl M;
PI
DR WPI; 2001-290930/30.
XX

PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.

PS Claim 1; Page 58; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence

XX SQ Sequence 18 BP; 2 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1021 GCCTCCCAAGCAGCTGG 1038
DB 18 GCCTCCCAAGCAGCTAGG 1

RESULT 1592
AAH39265
ID AAH39265 standard; DNA; 18 BP.
XX AAH39265;
AC
XX
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX
XX SNP specific upper PCR primer SEQ ID 2061.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200129262-A2.
PN
XX
XX 26-APR-2001.
PD
XX
XX 13-OCT-2000; 2000MO-US028436.
PF
XX
XX 15-OCT-1999; 99US-0160096P.
PR
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX Picoult-Newburg L, Pohl M,
PI
XX WPI; 2001-290930/30.
DR

XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polymorphic polymorphism in a nucleic
PT acid sample.

PS Claim 1; Page 60; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence

XX SQ Sequence 18 BP; 5 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 375 TGCTCAGCTCCCAAG 392
DB 1 TGCTCAGCTCCCAAG 18

RESULT 1593
AAH47615
ID AAH47615 standard; DNA; 18 BP.
XX AAH47615;
AC
XX
XX
XX 30-NOV-2001 (first entry)
DT
XX
XX
XX Human Her-3 mRNA inhibiting antisense oligo ISIS # 19628.
DE
XX
XX Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;
XX antiinflammatory; cytosolic; antibacterial; antisense; ss.
XX
XX Synthetic.
OS
XX
XX US6277640-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 31-JUL-2000; 2000US-00630706.
PF
XX
XX 31-JUL-2000; 2000US-00630706.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Cowart LM,
PI
XX WPI; 2001-535134/59.
DR
XX
XX Antisense compounds capable of modulating expression of human Her-3,
PT

PT member of epidermal growth factor family of receptor/tyrosine kinases,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
XX
PS Claim 1; Col 43-44; 49pp; English.
XX
CC The invention provides antisense compounds capable of inhibiting the
CC expression of human Her-3, a member of epidermal growth factor (EGF)
CC family of receptor/tyrosine kinases. The antisense oligonucleotides are
CC useful for inhibiting the expression of Her-3 in cells or tissues. They
CC are commonly used as research reagents and in diagnostics for example, to
CC elucidate the function of particular genes. The antisense compounds are
CC also useful for distinguishing between functions of various members of a
CC biological pathway and for research use. They are also utilized for
CC diagnostics, therapeutics, prophylaxis and in kits. They are useful
CC prophylactically, e.g. to prevent or delay infection, inflammation or
CC tumor formation. Sequences AAH47532-47615 represent chimeric antisense
CC phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,
CC used for the inhibition of Her-3 mRNA expression
XX
SQ Sequence 18 BP; 7 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 388 CAAAGTCTGAGATTACA 405
Db 1 CAAAGTCTGAGATTACA 18
XX
RESULT 1594
ABAB2413
ID ABA82413 standard; DNA; 18 BP.
XX
AC ABA82413;
XX
DT 25-JAN-2002 (first entry)
XX
DE Zmax1 gene region physical map preparation STS marker #372.
XX
KW Human; high bone mass; HBM gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177327-A1.
XX
PD 18-OCT-2001.
XX
PF 21-JUN-2000; 2000WO-US016951.
XX
PR 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2001-657171/75.
XX
PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS Disclosure; Page 36; 443pp; English.
XX
CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in

CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and ABA68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 392 GTGCTGGATTACAGCG 409
Db 1 GTGCTGGATTACAGCG 18
XX
RESULT 1595
ABA82195/C
ID ABA82195 standard; DNA; 18 BP.
XX
AC ABA82195;
XX
DT 25-JAN-2002 (first entry)
XX
DE Zmax1 gene region physical map preparation STS marker #154.
XX
KW Human; high bone mass; HBM gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177327-A1.
XX
PD 18-OCT-2001.
XX
PF 21-JUN-2000; 2000WO-US016951.
XX
PR 05-APR-2000; 2000US-00543771.
PR 05-APR-2000; 2000US-00544398.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2001-657171/75.
XX
PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS Disclosure; Page 34; 443pp; English.
XX
CC The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 685 CTTCTGCTCCCGGGTTCA 702
Db 18 CTTCTGCTCCCGGGTTCA 1

RESULT 1596
ABS98053
ID ABS98053 standard; DNA, 18 BP.
XX
AC ABS98053;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance gene PCR primer #17.
XX
KW Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP4502B1; LTF;
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxigenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLR2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
XX
PD 25-UTL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 22; Page 141; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxigenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLR2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), uridine kinase receptor (UPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing

CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLR2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention
XX
SQ Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
CY 867 GGGATTACGGCGGTGAGC 884
DB 1 GGGATTACGGGTGAGC 18
XX
RESULT 1597
ABK22992/C
ID ABK22992 standard; DNA, 18 BP.
XX
XX
AC ABK22992;
XX
DT 09-APR-2002 (first entry)
XX
XX
DE Human Zmax1 cDNA reverse PCR primer #77.
XX
KW Human; mouse; Zmax1; HMW; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
XX WPI; 2002-097784/13.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
PS Disclosure; Page 39; 409pp; English.
XX
CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-

CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
CC
CC
SQ Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 685 CTCGCTCCCGGGTTCA 702
DB 18 CTCGCTCCCGGGTTCA 1
RESULT 1598
ABK23210
ID ABK23210 standard; DNA; 18 BP.
XX
XX ABK23210;
AC
XX
DT 09-APR-2002 (first entry)
DE Human Zmax1 cDNA reverse PCR primer #186.
XX
XX Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteoprotective; cerebroprotective.
XX
XX Homo sapiens.
OS
XX
XX W0200192891-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016946.
PF
XX
XX 26-MAY-2000; 2000US-00578900.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
XX WPI; 2002-097784/13.
DR
XX
XX Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
XX
XX Disclosure; Page 41; 409pp; English.
PS
XX The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular

CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
CC
CC
SQ Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 392 GTGCTGGATTACAGCG 409
DB 1 GTGCTGGATTACAGCG 18
RESULT 1599
ACC49483
ID ACC49483 standard; DNA; 18 BP.
XX
XX ACC49483;
AC
XX
DT 27-JUN-2003 (first entry)
DE Human GAPDH reverse PCR primer SEQ ID NO:4.
XX
XX Human; NEDL-1; neuroblastoma; GAPDH; PCR primer; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX W02003018842-A1.
PN
XX
XX 06-MAR-2003.
PD
XX
XX 23-AUG-2002; 2002WO-JP008524.
PF
XX
XX 24-AUG-2001; 2001JP-00254974.
PR
XX 18-APR-2002; 2002JP-00116753.
PR
XX
XX (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
XX Nakagawara A, Miyazaki K;
PI
XX
XX WPI; 2003-278676/27.
DR
XX
XX Novel gene NEDL-1 as probes or primers for PCR in diagnosis and prognosis
PT of neuroblastoma.
PT
XX
XX Example 5; Page 34; 86pp; Japanese.
PS
XX
XX The present invention describes human NEDL-1. NEDL-1 is located to
CC chromosome 7, more specifically to 7p. The present invention also
CC describes a nucleic acid probe comprising: (a) a nucleic acid with a part
CC of the base sequence of the 6200 base pair sequence given in ACC49481
CC (1), or its complementary base sequence; or (b) a nucleic acid
CC hybridizable with the nucleic acid with a base sequence of (1) or its
CC complementary base sequence under stringent conditions. The NEDL-1 gene
CC and its encoded protein can be used in the diagnosis and prognosis of
CC neuroblastoma. The present sequence represents a PCR primer for GAPDH,
CC which is used in an example from the present invention
CC
CC
SQ Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 316 GTGAAACAGGGTTTCAC 333
|||
Db 1 GTAGAGACAGGGTTTCAC 18

RESULT 1600

ACCA5793
ID ACCA5793 standard; DNA; 18 BP.

ACCA5793;

02-JUN-2003 (first entry)

Human HBM STS marker reverse primer #186.

Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

Homo sapiens.

WO200292764-A2.

21-NOV-2002.

13-MAY-2002; 2002WO-US014876.

11-MAY-2001; 2001US-0290071P.

17-MAY-2001; 2001US-0291311P.

01-FEB-2002; 2002US-0353058P.

04-MAR-2002; 2002US-0361293P.

(GENO-) GENOME THERAPEUTICS CORP.

(AMHP) WYETH.

Babij P, Bex FJ, Yaworsky PJ, Bodine PV;

WPI; 2003-129278/12.

New transgenic animals (e.g. mice), useful as models for studying bone
density modulation, developing drugs for treating or preventing bone
diseases (e.g. osteoporosis), or diagnosing diseases characterized by
reduced bone density.

Disclosure; Page 57; 603pp; English.

The invention relates to novel transgenic animals expressing the high
bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
an LRP5 that is modulated by an altered gene control sequence introduced
by homologous or non-homologous recombination. The transgenic animals are
for the study of bone density modulation or bone mass modulation. The
invention has osteopathic and cytostatic activity. The polynucleotides of
the invention may have a use in gene therapy. The transgenic animals and
nucleic acids are for the study of bone density modulation, where the
bone mass is modulated relative to non-transgenic animals of the same
species in more than one parameter selected from bone density, bone
strength, trabecular number, bone size, or bone tissue connectivity. The
transgenic animals, nucleic acids and methods are useful for identifying
molecules involved in bone development, and for developing pharmaceutical
compositions, which may be employed for treating or preventing bone
diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
neoplasms of the bone. The transgenic animals and nucleic acids are also
useful in methods for diagnosing diseases involved in bone development,
or characterised by reduced bone density or mass. The present sequence is
used in the exemplification of the invention

Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.7%; Score 16.4; DB 1; Length 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 392 GTGCTGGGATTACAGCG 409
|||
Db 1 GTACTGGGATTACAGCG 18

RESULT 1601

ACCA575/C
ID ACCA575 standard; DNA; 18 BP.

ACCA575;

02-JUN-2003 (first entry)

Human HBM STS marker reverse primer #77.

Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

Homo sapiens.

WO200292764-A2.

21-NOV-2002.

13-MAY-2002; 2002WO-US014876.

11-MAY-2001; 2001US-0290071P.

17-MAY-2001; 2001US-0291311P.

01-FEB-2002; 2002US-0353058P.

04-MAR-2002; 2002US-0361293P.

(GENO-) GENOME THERAPEUTICS CORP.

(AMHP) WYETH.

Babij P, Bex FJ, Yaworsky PJ, Bodine PV;

WPI; 2003-129278/12.

New transgenic animals (e.g. mice), useful as models for studying bone
density modulation, developing drugs for treating or preventing bone
diseases (e.g. osteoporosis), or diagnosing diseases characterized by
reduced bone density.

Disclosure; Page 55; 603pp; English.

The invention relates to novel transgenic animals expressing the high
bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
an LRP5 that is modulated by an altered gene control sequence introduced
by homologous or non-homologous recombination. The transgenic animals are
for the study of bone density modulation or bone mass modulation. The
invention has osteopathic and cytostatic activity. The polynucleotides of
the invention may have a use in gene therapy. The transgenic animals and
nucleic acids are for the study of bone density modulation, where the
bone mass is modulated relative to non-transgenic animals of the same
species in more than one parameter selected from bone density, bone
strength, trabecular number, bone size, or bone tissue connectivity. The
transgenic animals, nucleic acids and methods are useful for identifying
molecules involved in bone development, and for developing pharmaceutical
compositions, which may be employed for treating or preventing bone
diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
neoplasms of the bone. The transgenic animals and nucleic acids are also
useful in methods for diagnosing diseases involved in bone development,
or characterised by reduced bone density or mass. The present sequence is
used in the exemplification of the invention

Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.7%; Score 16.4; DB 1; Length 18;

	Best Local Similarity	94.4%	Pred. No. 1.5e+03;			
	Matches	17;	Conservative	0;	Mismatches	1;
					Indels	0;
					Gaps	0;
Oy	685	CTGTGCTCCCGGGTTCA	702			
Db	18	CTTGCTCTCAGGGTTCA	1			

RESULT 1602
ID ACC45283 standard; DNA; 18 BP.
XX AC ACC45283;
DT 16-JUN-2003 (first entry)
DE Human GAPDH PCR primer SEQ ID NO:49.
XX Human; BMCC1; chromosome 9; cytostatic; cancer; tumour; neuroblastoma;
KW GAPDH; PCR primer; ss.
XX Homo sapiens.
OS WO2003018806-A1.
PN 06-MAR-2003.
PD 23-AUG-2002; 2002MO-JP008520.
Pf 24-AUG-2001; 2001JP-00255198.
PR (HISM) HISAMITSU PHARM CO LTD.
XX (CHIB-) CHIBA PREFECTURE.
PA Nakagawara A, Hattori M, Sakaki Y;
PI WPI; 2003-278667/27.
DR Novel human BMCC1 protein and encoded gene having high homology with a
PT part of BNIP2, applicable in studying biology, pathology and onset of
PT cancer, as well as diagnosis, prognosis and screening of drugs for tumor
e.g. neuroblastoma.
PS Example 9; Page 27; 99pp; Japanese.
XX The present invention describes the human BMCC1 protein. The BMCC1 gene
CC has high homology with a part of BNIP2, and is located to the chromosome
CC 9. BMCC1 has cytostatic activity. The BMCC1 protein and its encoded gene
CC are applicable in studying biology, pathology and the onset of cancer.
CC BMCC1 can also be used in the diagnosis, prognosis and screening of drugs
CC for tumour e.g. neuroblastoma, including the provision of gene data and
CC protein function on human neuroblastoma. The present sequence represents
CC a PCR primer for human GAPDH, which is used in an example from the
present invention
CC SQ Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
QY Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Db 316 GTAGANAACAGGGTTTCAC 333
1 GTTAGAACAAGGTTTCAAC 18
RESULT 1603
ACA62881/c
ID ACA62881 standard; DNA; 18 BP.
XX ACA62881;
AC ACA62881;
DT 21-FEB-2003 (first entry)

XX Repeated nucleic acid detection method, human probe Alu1.
DE Repeated nucleic acid detection; human; alu; probe; ss.
XX Repeated nucleic acid detection; human; alu; probe; ss.
XX Repeated nucleic acid detection; human; alu; probe; ss.
OS Homo sapiens.
XX Homo sapiens.
EN US2003022163-A1.
XX US2003022163-A1.
PD 30-JAN-2003.
XX 30-JAN-2003.
PE 15-DEC-2000; 2000US-00739909.
XX 15-DEC-2000; 2000US-00739909.
PR 21-JUL-1999; 99US-00358972.
PR 25-AUG-1999; 99US-00383316.
XX 25-AUG-1999; 99US-00383316.
PA (MAND/) MANDREKAR M N.
PA (TERE/) TEREBA A.
PA (SHUL/) SHULTZ J W.
XX (SHUL/) SHULTZ J W.
PI Mandrekar MN, Tereba A, Shultz JW;
XX Mandrekar MN, Tereba A, Shultz JW;
DR WPI; 2003-479484/45.
XX WPI; 2003-479484/45.
PT Determining presence or absence of desired nucleic acids that contain
PR multiple repeats of predetermined nucleic acid target sequences in a
PI sample, by using nucleic acid hybridization methods.
XX Claim 1; Page 27; 31pp; English.

```

XX The invention describes a method of determining presence or absence of a
CC desired nucleic acid (NA) that contains multiple repeats of a
CC predetermined NA target sequence in a NA sample. The method involves
CC providing a treated sample that may contain the desired NA in which
CC several predetermined repeating NA target sequences are hybridised with a
CC NA probe, analysing for presence of hybridised NA containing the NA
CC probe, and thereby the presence or absence of the desired NA. The method
CC is useful for determining the presence or absence of desired nucleic
CC acids that contain multiple repeats of a predetermined NA target
CC sequence, in a NA sample obtained from a biological sample, where the
CC repeated sequence includes several predetermined repeated sequence that
CC differ in length and/or sequence. The methods can be efficiently used for
CC distinguishing human and bacterial NA. The method is highly sensitive,
CC and enables detection and quantification of the presence of a NA without
CC the need to undergo a NA target sequence enrichment step prior to a NA
CC hybrid detection step. The method enables rapid and accurate detection of
CC a desired NA that contains multiple repeats of a NA target sequence. This
CC sequence represents a probe used to detect the human Alu repeat sequences
XX
SQ Sequence 18 BP; 4 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 729 AGTACTGGGACTACAGG 746
| | | | | | | | | | | | | | | |
DB 18 AGTAGCTGGGATTACAGG 1
RESULT 1604
ADB98491
ID ADB98491 standard; DNA; 18 BP.
XX
AC ADB98491;
DT 04-DEC-2003 (first entry)
XX
DE Sequence tagged site #372 used to prepare Zmax1 (LRP5) gene region map.
XX
KW Osteopathic; Gene therapy; High Bone Mass; HBW; LRP5; Zmax1; LRP6;
XX bone mass modulation; osteoporosis; STS; Sequence tagged site; ds.
XX
```

```
OS Homo sapiens.
XX
XX WO200292000-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US014877.
XX
XX 11-MAY-2001; 2001US-0290071P.
XX 17-MAY-2001; 2001US-0291311P.
XX 01-FEB-2002; 2002US-0353058P.
XX 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX (AMHP ) WYETH.
XX
XX Allen K, Anisiewicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
XX diagnosing a HBM-like phenotype in a subject and for preparing a
XX composition for modulating bone mass and/or lipid levels in a subject
XX suffering from e.g. osteoporosis.
XX
XX Example 2; Page 63; 629pp; English.
XX
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
XX LRP6 mutants, which results in a HBM-like phenotype when expressed in a
XX cell. The HBM-like phenotype results in bone mass modulation and/or lipid
XX level modulation. The invention is useful for diagnosing a HBM-like
XX phenotype in a subject and for preparing a composition for modulating
XX bone mass and/or lipid levels in a subject suffering from e.g.
XX osteoporosis. The present sequence is a Sequence Tagged Site (STS)
XX marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
XX region.
XX
XX Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 392 GTGCTGGATTACAGGCG 409
XX |||||
XX 1 GTACTGGGATTACAGGCG 18
XX
XX RESULT 1605
XX ADB98273/C
XX ID ADB98273 standard; DNA; 18 BP.
XX
XX ADB98273;
XX
XX 04-DEC-2003 (first entry)
XX
XX Sequence tagged site #154 used to prepare Zmax1 (LRP5) gene region map.
XX
XX Osteopathic; Gene therapy; High Bone Mass; HBM, LRP5; Zmax1; LRP6;
XX bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
XX
XX Homo sapiens.
XX
XX WO200292000-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US014877.
XX
XX 11-MAY-2001; 2001US-0290071P.
XX 17-MAY-2001; 2001US-0291311P.
XX 01-FEB-2002; 2002US-0353058P.
XX 04-MAR-2002; 2002US-0361293P.
XX
```

```
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX (AMHP ) WYETH.
XX
XX Allen K, Anisiewicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
XX diagnosing a HBM-like phenotype in a subject and for preparing a
XX composition for modulating bone mass and/or lipid levels in a subject
XX suffering from e.g. osteoporosis.
XX
XX Example 2; Page 62; 629pp; English.
XX
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
XX LRP6 mutants, which results in a HBM-like phenotype when expressed in a
XX cell. The HBM-like phenotype results in bone mass modulation and/or lipid
XX level modulation. The invention is useful for diagnosing a HBM-like
XX phenotype in a subject and for preparing a composition for modulating
XX bone mass and/or lipid levels in a subject suffering from e.g.
XX osteoporosis. The present sequence is a Sequence Tagged Site (STS)
XX marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
XX region.
XX
XX Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 685 CTCTGCTTCCTCCGCGTTCA 702
XX |||||
XX 18 CTCTGCTTCCTCCGCGTTCA 1
XX
XX RESULT 1606
XX ADH59603
XX ID ADH59603 standard; DNA; 18 BP.
XX
XX ADH59603;
XX
XX 25-MAR-2004 (first entry)
XX
XX Non-nucleotide probe of the invention #7.
XX
XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
XX probe.
XX
XX Synthetic.
XX
XX WO2003027328-A2.
XX
XX 03-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030573.
XX
XX 24-SEP-2001; 2001US-0324499P.
XX
XX (BOST-) BOSTON PROBES INC.
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX Kirszen NV, Hyldig-Nielsen JD, Williams BF;
XX WPI; 2003-421160/39.
XX
XX Non-nucleotide probe for suppressing binding of detectable nucleic acid
XX probes to undesired sequences, has aggregate nucleobase sequence
XX homologous to randomly distributed repeat sequence of genomic nucleic
XX acid.
XX
XX Claim 10; SEQ ID NO 9; 103pp; English.
XX
```


CC The present sequence represents a non-nucleotide probe. The probe is
 CC useful for suppressing the binding of one or more detectable nucleic acid
 CC probes, that are greater than 100 base pairs and that have been derived
 CC from genomic nucleic acid, to one or more undesired sequences in an assay
 CC for determining target genomic nucleic acid of a sample. The method
 CC comprises contacting the sample with the mixture of probes (preferably
 CC comprising 5-50 probes), contacting the sample with the one or more
 CC detectable nucleic acid probes, and determining the hybridization of the one
 CC or more detectable nucleic acid probes to the target genomic nucleic acid of
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic
 CC found in paraffin embedded tissue material or frozen tissue sections. The
 CC probe is also useful in comparing a sample of genomic nucleic acid with
 CC that of a control sample using a genomic nucleic acid reference array.
 CC The method comprises treating a sample of genomic nucleic acid and
 CC control genomic nucleic acid, which are differentially labelled, the
 CC array or both the sample and control genomic nucleic acid and the array
 CC with the mixture of the probe under suitable hybridization conditions,
 CC contacting the array with treated mixture of sample and control genomic
 CC nucleic acid under suitable hybridization conditions, and comparing the
 CC intensities of the signals from the differential labels of the array to
 CC that caused by hybridization of the probes to genomic nucleic acid, thus
 CC determining one or more variations in copy numbers of sequences in the
 CC sample as compared with the control. The hybridization of the genomic
 CC identical sequences in the control. The hybridization of the genomic
 CC array is determined using an intercalating dye or a detectable antibody,
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
 CC The sample of genomic nucleic acid to be tested and the reference of
 CC nucleic acid are labelled with detectable moiety such that hybridization
 CC of the genomic array is determined by determining the presence, absence,
 CC amount or location of the detectable label on the one or more genomic
 CC arrays. The genomic array comprises nucleic acid that is prepared from
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
 CC represents a non-nucleotide probe of the invention.

XX Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

XX Query Match 1.7%; Score 16.4; DB 1; Length 18;

XX Best Local Similarity 94.4%; Pred. No. 1.5e+03; Indels 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 TAGCTGGAGTACAGCGG 748

1 TAGCTGGAGTACAGCGG 18

Db

RESULT 1607

ADH59615/c

ID ADH59615 standard; DNA; 18 BP.

XX ADH59615;

XX 25-MAR-2004 (first entry)

XX Non-nucleotide probe of the invention #19.

XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;

XX probe.

XX Synthetic.

XX WO2003027328-A2.

XX 03-APR-2003.

XX 24-SEP-2002; 2002WO-US030573.

XX 24-SEP-2001; 2001US-0324499P.

XX (BOST-) BOSTON PROBES INC.

XX (DAKO-) DAKOCYTOMATION DENMARK AS.

XX

PI Kirszen NV, Hyldig-Nielsen JJ, Williams BF;
 XX WPI; 2003-421160/39.
 DR
 XX
 PT Non-nucleotide probe for suppressing binding of detectable nucleic acid
 PT probes to undesired sequences, has aggregate nucleobase sequence
 PT homologous to randomly distributed repeat sequence of genomic nucleic
 PT acid.
 XX
 XX Claim 10; SEQ ID NO 21; 103pp; English.

XX The present sequence represents a non-nucleotide probe. The probe is
 CC useful for suppressing the binding of one or more detectable nucleic acid
 CC probes, that are greater than 100 base pairs and that have been derived
 CC from genomic nucleic acid, to one or more undesired sequences in an assay
 CC for determining target genomic nucleic acid of a sample. The method
 CC comprises contacting the sample with the mixture of probes (preferably
 CC comprising 5-50 probes), contacting the sample with the one or more
 CC detectable nucleic acid probes, and determining the hybridization of the one
 CC or more detectable nucleic acid probes to the target genomic nucleic acid of
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic
 CC found in paraffin embedded tissue material or frozen tissue sections. The
 CC probe is also useful in comparing a sample of genomic nucleic acid with
 CC that of a control sample using a genomic nucleic acid reference array.
 CC The method comprises treating a sample of genomic nucleic acid and
 CC control genomic nucleic acid, which are differentially labelled, the
 CC array or both the sample and control genomic nucleic acid and the array
 CC with the mixture of the probe under suitable hybridization conditions,
 CC contacting the array with treated mixture of sample and control genomic
 CC nucleic acid under suitable hybridization conditions, and comparing the
 CC intensities of the signals from the differential labels of the array to
 CC that caused by hybridization of the probes to genomic nucleic acid, thus
 CC determining one or more variations in copy numbers of sequences in the
 CC sample as compared with the control. The hybridization of the genomic
 CC identical sequences in the control. The hybridization of the genomic
 CC array is determined using an intercalating dye or a detectable antibody,
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
 CC The sample of genomic nucleic acid to be tested and the reference of
 CC nucleic acid are labelled with detectable moiety such that hybridization
 CC of the genomic array is determined by determining the presence, absence,
 CC amount or location of the detectable label on the one or more genomic
 CC arrays. The genomic array comprises nucleic acid that is prepared from
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
 CC represents a non-nucleotide probe of the invention.

XX Sequence 18 BP; 4 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

XX Query Match 1.7%; Score 16.4; DB 1; Length 18;

XX Best Local Similarity 94.4%; Pred. No. 1.5e+03; Indels 0; Gaps 0;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 731 TAGCTGGAGTACAGCGG 748

18 TAGCTGGAGTACAGCGG 1

Db

RESULT 1608

ADH71082/c

ID ADH71082 standard; DNA; 18 BP.

XX ADH71082;

XX 25-MAR-2004 (first entry)

XX Human Vbeta microsatellite primer #25.

XX human; T-cell associated disease; Vbeta; autoimmune disease;

XX degenerative nervous system disease; graft versus host disease;

XX Addison's disease; atrophic gastritis;

XX degenerative nervous system disease; multiple sclerosis;

XX

KM Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
 KM allergy; type II hypersensitivity; Goodpasture's syndrome;
 KM type IV hypersensitivity; leprosy; infectious disease; viral infection;
 KM HIV; fungal infection; Candida; parasitic infection; schistosome;
 KM filaria; bacterial infection; Mycobacterium; neoplastic disease;
 KM lymphoproliferative disease; leukemia; lymphoma; cancer; brain cancer;
 KM breast cancer; ss; primer; microsatellite.
 XX
 OS Homo sapiens.
 XX
 PM US2002150891-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 05-MAR-1999; 99US-00263959.
 XX
 PR 19-SEP-1994; 94US-00309335.
 XX
 PR 19-SEP-1995; 95US-00531241.
 XX
 PA (HOOD/) HOOD L. E.
 XX (ROME/) ROME L.
 XX
 PI Hood LE, Rowen L;
 XX
 DR WPI; 2004-059052/06.
 XX
 PT Kit for diagnosing and treating T-cell associated diseases e.g.
 PT autoimmune; degenerative nervous system and infectious disease, comprises
 PT nucleic acid primers specifically priming and allowing amplification of a
 PT Vbeta gene.
 XX
 PS Disclosure; SEQ ID NO 1276; 164bp; English.
 XX
 CC The invention relates to a kit for diagnosing and treating T-cell
 CC associated diseases which comprises a panel of nucleic acid primers
 CC specifically priming and allowing amplification of each Vbeta gene,
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
 CC rejection and diagnosing and treating T-cell associated diseases
 CC including autoimmune diseases, degenerative nervous system diseases,
 CC graft versus host disease, hypersensitivity diseases, infectious diseases
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
 CC atrophic gastritis. Degenerative nervous system diseases include multiple
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
 CC I hypersensitivities such as contact with allergens that lead to
 CC allergies, Type II hypersensitivities such as those present in
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those
 CC manifested in leprosy. Infectious diseases include viral infections
 CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus Candida, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a Vbeta microsatellite primer.
 CC
 XX
 SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.7%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 641 CACCCAGGCTGGAGTGCA 658
 Db 18 CATCCAGGCTGGAGTGCA 1
 XX
 RESULT 1609
 ADH76753
 ID ADH76753 standard; DNA; 18 BP.
 XX
 AC ADH76753;
 XX
 DT 22-APR-2004 (first entry)
 XX

DB MCHRI genomic sequence analysis primer #62..
 XX
 XX melanin-concentrating hormone receptor 1; MCHRI; anorectic; gene therapy;
 KM obesity; primer; ss.
 XX
 OS unidentified.
 XX
 PM WO2003104489-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 05-JUN-2003; 2003WO-EP005917.
 XX
 PR 05-JUN-2002; 2002EP-00012569.
 XX
 PA (UYPH-) UNIV PHILIPPS MARBURG.
 XX
 PI Platzner M, Platzner C, Gudermann T, Hebebrand J, Hinney A;
 XX Reichwald K;
 XX
 DR WPI; 2004-062377/06.
 XX
 PT New diagnostic composition, useful for diagnosing obesity related to the
 PT presence of a molecular variant of the MCHRI gene or a susceptibility to
 PT the disorder.
 XX
 PS Example 2; Page 43; 76pp; English.
 XX
 CC The invention relates to a novel diagnostic polynucleotide composition.
 CC The polynucleotide composition comprises: a sequence encoding a
 CC polypeptide with defined sequences given in the specification; a sequence
 CC capable of hybridizing to a melanin-concentrating hormone receptor 1
 CC (MCHRI) gene; a polynucleotide encoding an MCHRI polypeptide; or a
 CC sequence comprising one or more of the nucleotide exchanges (SNP's) given
 CC in the specification and at least 8 bases of surrounding sequence of the
 CC MCHRI gene. The composition has anorectic activity. The polynucleotide
 CC composition may be used in gene therapy to treat the disorders of the
 CC invention. The composition is useful for diagnosing obesity related to
 CC the presence of a molecular variant of the MCHRI gene or a susceptibility
 CC to the disorder. The MCHRI protein or polynucleotide is useful for
 CC preparing a medicament for treating or preventing obesity related to the
 CC presence of a molecular variant of the MCHRI gene. This polynucleotide
 CC represents an MCHRI primer of the invention.
 CC
 XX
 SQ Sequence 18 BP; 5 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.7%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 729 AGTACTGGGACTACAGG 746
 Db 1 AGTACTGGGACTACAGG 18
 XX
 RESULT 1610
 ADP08780
 ID ADP08780 standard; DNA; 18 BP.
 XX
 AC ADP08780;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Extend primer 117 used to genotype human glycoprotein VI polymorphism.
 XX
 XX breast cancer; cytoabatic; gene therapy; human; platelet glycoprotein VI;
 KM GP6; GPIV; GPII; chromosome 19q13.4; ss; PCR; primer; SNP;
 KM single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO2004047767-A2.
 XX

PD 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
PR 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
XX WPI; 2004-441082/41.
DR
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
PT or absence of one or more nucleotide polymorphic variations, useful for
PT diagnosing, preventing and/or treating breast cancer.
XX
XX Example 3; Page 84; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of an extend primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
CC GPIV/GPVI) DNA which is located at chromosomal position 19q13.4.
XX
XX Sequence 18 BP; 3 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 876 GGGGTGAGCCACGCGCC 893
DB 1 GGTGTGAGCCACGCGCC 18
XX
XX RESULT 1611
ADP46226/c
ID ADP46226 standard; DNA; 18 BP.
XX
XX ADP46226;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Extend primer 7 used to genotype human KIAA0861 polymorphism.
DE
XX
XX breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
KW single nucleotide polymorphism;
KW Rho family guanine-nucleotide exchange factor; KIAA0861;
KW chromosome 3q27.3; probe.
XX
XX Homo sapiens.
OS
XX
XX WO2004047623-A2.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 25-NOV-2003; 2003WO-US037948.
PF
XX
XX 25-NOV-2002; 2002US-0429136P.
PR 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
PA
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI
XX
XX WPI; 2004-441051/41.
DR
XX

PT Identifying a subject at risk of breast cancer by detecting the presence
PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE
PT regions which are associated with breast cancer in a nucleic acid sample
PT from a subject.
XX
XX Example 6; Page 98; 289pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of one or
CC of breast cancer comprising detecting the presence or absence of one or
CC more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a subject at risk of
CC breast cancer, for early diagnosis, prevention and treatment of breast
CC cancer, possibly via gene therapy, as well as to analyse and predict a
CC response to a breast cancer treatment and in clinical drug trials. The
CC current sequence is that of an extend primer (also described as probe) of
CC the invention which was used to genotype human Rho family guanine-
CC nucleotide exchange factor KIAA0861 gDNA which has been mapped to
CC chromosomal position 3q27.3.
XX
XX Sequence 18 BP; 4 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 728 GAGTACTGGGACTACAG 745
DB 18 GAGTACTGGGACTACAG 1
XX
XX RESULT 1612
AAC92328/c
ID AAC92328 standard; DNA; 19 BP.
XX
XX AAC92328;
AC
XX
XX 22-MAR-2001 (first entry)
DT
XX
XX Human teratocarcinogenesis related protein PCR primer SEQ ID NO:5.
DE
XX
XX Human; teratocarcinoma; hTera; Tera; teratocarcinogenesis; PCR primer;
KW ss.
KW Homo sapiens.
OS
XX
XX CN1268566-A.
PN
XX
XX 04-OCT-2000.
PD
XX
XX 02-MAR-2000; 2000CN-00111771.
PF
XX
XX 02-MAR-2000; 2000CN-00111771.
PR
XX
XX (SCHR-) SOUTH CHINA RBS CENT NAT HUMAN GENE GROU.
PA
XX
XX Gao X, Xiao H, Qian B;
PI
XX
XX WPI; 2001-050470/07.
DR
XX
XX New human teratocarcinogenesis related protein and its coding sequence.
PS
XX
XX Example 1; Page 10; 21pp; Chinese.
XX
XX The present invention describes the human teratocarcinogenesis related
CC protein, designated htera, which is expressed in normal human marrow.
CC Also described is a method for the preparation of the htera protein and
CC nucleic acid sequences, and a method of detecting human htera nucleic
CC acid and polypeptide sequences in sample. The present sequence represents
CC a PCR primer used in the isolation of htera in an example from the
CC present invention
XX
XX Sequence 19 BP; 6 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

670 TTGGCTCACTGCACCTC 687
19 TTGGCTCACTGCACCTC 2

RESULT 1613

AAS13553
ID AAS13553 standard; DNA; 19 BP.

XX AAS13553;

XX 17-DEC-2001 (first entry)

DE PCR primer 1 used to amplify PAC 812f10 (54 T7) clone STS sequence.

XX Human; VMGLIOM; gliomulin; venous malformation gliomangioma; PCR primer;

KM STS; sequence tagged site; PAC 812f10; ss.

XX Homo sapiens.

OS WO200160856-A2.

PN 23-AUG-2001.

PF 16-FEB-2001; 2001WO-EP001760.

XX 16-FEB-2000; 2000EP-00870022.

PR 10-APR-2000; 2000US-0195777P.

PR 22-DEC-2000; 2000EP-00870320.

XX (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX VIKKULA M;

DR WPI; 2001-557643/62.

XX New VMGLIOM genes and polypeptides, useful in gene therapy or for

PT preventing, treating or alleviating disorders with vascular component,

PT e.g. varicosities, cardiopathies, cerebral disorders or cancer.

XX Disclosure; Page 70; 157pp; English.

XX The present invention relates to the isolation of novel human and mouse

CC VMGLIOM polypeptides (long form and short form), and the nucleic acid

CC molecules encoding them. VMGLIOMs (also referred to as gliomulins) are a

CC subtype of venous malformations (VMs) called gliomangiomas. In humans,

CC VMGLIOM has been mapped to chromosome 1p21-22. VMGLIOMs and the nucleic

CC acids encoding for them are useful as a medicament or for incorporation

CC into a diagnostic kit. Such medicaments are useful for preventing,

CC treating or alleviating disorders with a vascular component, particularly

CC where alteration of vascular smooth muscle cell phenotype is needed, e.g.

CC varicosities, cardiopathies or cardiomyopathies, cerebral disorders and

CC cancer. The nucleic acids are also useful in gene therapy. The present

CC sequence for PCR primer 1 is used to amplify PAC 812f10 (54 T7) clone STS

XX sequence in the methods of the present invention

SO Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1111 CAGGCTGCTCAACTC 1128

2 CAGGCTGCTCAACTC 19

RESULT 1614

AAS21179/c
ID AAS21179 standard; DNA; 19 BP.

XX AAS21179;

XX 09-APR-2002 (first entry)

DE Reverse primer used to isolate human liver gene.

XX Chimeric animal; liver; liver metabolism; toxicity; human;

KM liver disorder; transgenic primer; ss.

XX Homo sapiens.

OS WO200187059-A1.

PN 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP004193.

PR 19-MAY-2000; 2000JP-00149079.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Mukaidani C, Yoshizato K, Furukawa T;

DR WPI; 2002-097571/13.

XX Chimeric animal with functioning foreign liver cells for testing toxicity

PT and metabolism of drugs.

XX Example 2; Page 12; 26pp; Japanese.

XX The invention describes a chimeric (transgenic) animal with functioning

CC liver cells derived from another type of animal. The invention also

CC details methods for testing toxicity of substances on the human liver

CC cells and the metabolic conditions of substances by the liver cells. The

CC invention also discusses methods for screening new treatments and drugs

CC for human liver function disorder. This sequence is the reverse primer

CC used to isolate a gene from human liver cells, described in the method of

CC the invention

SO Sequence 19 BP; 5 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

535 CTCCTGCTCAAGCTCCC 552

19 CTCCTGCTCAAGCTCCC 2

RESULT 1615

ABX15007
ID ABX15007 standard; DNA; 19 BP.

XX ABX15007;

XX 14-MAR-2003 (first entry)

DE Human delta opioid receptor OPRD1-1 sequencing/PCR primer PF-0081.

XX Human; delta opioid receptor; OPRD1; ss; PCR; primer; SNP;

KM single nucleotide polymorphism; eating disorder; anorexia nervosa;

XX energy homeostasis disorder; chromosome 1.

OS Homo sapiens.

PN WO200292838-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014940.
XX
XX 11-MAY-2001; 2001US-0290016P.
XX
XX (BIOT-) BIOINVEST LTD.
PI Bergen AW;
PI WPI; 2003-129306/12.
XX
XX
PT New isolated nucleic acid molecule encoding a delta opioid receptor
PT variant associated with an eating or energy homeostasis disorder, useful
PT for diagnosing a genetic predisposition to such disorder, e.g. anorexia
PT nervosa.
XX
XX
PS Example; Page 22; 39pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC delta opioid receptor variant associated with an eating or energy
CC homeostasis disorder. Also included are a delta opioid receptor variant
CC encoded by the nucleic acid, an isolated antibody that specifically
CC recognises the delta opioid receptor variant, a vector comprising the
CC nucleic acid, a host cell transformed to contain the vector, producing
CC the polypeptide by culturing the host cell, identifying an agent which
CC modulates the expression of the nucleic acid, diagnosing a genetic
CC predisposition to an eating or energy homeostasis disorder by detecting
CC the presence or absence of the variant nucleic acid in a patient sample,
CC an allele specific primer that detects a polymorphism in the gene
CC encoding a delta opioid receptor associated with an eating or energy
CC homeostasis disorder and a non-human transgenic animal modified to
CC contain the variant nucleic acids. The variants are named OPRD1-1 to
CC OPRD1-8. The human opioid receptor gene is located on chromosome 1. The
CC nucleic acid molecules and delta opioid receptor variant are useful for
CC diagnosing a genetic predisposition to an eating or energy homeostasis
CC disorder, such as anorexia nervosa. The allele specific primer is useful
CC for detecting polymorphism in the gene encoding a delta opioid receptor
CC associated with the disorder cited. The present sequence is a sequencing
CC and PCR primer used to resequence the human delta opioid receptor gene
CC region surrounding a single nucleotide polymorphism (SNP)
XX
SQ Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 361 TCAAGCAGTCCACCTGCC 378
Db 1 TCAAGCAATCCACCTGCC 18
RESULT 1616
ACAB8919
ID ACAB8919 standard; DNA; 19 BP.
XX
XX ACAB8919;
AC
AC
DT 08-JUL-2003 (first entry)
XX
XX Selection and amplification of genetic markers PCR related primer #30.
DE
XX Genetic marker selection; multiplex PCR amplification;
KW prenatal diagnostic testing; foetal sex determination;
KW genetic identification; DNA profiling; DNA fingerprinting;
KW forensic analysis; PCR; primer; ss.
XX
XX Homo sapiens.
XX OS
XX WO2003031646-A1.
XX PN
XX 17-APR-2003.
XX PD
XX 14-OCT-2002; 2002WO-AU001388.
XX PF

XX
XX 12-OCT-2001; 2001AU-00008234.
PR 12-OCT-2001; 2001AU-00008235.
XX
XX (UYQU) UNIV QUEENSLAND.
PI Findlay I, Matthews PL, Mulcahy BK;
PI WPI; 2003-381725/36.
XX
XX
XX
XX
PT Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.
XX
XX
XX Claim 36; Page 39; 64pp; English.
XX
XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
SQ Sequence 19 BP; 3 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 392 GTGCTGGATTACAGCG 409
Db 2 GTGCTGGATTACAGCG 19
RESULT 1617
ABT34249
ID ABT34249 standard; DNA; 19 BP.
XX
XX ABT34249;
AC
AC
DT 12-JUN-2003 (first entry)
XX
XX
XX Opioid receptor D1 PCR primer SEQ ID No 35.
DE
XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;
KW serotonin receptor ID; delta-opioid receptor; dopamine receptor D2;
KW anorexia nervosa; bulimia nervosa; PCR; primer; ss.
XX
XX Unidentified.
XX OS
XX WO2003012143-A1.
XX PN
XX 13-FEB-2003.
XX PD
XX 16-JUL-2002; 2002WO-US022555.
XX PF
XX 16-JUL-2001; 2001US-0305153P.
XX 20-JUL-2001; 2001US-0306440P.
XX 13-NOV-2001; 2001US-0311285P.
XX 19-DEC-2001; 2001US-0340843P.
XX 19-DEC-2001; 2001US-0340844P.
XX
XX (PRIC-) PRICE FOUND LTD.
XX PA
XX Bergen AW, Yeager M;
XX PI

```
XX DR WPI; 2003-268122/26.
XX PT New nucleic acid molecule having polymorphisms in the serotonin receptor
XX PT ID, delta-opioid receptor, or dopamine receptor D2, useful in diagnostic
XX PT and prognostic assays for eating disorders, such as anorexia and bulimia
XX PT nervosa.
XX PS Example 3; Page 57; 149pp; English.
XX CC The invention relates to a novel isolated nucleic acid molecule
XX CC comprising a variant gene associated with an eating disorder and selected
XX CC from any of 119 polymorphisms with their corresponding genotyping in
XX CC database, alleles and HGBASE identification, given in the specification.
XX CC The novel nucleic acid molecule has polymorphisms in the serotonin
XX CC receptor ID, delta-opioid receptor, or dopamine receptor D2, which is
XX CC useful in diagnostic and prognostic assays for eating disorders, in
XX CC particular anorexia nervosa and bulimia nervosa. This polynucleotide
XX CC sequence represents a opioid receptor ID PCR primer of the invention
SQ Sequence 19 BP; 5 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 361 TCAGCAGTCCACCTGCC 378
Db 1 TCAGCAGTCCACCTGCC 18
RESULT 1618
ADH70769
ID ADH70769 standard; DNA; 19 BP.
AC ADH70769;
XX ADH70769;
XX 25-MAR-2004 (first entry)
XX DE Human Vbeta gene repeat sequence #559.
XX KW human; T-cell associated disease; Vbeta; autoimmune disease;
XX KW degenerative nervous system disease; graft versus host disease;
XX KW hypersensitivity disease; infectious disease; neoplastic disease;
XX KW Addison's disease; atrophic gastritis;
XX KW degenerative nervous system disease; multiple sclerosis;
XX KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
XX KW allergy; type II hypersensitivity; Goodpasture's syndrome;
XX KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
XX KW HIV; fungal infection; Candida; parasitic infection; schistosoma;
XX KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
XX KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
XX KW breast cancer; ds.
XX OS Homo sapiens.
XX PN US2002150891-A1.
XX PD 17-OCT-2002.
XX PF 05-MAR-1999; 99US-00263959.
XX PR 19-SEP-1994; 94US-00309335.
XX PR 19-SEP-1995; 95US-00531241.
XX PA (HOOD/) HOOD L E.
XX PA (ROWE/) ROWEN L.
XX PI Hood LE, Rowen L;
XX DR WPI; 2004-059052/06.
XX PT Kit for diagnosing and treating T-cell associated diseases e.g.
```

```
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX PS Disclosure; SEQ ID NO 963; 164pp; English.
XX CC The invention relates to a kit for diagnosing and treating T-cell
XX CC associated diseases which comprises a panel of nucleic acid primers
XX CC specifically priming and allowing amplification of each Vbeta gene,
XX CC VbetarRNA or cDNA. The kit is useful for diagnosing organ transplant
XX CC rejection and diagnosing and treating T-cell associated diseases
XX CC including autoimmune diseases, degenerative nervous system diseases,
XX CC graft versus host disease, hypersensitivity diseases, infectious diseases
XX CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
XX CC atrophic gastritis. Degenerative nervous system diseases include multiple
XX CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
XX CC I hypersensitivities such as contact with allergens that lead to
XX CC allergies, Type II hypersensitivities such as those present in
XX CC Goodpasture's syndrome and Type IV hypersensitivities such as those
XX CC manifested in leprosy. Infectious diseases include viral infections
XX CC caused by viruses such as HIV, fungal infections such as those caused by
XX CC the yeast genus Candida, parasitic infections such as those caused by
XX CC schistosomes, filaria and bacterial infections include lymphoproliferative diseases
XX CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
XX CC breast. The present sequence represents a Vbeta gene repeat sequence.
SQ Sequence 19 BP; 3 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 428 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 18
RESULT 1619
ADH71084
ID ADH71084 standard; DNA; 19 BP.
AC ADH71084;
XX ADH71084;
XX 25-MAR-2004 (first entry)
XX DE Human Vbeta microsatellite primer #27.
XX KW human; T-cell associated disease; Vbeta; autoimmune disease;
XX KW degenerative nervous system disease; graft versus host disease;
XX KW hypersensitivity disease; infectious disease; neoplastic disease;
XX KW Addison's disease; atrophic gastritis;
XX KW degenerative nervous system disease; multiple sclerosis;
XX KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
XX KW allergy; type II hypersensitivity; Goodpasture's syndrome;
XX KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
XX KW HIV; fungal infection; Candida; parasitic infection; schistosoma;
XX KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
XX KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
XX KW breast cancer; ss; primer; microsatellite.
XX OS Homo sapiens.
XX PN US2002150891-A1.
XX PD 17-OCT-2002.
XX PF 05-MAR-1999; 99US-00263959.
XX PR 19-SEP-1994; 94US-00309335.
XX PR 19-SEP-1995; 95US-00531241.
XX PA (HOOD/) HOOD L E.
```

PA (ROME/) ROWEN L.
 XX Hood LE, Rowen L.;
 PI
 XX
 DR WPI; 2004-059052/06.
 XX
 XX Kit for diagnosing and treating T-cell associated diseases e.g.
 PT autoimmune, degenerative nervous system and infectious disease, comprises
 PT nucleic acid primers specifically priming and allowing amplification of a
 PT Vbeta gene.
 XX
 PS Disclosure; SEQ ID NO 1278; 164pp; English.
 XX
 CC The invention relates to a kit for diagnosing and treating T-cell
 CC associated diseases which comprises a panel of nucleic acid primers
 CC specifically priming and allowing amplification of each Vbeta gene,
 CC VbetarNA or cDNA. The kit is useful for diagnosing organ transplant
 CC rejection and diagnosing and treating T-cell associated diseases
 CC including autoimmune diseases, degenerative nervous system diseases,
 CC graft versus host disease, hypersensitivity diseases, infectious diseases
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
 CC atrophic gastritis. Degenerative nervous system diseases include multiple
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
 CC I hypersensitivities such as contact with allergens that lead to
 CC allergies, Type II hypersensitivities such as those present in
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those
 CC manifested in leprosy. Infectious diseases include viral infections
 CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus Candida, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a Vbeta microsatellite primer.
 XX
 SQ Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.7%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 719 CAGCCTCTGAGTAGCTG 736
 Db 2 CAGCCTCTGAGTAGCTG 19
 RESULT 1620
 ADH70436/c
 ID ADH70436 standard; DNA, 19 BP.
 XX
 AC ADH70436;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human Vbeta gene repeat sequence #226.
 XX
 KM human; T-cell associated disease; Vbeta; autoimmune disease;
 KM degenerative nervous system disease; graft versus host disease;
 KM hypersensitivity disease; infectious disease; neoplastic disease;
 KM Addison's disease; atrophic gastritis;
 KM degenerative nervous system disease; multiple sclerosis;
 KM Alzheimer's disease; hypersensitivity disease; Type I hypersensitivity;
 KM allergy; Type II hypersensitivity; Goodpasture's syndrome;
 KM Type IV hypersensitivity; leprosy; infectious disease; viral infection;
 KM HIV; fungal infection; Candida; parasitic infection; schistosome;
 KM filaria; bacterial infection; Mycobacterium; neoplastic disease;
 KM lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
 KM breast cancer; ds.
 XX
 XX Homo sapiens.
 XX OS
 XX US2002150891-A1.
 XX PN
 XX 17-OCT-2002.

XX
 PF 05-MAR-1999; 99US-00263959.
 XX
 PR 19-SEP-1994; 94US-00309335.
 PR 19-SEP-1995; 95US-00531241.
 XX
 PA (HOOD/) HOOD L. E.
 XX (ROME/) ROWEN L.
 PI
 XX Hood LE, Rowen L.;
 DR WPI; 2004-059052/06.
 XX
 PT Kit for diagnosing and treating T-cell associated diseases e.g.
 PT autoimmune, degenerative nervous system and infectious disease, comprises
 PT nucleic acid primers specifically priming and allowing amplification of a
 PT Vbeta gene.
 XX
 PS Disclosure; SEQ ID NO 630; 164pp; English.
 XX
 CC The invention relates to a kit for diagnosing and treating T-cell
 CC associated diseases which comprises a panel of nucleic acid primers
 CC specifically priming and allowing amplification of each Vbeta gene,
 CC VbetarNA or cDNA. The kit is useful for diagnosing organ transplant
 CC rejection and diagnosing and treating T-cell associated diseases
 CC including autoimmune diseases, degenerative nervous system diseases,
 CC graft versus host disease, hypersensitivity diseases, infectious diseases
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
 CC atrophic gastritis. Degenerative nervous system diseases include multiple
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
 CC I hypersensitivities such as contact with allergens that lead to
 CC allergies, Type II hypersensitivities such as those present in
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those
 CC manifested in leprosy. Infectious diseases include viral infections
 CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus Candida, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a Vbeta gene repeat sequence.
 XX
 SQ Sequence 19 BP; 16 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 1.7%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTTATTTT 445
 Db 19 TTTTATTTTATTTTATTTT 2
 RESULT 1621
 ADK70924/c
 ID ADK70924 standard; DNA, 19 BP.
 XX
 AC ADK70924;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human hepatocyte related PCR primer R SEQ ID NO:2.
 XX
 KM human; hepatocyte; proliferation; human hepatocyte transplantation;
 KM immunodeficient hepatopathy; liver; PCR; primer; ss.
 XX
 XX Homo sapiens.
 XX OS
 XX Synthetic.
 XX WO2003080821-A1.
 XX PN
 XX 02-OCT-2003.
 XX PD
 XX 25-MAR-2003; 2003WO-JP003623.

```
XX 25-MAR-2002; 2002JP-00084280.
PR (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (HIRO-) HIROSHIMA IND PROMOTION ORG.
XX
PI Mukaidani C, Yoshizato K;
DR WPI; 2004-203365/19.
PT Proliferating human hepatocytes for producing an artificial liver.
XX
PS Example 1; SEQ ID NO 2; 73bp; Japanese.
XX
CC The present invention describes a human hepatocyte proliferation method
CC comprising transplanting human hepatocytes into a mouse suffering from
CC immunodeficient hepatopathy and feeding this mouse in a state protected
CC from attack from a human complement produced by the human complement to
CC proliferate the transplanted human hepatocytes in the mouse liver. Also
CC described: (1) a chimera mouse having transplanted human hepatocytes in
CC the liver; (2) a method of obtaining human hepatocytes by separating the
CC human hepatocytes from the liver of the chimera mouse; (3) the human
CC hepatocytes obtained; (4) a cell kit containing the human hepatocytes;
CC and (5) a hybrid artificial liver in which human hepatocytes are filled.
CC The method can be used as a human hepatocytes proliferation method for
CC producing an artificial liver in which human hepatocytes are filled. The
CC present sequence represents a PCR primer which is used in an example from
CC the present invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 535 CTCCTGCTCAGCTCC 552
DB 19 CTCCTGCTCAGCTCC 2
XX
RESULT 1622
ADP26951/C
ID ADP26951 standard; DNA; 19 BP.
XX
AC ADP26951;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human P-cadherin PCR primer SEQ ID NO:52.
XX
KW hair growth modulator; P-cadherin modulator; endocrine; depilatory;
KW gene therapy; antisense therapy; hair growth; alopecia; baldness;
KW unwanted hair growth; hirsutism;
KW hypotrichosis associated with juvenile macular dystrophy; HJMD; human;
KW P-cadherin; PCR; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP1428893-A2.
PD 16-JUN-2004.
XX
PF 10-OCT-2003; 2003EP-00256411.
XX
PR 15-OCT-2002; 2002US-0418163P.
XX
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
XX
PI Sprecher E, Bergman R;
XX
DR WPI; 2004-469945/45.
```

```
XX Identifying a hair growth modulator for treating alopecia and unwanted
PT hair growth such as hirsutism, comprises identifying a P-cadherin
PT modulator and testing whether the P-cadherin modulator is functional as a
PT hair growth modulator.
XX
PS Example; SEQ ID NO 52; 121bp; English.
XX
CC The present invention describes a method (M1) for identifying a hair
CC growth modulator. (M1) comprises identifying a P-cadherin modulator, and
CC testing whether the P-cadherin modulator is functional as a hair growth
CC modulator. Also described: (1) a hair growth modulator (I) identified by
CC (M1); and (2) a composition (II) for modulating hair growth, comprising
CC as an active ingredient, a P-cadherin modulator functional as a hair
CC growth modulator. (I) and (II) have endocrine and depilatory activities,
CC and can be used as hair growth modulators, P-cadherin function
CC modulators, and in gene and antisense therapy. (M1) is useful for
CC identifying a hair growth modulator. (I) is useful in a method of medical
CC treatment. (I) or (II) is useful for modulating hair growth for non-
CC therapeutic cosmetic purposes which involves administering to a subject,
CC (I) or (II). (I) can be used in the manufacture of a medicament for the
CC therapeutic modulation of hair growth. (I) or (II) is useful for treating
CC alopecia (baldness) and unwanted hair growth such as hirsutism. (I) or
CC (II) comprising P-cadherin inducer is useful for correction of hair loss
CC in congenital hypotrichosis associated with juvenile macular dystrophy
CC (HJMD) and other alopecia patients. The present sequence represents a PCR
CC primer human P-cadherin, which is used in an example from the present
CC invention.
XX
SQ Sequence 19 BP; 5 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 930 TCTCACTCTGTATCCAG 947
DB 18 TCTCACTCTGTATCCAG 1
XX
RESULT 1623
AAQ95565
ID AAQ95565 standard; DNA; 20 BP.
XX
AC AAQ95565;
XX
DT 14-FEB-1996 (first entry)
XX
DE Primer A7 (Group 4, set C) for a human chromosomal marker.
XX
KW primer; polymerase chain reaction; PCR; linkage study; locus;
KW microsatellite marker sequence; automated genotyping; allele;
KW polymorphism; detection; Homo sapiens; ss.
XX
OS Synthetic.
XX
PN WO9515400-A1.
PD 08-JUN-1995.
XX
PF 05-DEC-1994; 94WO-US013945.
XX
PR 03-DEC-1993; 93US-00160837.
XX
PA (UYUD ) UNIV JOHNS HOPKINS.
XX
PI Levitt RC;
XX
DR WPI; 1995-215278/28.
XX
PT kit for automated genotyping contg. pairs of PCR primers - designed to
PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT with a characteristic fluorescence label, useful e.g. in detection of
```


PT disease related genetic rearrangement.
XX
PS Disclosure; Fig 7D-2; 104pp; English.
XX
CC The method aims to provide a collection of highly reproducible
microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
throughout the human genome which can be detectably labelled. The MMS are
polymorphic, simple sequence repeats and can be used in automated
genotyping, esp. fluorescence-based. The primers correspond to the unique
DNA sequence surrounding each marker, and PCR is used to detect each
polymorphism. When the MMS show considerable polymorphism (ie. a
difference in the number of repeats) between individuals, the markers can
be particularly informative. The MMS can be ideal for linkage studies.
CC Kits comprise at least 4 groups, of at least 3 sets, each comprising
labelled primers for PCR amplification of the DNA. Group 4 primer pairs
are shown in AAQ95465-480 and AAQ95559-590. The chromosomal markers,
CC published size range of the allele and degree of heterozygosity in the
population for the markers covered by these primer pairs are not given in
the specification
CC
CC
SQ Sequence 20 BP; 4 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 187 TGGAGTTTCTCCATGTTG 204
1 TGGATTTCCTCATGTTG 18
DB
RESULT 1624
AAQ95680
ID AAQ95680 standard; DNA; 20 BP.
XX
AC AAQ95680;
XX
DT 15-FEB-1996 (first entry)
XX
DE Primer B (Group 6, set C) for marker D8S265, chromosome 8.
XX
KW primer; polymerase chain reaction; PCR; linkage study; locus;
microsatellite marker sequence; automated genotyping; allele;
KM polymorphism; detection; Homo sapiens; ss.
XX
OS Synthetic.
XX
PN WO9515400-A1.
XX
PD 08-JUN-1995.
XX
PF 05-DEC-1994; 94WO-US013945.
XX
PR 03-DEC-1993; 93US-00160837.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Levitt RC;
XX
DR WPI; 1995-215278/28.
XX
PT Kit for automated genotyping contg. pairs of PCR primers - designed to
amplify polymorphic nucleotide repeat sequences, arranged in sets each
with a characteristic fluorescence label, useful e.g. in detection of
PT disease related genetic rearrangement.
PS Disclosure; Fig 7F-3; 104pp; English.
XX
CC The method aims to provide a collection of highly reproducible
microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
throughout the human genome which can be detectably labelled. The MMS are
polymorphic, simple sequence repeats and can be used in automated
genotyping, esp. fluorescence-based. The primers correspond to the unique

CC DNA sequence surrounding each marker, and PCR is used to detect each
polymorphism. When the MMS show considerable polymorphism (ie. a
difference in the number of repeats) between individuals, the markers can
be particularly informative. The MMS can be ideal for linkage studies.
CC Kits comprise at least 4 groups, of at least 3 sets, each comprising
labelled primers for PCR amplification of the DNA. Group 6 primer pairs
are shown in AAQ95639-686. The published size range of the D8S265 allele
is 284-307 bp, and the degree of heterozygosity in the population is
about 75%
CC
CC
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 996 GGGCTCAGCGATTCTCC 1013
3 GGGTTCAGCGATTCTCC 20
DB
RESULT 1625
AAH91108/c
ID AAH91108 standard; DNA; 20 BP.
XX
AC AAH91108;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #183.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KM chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 15
FT /*tag= a
FT /note= "SNP, optionally A or T at this position"
XX
PN WO200142511-A2.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033632.
XX
PR 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI Daly M, Hudson TU, Lander ES, Rioux J, Siminovitch K;
XX
DR WPI; 2001-367874/38.
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
PS Claim 1; Page 46; 463pp; English.
XX
CC The present invention describes a method for detecting the presence of
polymorphisms associated with inflammatory bowel diseases such as
ulcerative colitis and Crohn's disease. The methods can be used to detect
the presence of genetic polymorphisms associated with inflammatory bowel
disease and correlating their occurrence with disease states. They may be
used in this way for phenotypic correlations, forensics, paternity
testing, medicine and genetic analysis. The present sequence is a
polymorphic site described in the exemplification of the invention
XX
SQ Sequence 20 BP; 8 A; 5 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 614 TTTTGTGAGACAGCTCTC 632
DB 20 TTTTGTGAGACAGCTCTC 2

RESULT 1626
ABL45527/C
ID ABL45527 standard; DNA; 20 BP.

XX ABL45527;

XX 11-APR-2002 (first entry)

XX Human chromosome 21q22.1 PCR primer SEQ ID NO:2571.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;

XX PCR primer; ss.

XX Homo sapiens.

XX JP2001321190-A.

XX 20-NOV-2001.

XX 12-MAR-2001; 2001JP-00068285.

XX 10-MAR-2000; 2000JP-00066716.

XX (RIKA) RIKAGAKU KENKUSHO.

XX (GENO-) GENOTEX YG.

XX WPI; 2002-144136/19.

XX Arraying genome clones.

XX Claim 6; Page 56; 528pp; Japanese.

CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

QY Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 496 ACAGCTCACTGCAGCCTT 513
DB 19 ACAGCTCACTGCAGCCTT 2

RESULT 1627
ACC55322/C
ID ACC55322 standard; DNA; 20 BP.

XX ACC55322;

XX 27-JUN-2003 (first entry)

XX Human ADAMTS13 STS marker GL2-1 5' PCR primer.

XX Human; thrombotic thrombocytopenic purpura; TTP; disintegrin;

XX metalloproteinase; thrombospondin 1-like domains 13; ADAMTS13;

XX thrombolytic; haemostatic; PCR; primer; RT-PCR; 5' RACE; 3' RACE; ss.

XX Homo sapiens.

XX WO2003016492-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026285.

XX 16-AUG-2001; 2001US-0312834P.

XX 16-AUG-2002; 2002US-00312834.

XX (UNMI) UNIV MICHIGAN.

XX Ginsburg D, Levy G, Tsai H;

XX WPI; 2003-268318/26.

XX Identifying risk of developing thrombotic thrombocytopenic purpura

XX disease, using a novel disintegrin and metalloproteinase containing

XX thrombospondin 1-like domains genes and proteases.

XX Example 1; Page 87; 98pp; English.

XX The invention relates to a novel method for identifying subjects at risk

XX of developing thrombotic thrombocytopenic purpura (TTP) disease,

XX comprising providing nucleic acid having a disintegrin and

XX metalloproteinase containing thrombospondin 1-like domains 13 (ADAMTS13)

XX gene from a subject, and detecting the presence or absence of one or more

XX variations in the ADAMTS13 gene. The method of the invention has

XX thrombolytic and haemostatic activity. The methods and compositions of

XX the present invention are useful for the diagnosis and treatment of,

XX and/or analysing risks for thrombotic thrombocytopenic purpura. The

XX present sequence is used in the exemplification of the invention

XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

QY Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 967 ATCTGAGCTCACTGCAC 984
DB 18 ATCTGAGCTCACTGCAC 1

RESULT 1628
AB271060/C
ID AB271060 standard; DNA; 20 BP.

XX AB271060;

XX 28-APR-2003 (first entry)

XX Human HKR1 phosphorothioate antisense oligonucleotide SEQ ID NO:88.

XX Human; HKR1; cytosolic; HKR1 inhibitor; hyperproliferative disorder;

XX cancer; antisense oligonucleotide; 2'-O-methoxyethyl; 2'-MOE; control;

KW phosphorothioate; ss.
XX Homo sapiens.
OS
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /+tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
FT modified_base 1..5
FT /+tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /+tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX WO2003004513-A1.
XX 16-JAN-2003.
XX
XX 02-JUL-2002; 2002WO-US021090.
XX
XX 03-JUL-2001; 2001US-00898556.
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Freier SM;
XX
XX WPI; 2003-210336/20.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding HKR1, useful for treating a disease/condition
PT associated with HKR1, such as hyperproliferative disorder, e.g. lung,
PT brain or breast cancer.
XX
XX Example 15; Page 74; 105pp; English.
XX
XX The present invention describes a compound 8-50 nucleobases in length
CC targeted to, and which specifically hybridises with a nucleic acid
CC molecule encoding HKR1, and inhibits the expression of HKR1. Also
CC described: (1) a compound 8-50 nucleobases in length that specifically
CC hybridises with at least an 8-nucleobase portion of an active site on a
CC nucleic acid molecule encoding HKR1; (2) a composition comprising the
CC compound and a carrier or diluent; (3) a method for inhibiting the
CC expression of HKR1 in cells or tissues by contacting the cells or tissues
CC with the compound so that expression of HKR1 is inhibited; and (4) a
CC method of treating an animal having a disease or condition associated
CC with HKR1 by administering to the animal a therapeutic or prophylactic
CC amount of the compound so that expression of HKR1 is inhibited. HKR1
CC antisense oligonucleotides have cytostatic activities and can be used as
CC HKR1 inhibitors. The compound, composition and methods are useful for
CC treating a disease or condition associated with HKR1, such as a
CC hyperproliferative disorder, e.g. lung, brain or breast cancer, by
CC inhibiting the expression of HKR1. They are also useful in research and
CC diagnostics for modulating the expression of HKR1. The present sequence
CC represents a human HKR1 chimeric phosphorothioate oligonucleotide having
CC 2'-O-methoxyethyl (2'-MOE) wings and a deoxy gap, which is an antisense
CC oligonucleotide used in the inhibition of human HKR1 in an example from
CC the present invention
XX
XX Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GAGTAGCTGGGACTACAG 745
|||
20 GATTGCTGGGACTACAG 3

RESULT 1629
ID ABT44200/C
ID ABT44200 standard; DNA; 20 BP.
XX
XX ABT44200;
AC
XX
DT 06-NOV-2003 (first entry)
DE
XX Chimeric antisense oligonucleotide ISIS 199196 to inhibit human NOD1.
XX
XX Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;
KW caspase associated recruitment domain 4; programmed cell death; cancer;
KW apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;
KW amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;
KW viral infection; human; chimeric.
XX
XX Chimeric - Homo sapiens.
OS
XX
XX WO2003050246-A2.
XX
XX 19-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US038606.
XX
XX 05-DEC-2001; 2001US-00006883.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX
XX Dobie KM, Roach MP;
XX
XX WPI; 2003-577293/54.
XX
XX New compound, comprising a sequence targeted to a nucleic acid encoding
PT nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing
PT a composition for treating hyperproliferative disease, e.g., cancer.
XX
XX Claim 3; Page 76; 138pp; English.
XX
XX This invention relates to novel chimeric antisense oligonucleotides that
CC specifically hybridise to and inhibit the expression of the nucleotide
CC binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4
CC (caspase associated recruitment domain 4) is a domain that is involved in
CC the elimination of cells via programmed cell death and in the host
CC defence against pathogens, i.e. it works to regulate apoptosis. Apoptosis
CC is a naturally occurring process, however, if it becomes overstimulated
CC it can lead to cell loss and neurodegenerative conditions including
CC Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis
CC pigmentosa and blood cell disorders. Conversely, insufficient apoptosis
CC can contribute to the development of cancer, autoimmune disorders and
CC viral infections. The present invention describes antisense
CC oligonucleotides that can modulate NOD1 expression (and variants
CC thereof), such that these compounds, via gene therapy, can be used to
CC treat various human diseases caused by aberrant apoptosis. This
CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit
CC expression of human NOD1, the aim of the invention. Note that it has two
CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a
CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate
CC throughout
XX
XX Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1019 CAGGCTCCAGCAGCTG 1036
|||
18 CTGCTCCAGCAGCTG 1
Db
RESULT 1630
ADE15817/C
ID ADE15817 standard; DNA; 20 BP.

XX ADE15817;
AC 29-JAN-2004 (first entry)
XX
XX Human PKR exon 17 PCR primer PK17A.
XX
XX ss; primer: PCR; 2',5'-oligoadenylate synthetase; OAS; RNase L;
XX 2',5' phosphodiesterase; hepatitis C; virucide; hepatotropic;
XX gene therapy; vaccine; human.
XX
XX Homo sapiens.
XX
XX WO2003089003-A1.
XX
XX 30-OCT-2003.
XX
XX 15-APR-2003; 2003WO-GB001625.
XX
XX 19-APR-2002; 2002GB-00008928.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Hill A, Thursz M, Knapp S;
XX
XX WPI; 2003-854045/79.
XX
XX
XX Use of a compound capable of modulating the level of activity of the OAS,
XX RNase L or 2',5' phosphodiesterase gene or protein in the manufacture of
XX a medicament for treating a patient with or at risk of hepatitis C
XX infection.
XX
XX Example 1; Page 43; 67pp; English.
XX
XX The invention relates to a novel compound capable of modulating the level
XX of activity of the 2',5'-oligoadenylate synthetase (OAS), RNase L or 2'-
XX 5' phosphodiesterase gene or protein, useful in the manufacture of a
XX medicament for treating a patient with or at risk of hepatitis C
XX infection, where the compound is not an interferon or an isoprenoid, such
XX as geranylgeranylacetone (GGA). The method of the invention has virucide
XX and hepatotropic activity. A polynucleotide of the invention may have a
XX use in gene therapy, or in a vaccine. The compound capable of modulating
XX the level of activity of the OAS, RNase L or 2',5' phosphodiesterase gene
XX and/or activity of the OAS, RNase L or 2',5' phosphodiesterase protein is
XX useful in the manufacture of a medicament for treating a patient with or
XX at risk of hepatitis C infection. The nucleic acid that hybridises
XX selectively to OAS nucleic acid is useful in the manufacture of a
XX medicament or diagnostic reagent for treating or diagnosing a patient
XX with or at risk of hepatitis C infection. The present sequence is used in
XX the exemplification of the invention.
XX
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 1.6e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 946 AGGCTGAGTGCATGCG 963
XX |||||
XX DB 20 AGGCTGAGTGCATGAC 3

RESULT 1631
ABZ99052
ID ABZ99052 standard; DNA; 20 BP.
XX
XX ABZ99052;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human PDE4C oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX
XX

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPTGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D,
XX Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 14294; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, for reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.7%; Score 16.4; DB 1; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 1.6e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 614 TTTTGGACGAGTCT 631
XX |||||
XX DB 1 TTTTGGACGAGTGTCT 18

RESULT 1632
ABD32083
ID ABD32083 standard; DNA; 20 BP.
XX
XX ABD32083;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human PDE4C-derived oligonucleotide SEQ ID 14294.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX
XX

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
OS Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US011143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 14294; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has antiallergic, antiinflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
SO
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 614 TTTTGGACAGAGCTC 631
DB 1 TTTTGGACAGAGCTC 18

RESULT 1633
ADH56987/c
ID ADH56987 standard; DNA; 20 BP.
XX
XX ADH56987;
XX
XX 25-MAR-2004 (first entry)
XX
XX PCR primer used to amplify human CARD4 DNA oligo allelic variant SeqID75.
XX
XX 99; human; CARD4; NOD1; CED4/Apaf-1; caspase-9 induced apoptosis;
XX inflammation; chronic obstructive pulmonary disease;
XX rheumatoid arthritis; inflammatory bowel; psoriasis; asthma;
XX antiasthmatic; antiinflammatory; antiallergic; pharmacogenomic; forensic;
XX paternity testing; PCR; primer.
XX
XX Homo sapiens.
XX
XX US2003219810-A1.
XX
XX 27-NOV-2003.
XX
XX 27-MAR-2003; 2003US-00401194.
XX
XX 27-MAR-2002; 2002US-0368184P.
XX
XX (BARN/) BARNES G.
XX (BERT/) BERTIN J.
XX
XX Barnes G, Bertin J;
XX WPI; 2004-010870/01.
XX
XX New isolated nucleic acid molecule comprising an allelic variant of a
XX CARD4 gene, useful for diagnosing, preventing or treating asthma or an
XX apoptotic, inflammatory or allergic disorder, or in pharmacogenomics.
XX
XX Example 6; SEQ ID NO 75; 77bp; English.
XX
XX This invention relates to novel single nucleotide polymorphisms within
XX the human CARD4 gene. Specifically, it refers to allelic variants of
XX CARD4 (NOD1), a member of the CED4/Apaf-1 family that is involved in
XX caspase-9 induced apoptosis and inflammation. The present invention
XX describes a kit for determining the allelic variants of CARD4 polymorphic
XX regions of an individual, which can be useful for predicting
XX susceptibility, as well as diagnosis, prevention and treatment of various
XX disorders including chronic obstructive pulmonary disease, rheumatoid
XX arthritis, inflammatory bowel disease, psoriasis or asthma. Accordingly,
XX the compositions of this invention exhibit antiasthmatic,
XX antiinflammatory and antiallergic activities. Furthermore, they may be
XX used to identify patients that would be strong candidates for effective
XX treatment with a CARD4 modulator, in pharmacogenomics, or in monitoring
XX the effects of CARD4 therapeutics during clinical trials. The nucleic
XX acid molecule may also be used in forensics or paternity testing. This
XX oligonucleotide sequence is a PCR primer used to amplify a human CARD4
XX DNA oligo comprising an allelic variant of the invention.
XX
XX Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
SO
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1019 CAGCTCCGACGAGCTG 1036
DB 19 CTGCTCCGACGAGCTG 2
RESULT 1634
AD138842/c
ID AD138842 standard; DNA; 20 BP.

AC	AD138842;
XX	
DT	22-APR-2004 (first entry)
XX	
XX	Human LIM domain kinase 1 antisense oligonucleotide #126.
KW	neuroprotective; LIM domain kinase 1; developmental disorder;
KM	neurological disorder; diagnostic; prophylaxis; human; ss.
XX	
OS	Homo sapiens.
FH	
FH	Key
FT	modified_base
FT	1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "OTHER= Phosphorothioate backbone. All cytidines are 5-methylcytidines"
FT	modified_base
FT	1..5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT	modified_base
FT	15..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX	
PN	US2004014047-A1.
PD	
PD	22-JAN-2004.
XX	
PF	18-JUL-2002; 2002US-00199199.
PR	
PR	18-JUL-2002; 2002US-00199199.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Cowseart LM, Dobie KW;
DR	
XX	WPI; 2004-121553/12.
XX	
PT	New antisense oligonucleotides for modulating LIM domain kinase 1
PT	expression, useful for diagnosing, preventing or treating conditions
PT	associated with the kinase, e.g. neurological or developmental disorders.
XX	
PS	
XX	Example 15; SEQ ID NO 141; 81bp; English.
CC	
CC	The invention describes a compound 8-80 nucleobases in length targeted to
CC	a nucleic acid molecule encoding LIM domain kinase 1. The compound
CC	specifically hybridises with the nucleic acid molecule encoding LIM
CC	domain kinase 1 and inhibits the expression of LIM domain kinase 1. It
CC	specifically hybridises with at least an 8-nucleobase portion of a
CC	preferred target region on the nucleic acid molecule encoding LIM domain
CC	kinase 1. The antisense oligonucleotide is useful for modulating the
CC	expression of LIM domain kinase 1 in cells or tissues to treat diseases
CC	associated with their expression, such as a developmental disorder or a
CC	neurological disorder. In addition, the compound is used for diagnostics,
CC	prophylaxis, or as research reagents or kits. This sequence represents a
CC	human LIM domain kinase 1 antisense oligonucleotide.
XX	
SQ	Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
QY	
Query Match	1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity	94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0.
DB	
687 CTGCCTCCCGGTTCAAG 704	
19 CTGCCTCTCGGGTTCAG 2	

```

XX AC ADI38764;
XX DT 22-APR-2004 (first entry)
XX XX Human LIM domain kinase 1 antisense oligonucleotide #68.
DE DE neuroprotective; LIM domain kinase 1; developmental disorder;
XX KM neurological disorder; diagnostic; prophylaxis; human; ss.
XX OS Homo sapiens.
FH Key location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT 1..5
FT modified_base
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX FT
XX PN US2004014047-A1.
XX PD 22-JAN-2004.
XX PF 18-JUL-2002; 2002US-00199199.
XX PR 18-JUL-2002; 2002US-00199199.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowseert LM, Dobie KW;
XX WPI, 2004-121553/12.
XX DR
XX PT New antisense oligonucleotides for modulating LIM domain kinase 1
PT expression, useful for diagnosing, preventing or treating conditions
PT associated with the kinase, e.g. neurological or developmental disorders.
XX PS Example 15; SEQ ID NO 83; 81bp; English.
XX CC The invention describes a compound 8-80 nucleobases in length targeted to
CC a nucleic acid molecule encoding LIM domain kinase 1. The compound
CC specifically hybridizes with the nucleic acid molecule encoding LIM
CC domain kinase 1 and inhibits the expression of LIM domain kinase 1. It
CC specifically hybridizes with at least an 8-nucleobase portion of a
CC preferred target region on the nucleic acid molecule encoding LIM domain
CC kinase 1. The antisense oligonucleotide is useful for modulating the
CC expression of LIM domain kinase 1 in cells or tissues to treat diseases
CC associated with their expression, such as a developmental disorder or a
CC neurological disorder. In addition, the compound is used for diagnostics,
CC prophylaxis, or as research reagents or kits. This sequence represents a
CC human LIM domain kinase 1 antisense oligonucleotide.
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 687 CTGCCCTCCCGGTTCAAG 704
|||||
DB 2 CTGCCTCTCGGGTTCACG 19

```

ID ADJ60937 standard; DNA; 20 BP.
XX
AC ADJ60937;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDE4C #3.
XX
KW Interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-039076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JM, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahbuddin S, Lu H, Cong H;
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 1793; 85pp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
XX
Query Match 1.7%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 614 TTTTGGACAGAGTCT 631
Db 1 TTTTGGACAGAGTCT 18
XX
RESULT 1637
ADM15371/C
ID ADM15371 standard; DNA; 20 BP.
XX
AC ADM15371;
XX
DT 01-JUL-2004 (first entry)

XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1558.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsome prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsome prostaglandin E2 synthase inhibitor; cyclooxygenase; anti-diabetic;
KW immunomodulator; cardiant; neuroprotective; anti-inflammatory;
KW neuroprotective; noctropic; anti-arthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
XX
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse UK;
XX
PI WPI; 2004-305094/28.
XX
DR New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 1558; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC anti-diabetic, immunomodulatory, cardiant, neuroprotective,
CC anti-inflammatory, neuroprotective, noctropic, anti-arthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.7% Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 732 AGCTGGACTACAGCGC 749
 Db 20 AGCTGGACTACAGCGC 3

RESULT 1638
 ADO46426
 ADO46426 standard; DNA; 20 BP.

AC ADO46426;
 XX
 XX
 XX 15-JUL-2004 (first entry)
 DE Human oligonucleotide #1792.

XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KM lung disease; hyper-responsiveness; adenosis; adenosis A receptor;
 KM asthma; lung allergy; inflammation; inflammatory disease;
 KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KM acute respiratory distress syndrome; pulmonary hypertension;
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.
 OS
 XX US2004049022-A1.
 XX
 XX 11-MAR-2004.
 XX
 XX 25-JUL-2003; 2003US-00627930.
 XX PF 23-APR-2002; 2002WO-US013135.
 XX PR 23-APR-2002; 2002WO-US013143.
 XX PA (NYCE/) NYCE J W.
 XX PA (SAND/) SANDRASAGRA A.
 XX PA (TANG/) TANG L.
 XX PA (AGUI/) AGUILAR D.
 XX PA (MILL/) MILLER S.
 XX PA (SHAH/) SHAHABUDDIN S.
 XX PA (LUH/) LU H.
 XX PA (CONG/) CONG H.
 XX PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 XX PI Shahabuddin S, Lu H, Cong H;
 XX DR WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.

XX Claim 2; SEQ ID NO 1793; 174pp; English.

XX The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,

CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosis and/or levels of adenosis A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.

XX Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
 SQ

Query Match 1.7% Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 614 TTTTGGAGACAGTCT 631
 Db 1 TTTTGGAGACAGTCT 18

RESULT 1639
 ADP45846
 ADP45846 standard; DNA; 20 BP.

AC ADP45846;
 XX
 XX 26-AUG-2004 (first entry)
 DE Extend primer 38 used to genotype human ICAM-1/ICAM-4/ICAM-5 SNP.

XX breast cancer; cytostatic; gene therapy; human;
 KM intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;
 KM CD54; cell surface glycoprotein P3.58; ICAM-4;
 KM Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;
 KM ss; primer; PCR; SNP; single nucleotide polymorphism; probe.

XX Homo sapiens.
 OS
 XX WO2004047623-A2.
 XX
 XX 10-JUN-2004.
 XX PD 25-NOV-2003; 2003WO-US037948.
 XX PF 25-NOV-2002; 2002US-0429136P.
 XX PR 24-JUL-2003; 2003US-0490234P.
 XX PA (SEQU-) SEQUENOM INC.
 XX PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 XX PI WPI; 2004-441051/41.

XX Identifying a subject at risk of breast cancer by detecting the presence
 PT of polymorphic variations in the ICAM, MAPK10, KIA0061, NIMA1 or GALE
 PT regions which are associated with breast cancer in a nucleic acid sample
 PT from a subject.

XX Example 4; Page 83; 289pp; English.

XX The invention relates to a novel method for identifying a subject at risk
 CC of breast cancer comprising detecting the presence or absence of one or
 CC more polymorphic variations associated with breast cancer in a nucleic
 CC acid sample from a subject. The method of the invention has cytostatic
 CC applications and may be useful for identifying a subject at risk of
 CC breast cancer, for early diagnosis, prevention and treatment of breast
 CC cancer, possibly via gene therapy, as well as to analyse and predict a
 CC response to a breast cancer treatment and in clinical drug trials. The
 CC current sequence is that of an Extend primer (also described as probe) of

Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

DT 17-JUL-2001 (first entry)

```
XX DE Human thyroid malfunction-associated protein RITA PCR primer #2.
XX KM KRB domain; hyperplasia; thyroid; tumor; zinc finger motif; primer;
XX KM cytosolic; antithyroid; gene therapy; chromosome 19; 19q13; ss.
XX OS Homo sapiens.
XX PN MO200127265-A1.
XX PD 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-DE003600.
XX PR 12-OCT-1999; 99DE-01049179.
XX PA (UTBR-) UNITV BREMEN.
XX PI Bullerdiek J, Rippe V, Meiboom M, Belge G;
XX DR WPI; 2001-290723/30.
XX PT New nucleic acid useful for the diagnosis and treatment of thyroid
XX PT disorders, e.g. tumors.
XX PS Example 8; Page 29; 59pp; German.
XX CC This invention describes a novel nucleic acid (N1) encoding a polypeptide
XX CC which comprises a KRB-domain and/or at least one zinc finger motif. The
XX CC products of the invention have cytosolic and antithyroid activity and
XX CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies
XX CC of the invention may be used in the diagnosis and/or the therapy of the
XX CC malfunction of the thyroid and/or hyperplasia of the thyroid and/or
XX CC thyroid tumors. They may also be used in the production of medicaments.
XX CC (N1) can also be used to diagnose thyroid tumors which are located on
XX CC chromosome 19 at band 19q13. This sequence represents a PCR primer used
XX CC in the isolation of the thyroid malfunction-associated protein, RITA
XX CC which is described in the method of the invention
XX SQ Sequence 16 BP; 2 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 644 CCAAGCTGAGTGCAG 659
DB 16 CCAAGCTGAGTGCAG 1
RESULT 1643
ABS97400
ID ABS97400 standard; DNA; 16 BP.
XX
XX ABS97400;
AC 23-DEC-2002 (first entry)
XX
XX
XX
XX
XX Human cyclooxygenase 2 (COX2) PCR primer #13.
DE
XX
XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
XX KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
XX KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;
XX KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX KM NADH quinone oxidoreductase 2; NOQ2; sulfoxtransferase thermolabile; STM;
XX KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
XX KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX KM multidrug resistance associated protein 3; cancer; prostate;
```

```
XX KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX KM altered drug metabolism; cardiovascular function; colorectal tumour;
XX KM central nervous system; pulmonary; immunological.
XX OS Homo sapiens.
XX PN WO200257410-A2.
XX PD 25-JUL-2002.
XX PF 28-NOV-2001; 2001WO-US044838.
XX PR 28-NOV-2000; 2000US-00724389.
XX PA (DNAS-) DNA SCI LAB INC.
XX PI Guida M, Hall J;
XX DR WPI; 2002-698522/75.
XX PT Isolated nucleic acid molecules having polymorphisms in known human genes
XX PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
XX PT for locating, identifying and characterizing the genes responsible for
XX PT disorder-related traits.
XX PS Example 8; Page 112; 714pp; English.
XX CC This invention relates to the sequence of an isolated nucleic acid
XX CC molecule comprising at least one base variation from that of a known
XX CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
XX CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
XX CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
XX CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
XX CC transferase (NNMT), NADH quinone oxidoreductase 2 (NOQ2),
XX CC sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
XX CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
XX CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
XX CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX CC The polymorphisms in the human genes cited in the invention are useful as
XX CC genetic linkage markers for locating and characterizing the genes that
XX CC are responsible for specific traits within the genome and eventually
XX CC identifying the genes responsible for a variety of disorder-related
XX CC traits as a result of their e.g., overexpression, constitutive
XX CC expression, mutation or underexpression, which may be used in diagnosing
XX CC and/or treating the disorders. The nucleic acid molecules comprising the
XX CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
XX CC ARNT, EPHX2, GST12, NNMT, NOQ2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
XX CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
XX CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX CC used to screen for altered cardiovascular function. In COX2 for altered
XX CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
XX CC nervous system function, in FLAP and HNMT for altered pulmonary,
XX CC immunological or haematological function, in KLK2 for altered serine
XX CC protease activity in the prostate, in LTF for altered immunological or
XX CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
XX CC peripheral nervous system function. The present sequence represents a PCR
XX CC primer used to amplify the sequences of the invention
XX SQ Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 868 GGATTACAGGCGTGAG 883
|||||
```

Db 1 GGATTACAGCGCTGAG 16

RESULT 1644
 ABS98039/c
 ID ABS98039 standard; DNA; 16 BP.
 XX
 AC ABS98039;
 XX
 DT 23-DEC-2002 (first entry)
 DE Human multilocus resistance gene PCR primer #3.
 XX
 KM Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTR;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; NRP3; NR112;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KM multilocus resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multilocus resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological.
 XX
 OS Homo sapiens.
 XX
 PN MO200257410-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 28-NOV-2001; 2001WO-US044838.
 XX
 PR 28-NOV-2000; 2000US-00724389.
 XX
 PA (DNAS-) DNA SCI LAB INC.
 XX
 PI Guida M, Hall J;
 XX
 DR WPI; 2002-698522/75.
 XX
 PT Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 PS Example 22; Page 141; 714pp; English.
 XX
 CC This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multilocus resistance 1
 CC (MDR1), lactotransferrin (LTF), multilocus resistance associated protein 3
 CC (NRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related

traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTR for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered drug
 CC peripheral nervous system function. The present sequence represents a PCR
 CC primer used to amplify the sequences of the invention
 XX

SQ Sequence 16 BP; 3 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGCTGAG 883
 Db 16 GGATTACAGCGCTGAG 1

RESULT 1645
 ACA62885/c
 ID ACA62885 standard; DNA; 16 BP.
 XX
 AC ACA62885;
 XX
 DT 21-AUG-2003 (first entry)
 XX
 DE Repeated nucleic acid detection method, human probe Alu13.
 XX
 KM Repeated nucleic acid detection; human; alu; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003022163-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 15-DEC-2000; 2000US-00739909.
 XX
 PR 21-JUL-1999; 99US-00358972.
 XX
 PR 25-AUG-1999; 99US-00383316.
 XX
 PA (MAND/) MANDEKAR M N.
 PA (TERE/) TEREBA A.
 PA (SHUL/) SHULTZ J W.
 PI Mandrekar MN, Tereba A, Shultz JW;
 XX
 DR WPI; 2003-479484/45.
 XX
 PT Determining presence or absence of desired nucleic acids that contain
 PT multiple repeats of predetermined nucleic acid target sequences in a
 PT sample, by using nucleic acid hybridization methods.
 XX
 PS Claim 1; Page 27; 31pp; English.
 XX
 CC The invention describes a method of determining presence or absence of a
 CC desired nucleic acid (NA) that contains multiple repeats of a
 CC predetermined NA target sequence in a NA sample. The method involves
 CC providing a treated sample that may contain the desired NA in which
 CC several predetermined repeating NA target sequences are hybridised with a
 CC NA probe, analysing for presence of hybridised NA containing the NA
 CC probe, and thereby the presence or absence of the desired NA. The method

is useful for determining the presence or absence of desired nucleic acids that contain multiple repeats of a predetermined NA target sequence, in a NA sample obtained from a biological sample, where the repeated sequence includes several predetermined repeated sequence that differ in length and/or sequence. The method is highly sensitive, and enables detection and quantification of the presence of a NA without the need to undergo a NA target sequence enrichment step prior to a NA hybrid detection step. The method enables rapid and accurate detection of a desired NA that contains multiple repeats of a NA target sequence. This sequence represents a probe used to detect the human Alu repeat sequences

Sequence 16 BP; 3 A; 9 C; 2 G; 2 T; 0 U; 0 Other;

Query Match. 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

647 GGCTGAGTCAGTCG 662
16 GGCTGAGTCAGTCG 1

RESULT 1646
ACAE2878 standard; DNA; 16 BP.
ACAE2878;
21-AUG-2003 (first entry)
Repeated nucleic acid detection method, human probe Alu4.
Repeated nucleic acid detection; human; alu; probe; ss.
Homo sapiens.
US2003022163-A1.
30-JAN-2003.
15-DEC-2000; 2000US-00739909.
21-JUL-1999; 99US-00358972.
25-AUG-1999; 99US-00383316.
(MAND/) MANDREKAR M N.
(TERE/) TEREBA A.
(SHUL/) SHULTZ J W.
Mandrekar MN, Tereba A, Shultz JW;
WPI; 2003-479484/45.
Determining presence or absence of desired nucleic acids that contain multiple repeats of predetermined nucleic acid target sequences in a sample, by using nucleic acid hybridization methods.
Claim 1; Page 27; 31pp; English.
The invention describes a method of determining presence or absence of a predetermined NA target sequence in a NA sample. The method involves providing a treated sample that may contain the desired NA in which several predetermined repeating NA target sequences are hybridised with a NA probe, analysing for presence of hybridised NA containing the NA probe, and thereby the presence or absence of the desired NA. The method is useful for determining the presence or absence of desired nucleic acids that contain multiple repeats of a predetermined NA target sequence, in a NA sample obtained from a biological sample, where the repeated sequence includes several predetermined repeated sequence that differ in length and/or sequence. The method is highly sensitive, and enables detection and quantification of the presence of a NA without the need to undergo a NA target sequence enrichment step prior to a NA hybrid detection step. The method enables rapid and accurate detection of a desired NA that contains multiple repeats of a NA target sequence. This sequence represents a probe used to detect the human Alu repeat sequences

and enables detection and quantification of the presence of a NA without the need to undergo a NA target sequence enrichment step prior to a NA hybrid detection step. The method enables rapid and accurate detection of a desired NA that contains multiple repeats of a NA target sequence. This sequence represents a probe used to detect the human Alu repeat sequences

Sequence 16 BP; 3 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match. 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

968 TCTCGGCTCAGTCGAA 983
1 TCTCGGCTCAGTCGAA 16

RESULT 1647
ACAE2880 standard; DNA; 16 BP.
ACAE2880;
21-AUG-2003 (first entry)
Repeated nucleic acid detection method, human probe Alu10.
Repeated nucleic acid detection; human; alu; probe; ss.
Homo sapiens.
US2003022163-A1.
30-JAN-2003.
15-DEC-2000; 2000US-00739909.
21-JUL-1999; 99US-00358972.
25-AUG-1999; 99US-00383316.
(MAND/) MANDREKAR M N.
(TERE/) TEREBA A.
(SHUL/) SHULTZ J W.
Mandrekar MN, Tereba A, Shultz JW;
WPI; 2003-479484/45.
Determining presence or absence of desired nucleic acids that contain multiple repeats of predetermined nucleic acid target sequences in a sample, by using nucleic acid hybridization methods.
Claim 1; Page 27; 31pp; English.
The invention describes a method of determining presence or absence of a predetermined NA target sequence in a NA sample. The method involves providing a treated sample that may contain the desired NA in which several predetermined repeating NA target sequences are hybridised with a NA probe, analysing for presence of hybridised NA containing the NA probe, and thereby the presence or absence of the desired NA. The method is useful for determining the presence or absence of desired nucleic acids that contain multiple repeats of a predetermined NA target sequence, in a NA sample obtained from a biological sample, where the repeated sequence includes several predetermined repeated sequence that differ in length and/or sequence. The methods can be efficiently used for distinguishing human and bacterial NA. The method is highly sensitive, and enables detection and quantification of the presence of a NA without the need to undergo a NA target sequence enrichment step prior to a NA hybrid detection step. The method enables rapid and accurate detection of a desired NA that contains multiple repeats of a NA target sequence. This sequence represents a probe used to detect the human Alu repeat sequences

and enables detection and quantification of the presence of a NA without the need to undergo a NA target sequence enrichment step prior to a NA hybrid detection step. The method enables rapid and accurate detection of a desired NA that contains multiple repeats of a NA target sequence. This sequence represents a probe used to detect the human Alu repeat sequences

SQ Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 868 GGATTACAGCGCTGAG 883
DB 1 GGATTACAGCGCTGAG 16
RESULT 1648
ID ACA62882
ACA62882 standard; DNA; 16 BP.
XX
AC ACA62882;
XX
DT 21-AUG-2003 (first entry)
XX
DE Repeated nucleic acid detection method, human probe Alu12.
XX
KM Repeated nucleic acid detection; human; alu; probe; ss.
XX
OS Homo sapiens.
XX
PN US2003022163-A1.
XX
PD 30-JAN-2003.
XX
PF 15-DEC-2000; 2000US-00739909.
XX
PR 21-JUL-1999; 99US-00358972.
PR 25-AUG-1999; 99US-00383316.
XX
PA (MAND/) MANDREKAR M N.
PA (TERE/) TERESA A.
PA (SHUL/) SHULTZ J W.
XX
PI Mandrekar MN, Tereba A, Shultz JW;
XX
DR WPI; 2003-479484/45.
XX
PT Determining presence or absence of desired nucleic acids that contain
PT multiple repeats of predetermined nucleic acid target sequences in a
PT sample, by using nucleic acid hybridization methods.
XX
PS Claim 1; Page 27; 31pp; English.
XX
CC The invention describes a method of determining presence or absence of a
CC desired nucleic acid (NA) that contains multiple repeats of a
CC predetermined NA target sequence in a NA sample. The method involves
CC providing a treated sample that may contain the desired NA in which
CC several predetermined repeating NA target sequences are hybridised with a
CC NA probe, and analysing for presence or absence of the desired NA. The method
CC is useful for determining the presence or absence of desired nucleic
CC acids that contain multiple repeats of a predetermined NA target
CC sequence, in a NA sample obtained from a biological sample, where the
CC repeated sequence includes several predetermined repeated sequence that
CC differ in length and/or sequence. The methods can be efficiently used for
CC distinguishing human and bacterial NA. The method is highly sensitive,
CC and enables detection and quantification of the presence of a NA without
CC the need to undergo a NA target sequence enrichment step prior to a NA
CC hybrid detection step. The method enables rapid and accurate detection of
CC a desired NA that contains multiple repeats of a NA target sequence. This
CC sequence represents a probe used to detect the human Alu repeat sequences
XX
SQ Sequence 16 BP; 2 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 647 GGCTGAGTGCAGTGG 662
DB 1 GGCTGAGTGCAGTGG 16
RESULT 1649
ID ACA62879
ACA62879 standard; DNA; 16 BP.
XX
AC ACA62879;
XX
DT 21-AUG-2003 (first entry)
XX
DE Repeated nucleic acid detection method, human probe Alu8.
XX
KM Repeated nucleic acid detection; human; alu; probe; ss.
XX
OS Homo sapiens.
XX
PN US2003022163-A1.
XX
PD 30-JAN-2003.
XX
PF 15-DEC-2000; 2000US-00739909.
XX
PR 21-JUL-1999; 99US-00358972.
PR 25-AUG-1999; 99US-00383316.
XX
PA (MAND/) MANDREKAR M N.
PA (TERE/) TERESA A.
PA (SHUL/) SHULTZ J W.
XX
PI Mandrekar MN, Tereba A, Shultz JW;
XX
DR WPI; 2003-479484/45.
XX
PT Determining presence or absence of desired nucleic acids that contain
PT multiple repeats of predetermined nucleic acid target sequences in a
PT sample, by using nucleic acid hybridization methods.
XX
PS Claim 1; Page 27; 31pp; English.
XX
CC The invention describes a method of determining presence or absence of a
CC desired nucleic acid (NA) that contains multiple repeats of a
CC predetermined NA target sequence in a NA sample. The method involves
CC providing a treated sample that may contain the desired NA in which
CC several predetermined repeating NA target sequences are hybridised with a
CC NA probe, and analysing for presence or absence of the desired NA. The method
CC is useful for determining the presence or absence of desired nucleic
CC acids that contain multiple repeats of a predetermined NA target
CC sequence, in a NA sample obtained from a biological sample, where the
CC repeated sequence includes several predetermined repeated sequence that
CC differ in length and/or sequence. The methods can be efficiently used for
CC distinguishing human and bacterial NA. The method is highly sensitive,
CC and enables detection and quantification of the presence of a NA without
CC the need to undergo a NA target sequence enrichment step prior to a NA
CC hybrid detection step. The method enables rapid and accurate detection of
CC a desired NA that contains multiple repeats of a NA target sequence. This
CC sequence represents a probe used to detect the human Alu repeat sequences
XX
SQ Sequence 16 BP; 3 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 968 TCTGGCTCACTGCAA 983
DB 1 TCTGGCTCACTGCAA 16
RESULT 1650

AAD63080/c
ID AAD63080 standard; DNA; 16 BP.
XX
AC AAD63080;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tandem tag DNA #14.
XX
KM Tandem tag; concatenated tag; human; ds.
XX
OS Homo sapiens.
XX
PN US2003190618-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00092885.
XX
PR 06-MAR-2002; 2002US-00092885.
XX
PA (SAMA/) SAMAL B.
PA (LIYY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOPP/) HOPPA N L.
PA (JOHE/) JOHE K K.
XX
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK,
XX
DR WPI; 2003-831617/77.
XX
PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
XX
PT sample of mRNAs, amplifying the released tags, concatenating the
XX
PT amplified tags to form concatenated tags, amplifying and isolating the
XX
PT concatenated tags.
XX
PS Disclosure; Page 5; 0pp; English.
XX
CC The present invention discloses a method for generating five prime biased
XX
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
XX
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
XX
CC form concatenated tags, amplifying and isolating the concatenated tags.
XX
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 2 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 250 CGGCTCCCAAGTGC 265
Db 16 CGGCTCCCAAGTGC 1
XX
RESULT 1651
AAD63081/c
ID AAD63081 standard; DNA; 16 BP.
XX
AC AAD63081;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tandem tag DNA #15.
XX
KM Tandem tag; concatenated tag; human; ds.
XX
OS Homo sapiens.
XX
PN US2003190618-A1.
XX
PD 09-OCT-2003.
XX

PF 06-MAR-2002; 2002US-00092885.
XX
XX
PR 06-MAR-2002; 2002US-00092885.
XX
XX
PA (SAMA/) SAMAL B.
PA (LIYY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOPP/) HOPPA N L.
PA (JOHE/) JOHE K K.
XX
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK,
XX
DR WPI; 2003-831617/77.
XX
PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
XX
PT sample of mRNAs, amplifying the released tags, concatenating the
XX
PT amplified tags to form concatenated tags, amplifying and isolating the
XX
PT concatenated tags.
XX
PS Disclosure; Page 5; 0pp; English.
XX
CC The present invention discloses a method for generating five prime biased
XX
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
XX
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
XX
CC form concatenated tags, amplifying and isolating the concatenated tags.
XX
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 3 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 869 GATTACAGGCGTGAC 884
Db 16 GATTACAGGCGTGAC 1
XX
RESULT 1652
AAD63078/c
ID AAD63078 standard; DNA; 16 BP.
XX
AC AAD63078;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tandem tag DNA #12.
XX
KM Human tandem tag DNA #12.
XX
KM Tandem tag; concatenated tag; human; ds.
XX
OS Homo sapiens.
XX
PN US2003190618-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00092885.
XX
PR 06-MAR-2002; 2002US-00092885.
XX
PA (SAMA/) SAMAL B.
PA (LIYY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOPP/) HOPPA N L.
PA (JOHE/) JOHE K K.
XX
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK,
XX
DR WPI; 2003-831617/77.
XX
PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
XX
PT sample of mRNAs, amplifying the released tags, concatenating the
XX
PT amplified tags to form concatenated tags, amplifying and isolating the

```
PT concatenated tags.
XX
PS Disclosure; Page 5; Opp; English.
XX
CC The present invention discloses a method for generating five prime biased
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
CC form concatenated tags, amplifying and isolating the concatenated tags.
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 5 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      667 ATCTTGCTCCTCCTGCA 682
DB      16 ATCTTGCTCCTCCTGCA 1

RESULT 1653
AAD63084/C
ID AAD63084 standard; DNA; 16 BP.
XX
AC AAD63084;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tandem tag DNA #18.
XX
KM Tandem tag; concatenated tag; human; ds.
XX
OS Homo sapiens.
XX
PN US2003190618-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00092885.
XX
PR 06-MAR-2002; 2002US-00092885.
XX
PS (SAMA/) SAMAL B.
PA (LIYY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOPP/) HOPPA N L.
PA (JOHE/) JOHE K K.
XX
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;
XX
DR WPI; 2003-831617/77.
XX
PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
PT sample of mRNAs, amplifying the released tags, concatenating the
PT amplified tags to form concatenated tags, amplifying and isolating the
PT concatenated tags.
XX
PS Disclosure; Page 5; Opp; English.
XX
CC The present invention discloses a method for generating five prime biased
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
CC form concatenated tags, amplifying and isolating the concatenated tags.
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 3 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      381 AGCCTCCCAAGTGCT 396
DB      16 AGCCTCCCAAGTGCT 1
```

```
DB      16 AGCCTCCCAAGTGCT 1

RESULT 1654
AAD63086/C
ID AAD63086 standard; DNA; 16 BP.
XX
AC AAD63086;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human tandem tag DNA #20.
XX
KM Tandem tag; concatenated tag; human; ds.
XX
OS Homo sapiens.
XX
PN US2003190618-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00092885.
XX
PR 06-MAR-2002; 2002US-00092885.
XX
PS (SAMA/) SAMAL B.
PA (LIYY/) LI Y.
PA (HERM/) HERMIDA L C.
PA (HOPP/) HOPPA N L.
PA (JOHE/) JOHE K K.
XX
PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;
XX
DR WPI; 2003-831617/77.
XX
PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
PT sample of mRNAs, amplifying the released tags, concatenating the
PT amplified tags to form concatenated tags, amplifying and isolating the
PT concatenated tags.
XX
PS Disclosure; Page 6; Opp; English.
XX
CC The present invention discloses a method for generating five prime biased
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
CC mRNAs, amplifying the released tags, concatenating the amplified tags to
CC form concatenated tags, amplifying and isolating the concatenated tags.
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 3 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      1.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      381 AGCCTCCCAAGTGCT 396
DB      16 AGCCTCCCAAGTGCT 1

RESULT 1655
AAA22740
ID AAA22740 standard; RNA; 17 BP.
XX
AC AAA22740;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5966.
XX
KM Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cyostatic; antidiabetic;
```

ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberos sclerosi; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Homo sapiens. MO9950403-A2. 07-OCT-1999. 24-MAR-1999; 99WO-US006507. 27-MAR-1998; 98US-0079678P. (RIBO-) RIBOZYME PHARM INC. Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA; MPI; 1999-591315/50. Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors. Claim 54; Page 239; 305pp; English.

The present invention describes enzymatic cleave RNA molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA1688 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberos sclerosi, pot-wine stain, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 3 A; 1 C; 3 G; 0 T; 10 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17; Best Local Similarity 37.5%; Pred. No. 1.5e+03; Matches 6; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Db 1065 GCTAATTTTGTATT 1080
||:||||:||||:|
AAA22748
ID AAA22748 standard; RNA; 17 BP.
XX
XX AAA22748;
AC
XX
XX 19-JUN-2000 (first entry)
DT
XX

Integrin subunit beta 3 substrate sequence SEQ ID NO:5974.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberos sclerosi; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. Homo sapiens. MO9950403-A2. 07-OCT-1999. 24-MAR-1999; 99WO-US006507. 27-MAR-1998; 98US-0079678P. (RIBO-) RIBOZYME PHARM INC. Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA; MPI; 1999-591315/50. Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors. Claim 54; Page 240; 305pp; English.

The present invention describes enzymatic cleave RNA molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA1688 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberos sclerosi, pot-wine stain, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 5 A; 1 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17; Best Local Similarity 56.2%; Pred. No. 1.5e+03; Matches 9; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Db 774 GTATTTTAGTAGAGA 789
||:||||:||||:|
AAA22736
ID AAA22736 standard; RNA; 17 BP.

XX AC AAA22736;
XX DT 19-JUN-2000 (first entry)
XX DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5962.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antiproliferative; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Oster-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX OS
XX MO9950403-A2.
XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99MO-US006507.
XX PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX DR
XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
XX AA11767 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
XX AA11768 to AA17560 and AA17623 to AA17684 represent their
XX corresponding target sequences; AA17685 to AA18385 and AA19087 to
XX AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
XX and AA19155 to AA19222 represent their corresponding target sequences;
XX AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
XX AA21596 to AA21688 represent their corresponding target sequences;
XX AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
XX AA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Oster-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;
SQ

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 394 GCTGGATTACAGCG 409
DB 1 GCTGGATTACAGCG 16

RESULT 1658
ID AAA22742
AAA22742 standard; RNA; 17 BP.
XX
XX AAA22742;
XX
XX 19-JUN-2000 (first entry)
XX DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5968.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antiproliferative; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Oster-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX OS
XX MO9950403-A2.
XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99MO-US006507.
XX PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX DR
XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
XX AA11767 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
XX AA11768 to AA17560 and AA17623 to AA17684 represent their
XX corresponding target sequences; AA17685 to AA18385 and AA19087 to
XX AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
XX and AA19155 to AA19222 represent their corresponding target sequences;
XX AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
XX AA21596 to AA21688 represent their corresponding target sequences;
XX AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
XX AA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Oster-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 1 C; 1 G; 0 T; 12 U; 0 Other;
SQ

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 31.2%; Pred. No. 1.5e+03;

Matches 5; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1066 CTAATTTTGTATTTT 1081
 ||:||||:||||:
 Db 1 CUAAUUUUUUUUUU 16

RESULT 1659
 AAA22743
 ID AAA22743 standard; RNA; 17 BP.

XX AAA22743;
 AC
 XX
 XX
 DT 19-JUN-2000 (first entry)
 XX
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5969.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
 tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
 Kipfel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.
 OS
 XX
 XX WO9950403-A2.
 PN
 XX
 PD 07-OCT-1999.
 XX
 XX
 PF 24-MAR-1999; 99WO-US006507.
 PR
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.
 PS
 XX Claim 54; Page 239; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA2422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiodiroma of tubercous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kipfel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3

XX SQ Sequence 17 BP; 3 A; 0 C; 2 G; 0 T; 12 U; 0 Other;
 Query Match 1.6%; Score 16; DB 1; Length 17;
 Best Local Similarity 25.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 769 TTTTGTATTTTGT 784
 ||:||||:||||:
 Db 2 UUUUUUUUUUUUU 17

RESULT 1660
 AAA22957/C
 ID AAA22957 standard; RNA; 17 BP.

XX AAA22957;
 AC
 XX
 XX
 DT 19-JUN-2000 (first entry)
 XX
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6183.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
 tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;
 Kipfel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.
 OS
 XX
 XX WO9950403-A2.
 PN
 XX
 PD 07-OCT-1999.
 XX
 XX
 PF 24-MAR-1999; 99WO-US006507.
 PR
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.
 PS
 XX Claim 54; Page 253; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA2422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as

CC neovascular glaucoma, myopic degeneration, pteriosis, verruca vulgaris,
CC angioblastoma of tuberculous scleritis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 873 ACAGGCGTGAGCCACC 888
DB 17 ACAGGCGTGAGCCACC 2

RESULT 1661

AAf64147/c
ID AAF64147 standard; DNA; 17 BP.

XX AAF64147;

DT 06-APR-2001 (first entry)

DE Primer #89.

KM Human; lipoprotein lipase; LPL; stenosis; ss.

OS Homo sapiens.

PN WO200102606-A2.

PD 11-JAN-2001.

PF 30-JUN-2000; 2000WO-US018308.

PR 02-JUL-1999; 99US-00347114.

PA (CEDA-) CEDARS SINAI MEDICAL CENT.

PI Taylor KD, Scheuner M, Rotter J, Yang H;

DR WPI; 2001-138155/14.

PT Genetic testing for determining non-responsiveness to statin drug in
PT patients of a coronary artery disease, involves analyzing amplification
PT products for homozygosity for a variant allele in the human lipoprotein
PT lipase gene.

PS Claim 16; Page 20; 74pp; English.

CC The present invention relates to detecting a genetic predisposition in a
CC human subject for non-responsiveness to statin drug treatment, involving
CC amplifying nucleic acids including a non-coding or untranslated region
CC within the 3' end of the human lipoprotein lipase (LPL) gene from a
CC tissue sample. The method is useful for determining which patients
CC suffering from coronary artery disease, or which coronary artery bypass
CC graft (CABG) patients, will likely not respond positively to statin drugs
CC treatment with respect to stenosis of a coronary artery or bypass graft
XX
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;

QY 939 GTTACCCAGGCTGGAG 954

DB 16 GTTACCCAGGCTGGAG 1

RESULT 1662

ABN83022/c
ID ABN83022 standard; DNA; 17 BP.

XX ABN83022;

DT 16-AUG-2002 (first entry)

DE Ataxia telangiectasia locus 56594896-Wild-a capture probe.

KM Ataxia telangiectasia; probe; biochip; array; capture; ss.

OS Homo sapiens.

PN WO200180155-A2.

PD 25-OCT-2001.

PF 18-APR-2001; 2001WO-US012750.

PR 18-APR-2000; 2000US-0198045P.

PR 22-NOV-2000; 2000US-0252880P.

PA (COMB-) COMBIMATRIX CORP.

PI Anderson BP, Charles PA, Ghazvini S;

DR WPI; 2002-017664/02.

PT Automated process for custom-designed biochip design, comprises obtaining

PT desired target sequences from customer, creating sequence content motif

PT for an array and applying the motif to a surface suitable for later

PT detection.

PS Example 5; Page 21; 47pp; English.

CC The invention relates to a novel process for a manufacturer to obtain
CC customer orders for custom-designed biochips in an automated process. The
CC invention also includes an automated system and process for providing a
CC fully automated process for the design, manufacture and analysis of data
CC for biological array devices. The sequence represents a capture probe
CC designed in the invention for the "sample ataxia" set of targets, as an
CC example of an array that may be designed using the method of the
CC invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;

QY 676 CACTGCAACCTTGCC 691

DB 17 CACTGCAACCTTGCC 2

RESULT 1663

ABT38108
ID ABT38108 standard; DNA; 17 BP.

XX ABT38108;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 3745.

KM Cytostatic; vincristine; neuroprotective; neurotrophic; neuroleptic; gene chip;

KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

KM schizophrania; protein chip; gene therapy; tumour suppression;

OS human fukutin; ds.
XX Homo sapiens.
PN WO2003025175-A2.

XX 27-MAR-2003.
PD 17-SEP-2002; 2002MO-IB004208.
XX 17-SEP-2001; 2001FR-00011978.
PF 17-SEP-2001; 2001FR-00011978.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX (MOLE-) MOLECULAR ENGINES LAB.
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
DR WPI; 2003-313353/30.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PS Disclosure; Page 471; 720pp; French.
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 532 ATCTCTCTGCTCAGC 547
DB 2 ATCTCTCTGCTCAGC 17
RESULT 1664
ABT35067
ID ABT35067 standard; DNA; 17 BP.
XX ABT35067;
AC
XX 12-JUN-2003 (first entry)
DT
XX Tumour suppression related human fukutin oligo SEQ ID No 704.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
OS
XX WO2003025175-A2.
PN
XX 27-MAR-2003.
PD

XX 17-SEP-2002; 2002MO-IB004208.
PF 17-SEP-2001; 2001FR-00011978.
XX 17-SEP-2001; 2001FR-00011978.
PR (MOLE-) MOLECULAR ENGINES LAB.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX (MOLE-) MOLECULAR ENGINES LAB.
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
DR WPI; 2003-313353/30.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PS Disclosure; Page 116; 720pp; French.
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 837 GATCTGCTGCTCGG 852
DB 1 GATCTGCTGCTCGG 16
RESULT 1665
ADB04313
ID ADB04313 standard; DNA; 17 BP.
XX ADB04313;
AC
XX 20-NOV-2003 (first entry)
DT
XX Human MD27 scanning oligonucleotide SEQ ID 5299.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 10p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EP1281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF

```
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5299; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 2 C; 10 G; 3 T; 0 U; 0 Other:
XX
XX Query Match      1.6%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 647 GGCTGGAGTGCAGTGG 662
XX      |||||||||
XX      2 GGCTGGAGTGCAGTGG 17
XX
XX RESULT 1666
XX ADB04443
XX ID ADB04443 standard; DNA; 17 BP.
XX
XX ADB04443;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5429.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
```

```
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5429; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 5 A; 1 C; 4 G; 7 T; 0 U; 0 Other:
XX
XX Query Match      1.6%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 774 GTATTTTACTAGAGA 789
XX      |||||||||
XX      1 GTATTTTACTAGAGA 16
XX
XX RESULT 1667
XX ADB04438
XX ID ADB04438 standard; DNA; 17 BP.
XX
XX ADB04438;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5424.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5424; 103pp; English.
XX
```

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

SO Sequence 17 BP; 4 A; 0 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 770 TTTTGTATTTTACTA 785
DB 2 TTTTGTATTTTACTA 17

RESULT 1668

ADB04281

ID ADB04281 standard; DNA; 17 BP.

AC ADB04281;

DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5267.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5267; 103pp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

SO Sequence 17 BP; 4 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 614 TTTTGTAGACGAGT 629
DB 2 TTTTGTAGACGAGT 17

RESULT 1669

ADB04315

ID ADB04315 standard; DNA; 17 BP.

AC ADB04315;

DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5301.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5301; 103pp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

Seq Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 648 GCTGAGTGCAGTGGC 663
Db 1 GCTGAGTGCAGTGGC 16

RESULT 1670
ADB04284
ID ADB04284 standard; DNA; 17 BP.

AC ADB04284;

DT 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5270.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.

OS Homo sapiens.

PN EPI281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002BP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

DR WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5270; 103bp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 4 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Qy Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 TTTTGAGACAGAGTCT 631
|||||

Db 1 TTTTGAGACAGAGTCT 16

RESULT 1671
ABZ60605
ID ABZ60605 standard; RNA; 17 BP.

AC ABZ60605;

DT 21-MAR-2003 (first entry)

DE Human K-Ras DNAzyme substrate #717.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.

OS Homo sapiens.

PN W0200297114-A2.

PD 05-DEC-2002.

PF 29-MAY-2002; 2002MO-US016840.

PR 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Mcswiggen J;

DR WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer; modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 98; 185bp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ68524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

XX Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

Qy Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CAGCGTGTCTCGAAC 222
Db 2 CAGCGTGTCTCGAAC 17
|||||

RESULT 1672

ACC63031/C
ID ACC63031 standard; DNA; 17 BP.

AC ACC63031;

DT 01-JUL-2003 (first entry)

XX

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 278.
 XX
 XX Cytostatic; virostatic; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.
 XX
 XX Mus musculus.
 XX
 XX MO2003025176-A2.
 XX
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004210.
 XX
 XX 17-SEP-2001; 2001FR-00011979.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-333167/31.
 DR
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; Page 63; 739pp; French.
 PS
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 CC
 SQ Sequence 17 BP; 5 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
 QY
 Query Match 1.6%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 480 GTGCACTGGTGTGATC 495
 ID 16 GTGCACTGGTGTGATC 1
 AC
 XX
 XX ADB44260/
 ID ADB44260 standard; DNA; 17 BP.
 AC
 XX
 XX ADB44260;
 ID
 XX 18-DEC-2003 (first entry)
 DE Tumour suppression/reversion associated nucleotide #4583.
 XX
 XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO2003040369-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004219.
 PF

XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-441574/41.
 DR
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumours and viral infection, also related
 PT polypeptide and antibodies.
 XX
 XX Disclosure; Page 567; 771pp; French.
 PS
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 CC
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 QY
 Query Match 1.6%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 480 GTGCACTGGTGTGATC 495
 ID 16 GTGCACTGGTGTGATC 1
 AC
 XX
 XX ACC54382
 ID ACC54382 standard; DNA; 17 BP.
 XX
 XX ACC54382;
 ID
 XX 27-JUN-2003 (first entry)
 DE Human tumour suppressor sequence #3149.
 XX
 XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KM tumour regression; apoptosis; virus resistance; diagnosis;
 KM cellular degeneration.
 XX
 XX Homo sapiens.
 OS
 XX
 XX FR2826373-A1.
 PN
 XX 27-DEC-2002.
 PD
 XX 20-JUN-2001; 2001FR-00008139.
 PF
 XX 20-JUN-2001; 2001FR-00008139.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB SA.
 PA
 XX

PI Tuijnder M, Teleman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
XX apoptosis or virus resistance are useful to diagnose and treat viral
XX disease, development of tumor cells and cell degeneration.
PS Claim 1; Page 767; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;
QY 667 ATCTTGAGCTCAGTCA 682
2 ATCTTGAGCTCAGTCA 17
DB
RESULT 1675
ACCS1495/c
ID ACCS1495 standard; DNA; 17 BP.
XX
AC ACCS1495;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #262.
XX
KW SB; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Teleman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
XX apoptosis or virus resistance are useful to diagnose and treat viral
XX disease, development of tumor cells and cell degeneration.
PS Claim 1; Page 100; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 GTGCAGTGTGTGATC 495
16 GTGCAGTGTGTGATC 1
DB
RESULT 1676
ADL50194
ID ADL50194 standard; RNA; 17 BP.
XX
AC ADL50194;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1308.
XX
KW antiseize oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
OS Unidentified.
XX
OS
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowitra B, Haerberli P, Mcswigen J, Fonaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
PS Claim 59; SEQ ID NO 3727; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antiseize oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX

SQL Sequence 17 BP; 5 A; 2 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 946 AGGCTGAGTGCATG 961
|||:||||:||||:
DB 1 AGGCTGAGTGCATG 16

RESULT 1677

ADL50204

ID ADL50204 standard; RNA; 17 BP.

AC ADL50204;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1318.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX restenosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.

OS Unidentified.

PN WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fornaugh K;

XX WPI; 2003-058513/05.

DR Novel enzymatic nucleic acid that down-regulates expression of neurite

PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3737; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.

SQL Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 722 CCTCCTGAGTACTGG 737
|||:||||:||||:
DB 1 CCTCCTGAGTACTGG 16

RESULT 1678

ADL49433

ID ADL49433 standard; RNA; 17 BP.

AC ADL49433;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #547.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX restenosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.

OS Unidentified.

PN WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fornaugh K;

XX WPI; 2003-058513/05.

DR Novel enzymatic nucleic acid that down-regulates expression of neurite

PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2966; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.

Sequence 17 BP; 1 A; 9 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 536 TCCTGCTCAGCCTCC 551
:|||||:|||||:
DB 1 UCCGCCUCAGCCUCC 16
RESULT 1679
ADL49459
ID ADL49459 standard; RNA; 17 BP.
XX
AC ADL49459;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #573.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswiggen J, Fossnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2992; 317bp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX

Sequence 17 BP; 1 A; 10 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 843 CCCTGCTCAGCCTCC 858
:|||||:|||||:
DB 2 CCUGCCUCAGCCUCC 17
RESULT 1680
ADL50215
ID ADL50215 standard; RNA; 17 BP.
XX
AC ADL50215;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1329.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswiggen J, Fossnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3748; 317bp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX

SQL Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1111 CAGGCTGCTCAAC 1126

DB 2 CAGGCTGCTCAAC 17

RESULT 1681

ADL49914 ADL49914 standard; RNA; 17 BP.

XX ADL49914;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1028.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

KM protein kinase PKR; cerebrovascular accident;

KM central nervous system injury; CNS injury; spinal cord injury; cancer;

KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KM restenosis; asthma; Crohn's disease; diabetes; obesity;

KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;

KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

XX substrate; ds.

XX Unidentified.

OS WO200281628-A2.

XX 17-OCT-2002.

PD 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeblerli P, Mcswigen J, Fosnaugh K;

PI WPI; 2003-058513/05.

DR Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3447; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central

CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

CC disease, lupus, multiple sclerosis, transplant/graft rejection,

CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

CC nucleic acids of the invention are also useful for down-regulating the

CC expression of a target gene and as a diagnostic tool to examine genetic

CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human PKR

CC substrate sequence.

XX

SQL Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.5e+03;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 668 TCTTGCTCACTGCA 683

DB 2 UCUGGCTCAGCGCA 17

RESULT 1682

ADL49909 ADL49909 standard; RNA; 17 BP.

XX ADL49909;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1023.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

KM protein kinase PKR; cerebrovascular accident;

KM central nervous system injury; CNS injury; spinal cord injury; cancer;

KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KM restenosis; asthma; Crohn's disease; diabetes; obesity;

KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;

KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

XX substrate; ds.

XX Unidentified.

OS WO200281628-A2.

XX 17-OCT-2002.

PD 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeblerli P, Mcswigen J, Fosnaugh K;

PI WPI; 2003-058513/05.

DR Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3442; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central

CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

CC disease, lupus, multiple sclerosis, transplant/graft rejection,

CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

CC nucleic acids of the invention are also useful for down-regulating the

CC expression of a target gene and as a diagnostic tool to examine genetic

CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human PKR

CC substrate sequence.

XX

Sequence 17 BP, 3 A, 5 C, 7 G, 0 T, 2 U, 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCA 658
DB 2 CCCAGGCTGAGTGCA 17

RESULT 1683

ID ADL49932 standard; RNA; 17 BP.

AC ADL49932;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1046.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX restenosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.

XX Unidentified.

XX MO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002MO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blact L, Chowitra B, Haerberli P, Mcswiggen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3465; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.

Sequence 17 BP, 3 A, 6 C, 4 G, 0 T, 4 U, 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 719 CAGCCCTCGAGTACG 734
DB 2 CAGCCCTCGAGTACG 17

RESULT 1684

ID ADL49915 standard; RNA; 17 BP.

AC ADL49915;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1029.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX restenosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.

XX Unidentified.

XX MO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002MO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blact L, Chowitra B, Haerberli P, Mcswiggen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3448; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.

SQL Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.5e+03; Mismatches 12; Conservative 4; Indels 0; Gaps 0;

QY 669 CTTGGCTCAGTCAAC 684

DB 1 CUUGGUCACUGCAAC 16

RESULT 1685

ADL49927

ID ADL49927 standard; RNA; 17 BP.

XX ADL49927;

XX 20-MAY-2004 (first entry)

XX Human PKR substrate sequence #1041.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

XX protein kinase PKR; cerebrovascular accident;

XX central nervous system injury; CNS injury; spinal cord injury; cancer;

XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX restenosis; asthma; Crohn's disease; diabetes; obesity;

XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;

XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

XX substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeblerl P, Mewswigen J, Fornaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3460; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

XX that down regulate the expression or inhibit the function of a receptor

XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

XX invention are useful for treating: cerebrovascular accident, central

XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

XX disease, lupus, multiple sclerosis, transplant/graft rejection,

XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

XX nucleic acids of the invention are also useful for down-regulating the

XX expression of a target gene and as a diagnostic tool to examine genetic

XX drifts and mutations within diseased cells or to detect the presence of a

XX target RNA in a cell. The present RNA sequence represents a human PKR

SQL Sequence 17 BP; 1 A; 9 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.5e+03; Mismatches 12; Conservative 4; Indels 0; Gaps 0;

QY 535 CTCCTGCTCAGCCTC 550

DB 2 CUUCGUCUACGCCUC 17

RESULT 1686

ADL50427

ID ADL50427 standard; RNA; 17 BP.

XX ADL50427;

XX 20-MAY-2004 (first entry)

XX Human PKR substrate sequence #1541.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

XX protein kinase PKR; cerebrovascular accident;

XX central nervous system injury; CNS injury; spinal cord injury; cancer;

XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX restenosis; asthma; Crohn's disease; diabetes; obesity;

XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;

XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

XX allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

XX substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeblerl P, Mewswigen J, Fornaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3960; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

XX that down regulate the expression or inhibit the function of a receptor

XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

XX invention are useful for treating: cerebrovascular accident, central

XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

XX disease, lupus, multiple sclerosis, transplant/graft rejection,

XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

XX nucleic acids of the invention are also useful for down-regulating the

XX expression of a target gene and as a diagnostic tool to examine genetic

XX drifts and mutations within diseased cells or to detect the presence of a

XX target RNA in a cell. The present RNA sequence represents a human PKR

XX substrate sequence.

Sequence 17 BP; 3 A; 2 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.5e+03; Mismatches 12; Conservative 4; Indels 0; Gaps 0;

Matches 12; Conservative 4; Indels 0; Gaps 0;

392 GTGCTGGGATTACAG 407

1 GUGCUGGGAUUCACAG 16

RESULT 1687

ADL49957 standard; RNA; 17 BP.

ADL49957;

20-MAY-2004 (first entry)

Human PKR substrate sequence #1071.

antisense oligonucleotide; neurite growth inhibitor; NOGO;

prostaglandin D2 receptor; PGDR; IkappaB kinase; IKK;

central nervous system injury; CNS injury; spinal cord injury; cancer;

melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

restenosis; asthma; Crohn's disease; diabetes; obesity;

autoimmune disease; lupus; multiple sclerosis; transplant rejection;

graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;

allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

substrate; ds.

Unidentified.

WO200281628-A2.

17-OCT-2002.

03-APR-2002; 2002WO-US010512.

05-APR-2001; 2001US-00827395.

29-MAY-2001; 2001US-0294412P.

28-AUG-2001; 2001US-0315315P.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fornaugh K;

WPI; 2003-058513/05.

Novel enzymatic nucleic acid that down-regulates expression of neurite

protein inhibitor receptor; prostaglandin D2 receptor; IkappaB kinase or

protein kinase PKR genes, for treating cancer and inflammatory disease.

Claim 59; SEQ ID NO 3490; 317pp; English.

The invention comprises nucleic acids (e.g. antisense oligonucleotides)

that down regulate the expression or inhibit the function of a receptor

for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PGDR),

IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

invention are useful for treating: cerebrovascular accident, central

nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune

Sequence 17 BP; 6 A; 7 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 1.5e+03; Mismatches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1122 CAAACCTCGACTCA 1137

1 CAAACCTCGACTCA 16

RESULT 1688

ADP46267 standard; DNA; 17 BP.

ADP46267;

26-AUG-2004 (first entry)

Extend primer 48 used to genotype human KIAA0861 polymorphism.

breast cancer; cytoskeletal; gene therapy; human; ss; primer; PCR; SNP;

single nucleotide polymorphism;

Rho family guanine-nucleotide exchange factor; KIAA0861;

chromosome 3q27.3; probe.

Homo sapiens.

WO2004047623-A2.

10-JUN-2004.

25-NOV-2003; 2003WO-US037948.

25-NOV-2002; 2002US-0429136P.

24-JUL-2003; 2003US-0490234P.

(SEQU-) SEQUENOM INC.

Roch RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

WPI; 2004-441051/41.

Identifying a subject at risk of breast cancer by detecting the presence

of polymorphic variations in the ICM, MAPK10, KIAA0861, NDM1 or GALE

regions which are associated with breast cancer in a nucleic acid sample

from a subject.

Example 6; Page 99; 289pp; English.

The invention relates to a novel method for identifying a subject at risk

of breast cancer comprising detecting the presence or absence of one or

more polymorphic variations associated with breast cancer in a nucleic

acid sample from a subject. The method of the invention has cytostatic

applications and may be useful for identifying a subject at risk of

breast cancer, for early diagnosis, prevention and treatment of breast

cancer, possibly via gene therapy, as well as to analyse and predict a

response to a breast cancer treatment and in clinical drug trials. The

current sequence is that of an extend primer (also described as probe) of

the invention which was used to genotype human Rho family guanine-

nucleotide exchange factor KIAA0861 gDNA which has been mapped to

chromosomal position 3q27.3.

Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03; Mismatches 16; Conservative 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

1000 TCAAGCATTCCTCG 1015

1 TCAAGCATTCCTCG 16

```

RESULT 1689
AAT36226/c
ID AAT36226 standard; DNA; 18 BP.
XX
XX
AC AAT36226;
XX
XX
DT 25-MAR-2003 (revised)
DT 16-APR-1997 (first entry)
XX
XX
DE Antisense oligo targeting CD28 5'-UTR (nt -201 to -184).
XX
XX
KW Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type 1 diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease; antisense;
KW oligonucleotide; 5'-untranslated region; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO9624380-A1.
XX
XX
PD 15-AUG-1996.
XX
XX
PF 05-FEB-1996; 96WO-US001507.
XX
XX
PR 09-FEB-1995; 95US-00387041.
PR 18-SEP-1995; 95US-00529878.
XX
XX
PA (ICNC) ICN PHARM INC.
XX
XX
PI Tam RC;
XX
XX
PI WPI; 1996-384228/38.
XX
XX
PT Oligo:nucleotide which reduces CD28 gene expression in T cells - for
PT treating immune system diseases, e.g. graft vs. host disease, septic
PT shock, psoriasis, etc.
XX
XX
PS Example 1; Page 27; 77pp; English.
XX
XX
CC The present oligonucleotide reduces T cell CD28 gene expression, useful
CC in the treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral disease,
CC psoriasis, type 1 diabetes mellitus, thyroiditis, sarcoides, multiple
CC sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus,
CC inflammatory bowel disease, etc. . Reducing CD28 expression may reduce the
CC effects of antigenic stimulation of CD28 positive T cells, with a
CC consequent reduction in cytokine release. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
XX
SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 TACAGCGGTGAGCCAC 887
DB 18 TACAGCGGTGAGCCAC 3
XX
XX
RESULT 1690
AA90320/c
ID AAX90320 standard; DNA; 18 BP.
XX
XX
AC AAX90320;
XX
XX
DT 24-SEP-1999 (first entry)
XX
XX
DE Oligonucleotide RT27 used in an Example from US5932556.
XX

```

```

KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX
OS Synthetic.
XX
XX
PN US5932556-A.
XX
XX
PD 03-AUG-1999.
XX
XX
PF 18-SEP-1995; 95US-00529878.
XX
XX
PR 09-FEB-1995; 95US-00387041.
PR 18-SEP-1995; 95US-00529878.
XX
XX
PA (TAMR/) TAM R C.
XX
XX
PI Tam RC;
XX
XX
PI WPI; 1996-384228/38.
XX
XX
PT Oligo:nucleotide which reduces CD28 gene expression in T cells - for
PT treating immune system diseases, e.g. graft vs. host disease, septic
PT shock, psoriasis, etc.
XX
XX
PS Example; Col 15; 45pp; English.
XX
XX
CC The present invention describes a method for inhibiting the expression of
CC CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises
CC subcutaneous administration of an oligonucleotide (OGN). AAX90288 to
CC AAX90291 represent specifically claimed OGNs for use in the method. The
CC OGNs are used for the treatment of immune system-mediated diseases.
CC AAX90292 to AAX90323 represent oligonucleotides used in the
CC exemplification of the present invention
XX
XX
SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 TACAGCGGTGAGCCAC 887
DB 18 TACAGCGGTGAGCCAC 3
XX
XX
RESULT 1691
AB209942/c
ID AB209942 standard; DNA; 18 BP.
XX
XX
AC AB209942;
XX
XX
DT 16-JAN-2003 (first entry)
XX
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #82.
XX
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
PN WO20027272-A2.
XX
XX
PD 03-OCT-2002.
XX
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
XX
PA (EPIC-) EPIGENOMICS AG.
XX
XX
PI Berlin K, Braun A, Dieltier J, Guetig D, Howe A, Mueller J;

```


PI Olek A, Piepenbrock C, Adorian P, Grabs G, Iesche R, Leu E, Pelet C,
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C,
PI Schwobe I, Ziebarth H;
XX
XX
XX WPI; 2003-018942/01.
XX
XX
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX
XX Claim 37; SEQ ID NO 82; 117bp; English.
XX
XX
XX The present invention describes a method for detecting and
CC differentiating between hematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB211118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy hematopoietic cells and proliferative
CC disorder hematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of hematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC hematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of hematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
XX
XX Sequence 18 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 967 ATCTGGCTCACTGCA 982
Db 16 ATCTGGCTCACTGCA 1
XX
XX
XX RESULT 1692
ADOS6481
ID ADO56481 standard; DNA; 18 BP.
XX
XX
XX ADO56481;
AC
XX
XX 12-AUG-2004 (first entry)
DT
XX
XX
XX Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #6.
DE
XX
XX
XX gene therapy; human; ss; melanoma;
KM melanoma associated polymorphic variation; SNP;
KW single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
XX
XX
XX Homo sapiens.
OS
XX
XX W02004044164-A2.
PN
XX
XX 27-MAY-2004.
PD
XX
XX 06-NOV-2003; 2003WO-US035879.
PF
XX
XX 06-NOV-2002; 2002US-0424475P.
PR
XX
XX 23-JUL-2003; 2003US-0489703P.
PT
XX
XX (SEQU-) SEQUENOM INC.

PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
XX WPI; 2004-411721/38.
XX
XX
XX Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
XX
XX Example 5; Page 83; 295bp; English.
XX
XX
XX The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
XX
XX
XX Sequence 18 BP; 4 A; 6 C; 6 G; 1 T; 0 U; 1 Other;
SQ
XX
XX Query Match 1.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 873 ACAGGCGTGAAGCCACC 888
Db 1 ACAGGCGTGAAGCCACC 16
XX
XX
XX RESULT 1693
AAV57826/C
ID AAV57826 standard; DNA; 19 BP.
XX
XX
XX AAV57826;
AC
XX
XX 18-NOV-1998 (first entry)
DT
XX
XX
XX Human chromosome 18 PCR primer F for D18S378.
DE
XX
XX
XX Manic-depressive illness; susceptibility; genotype; diagnosis;
KM chromosomal marker; polymorphic marker; chromosome 18; human;
KW myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.
XX
XX
XX Synthetic.
OS
XX
XX Homo sapiens.
OS
XX
XX W09818963-A1.
PN
XX
XX 07-MAY-1998.
PD
XX
XX 28-OCT-1997; 97WO-US019381.
PF
XX
XX 28-OCT-1996; 96US-0029278P.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
XX DeCera-Wadleigh SD, Gershon ES, Badner JA, Goldin LR,
XX Berricini WH, Yoshikawa T, Sanders AR, Esterling LE;
XX
XX WPI; 1998-272247/24.
DR
XX
XX
XX New isolated IMP-18p myo-inositol monophosphatase - used to develop
PT products for determining susceptibility to manic depressive illness and
PT as targets for preventive and therapeutic treatments.
XX
XX
XX Disclosure; Page 3; 118bp; English.

XX Findlay I, Matthews PL, Mulcahy BK;
XX
XX WPI; 2003-381725/36.
XX
XX Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.
XX
XX Claim 36; Page 39; 64pp; English.
XX
XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
SQ Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 635 CTCTGTACCCAGGCT 650
DB 16 CTCTGTACCCAGGCT 1
RESULT 1696
AAH48599/C
ID AAH48599 standard; DNA; 20 BP.
XX
XX AAH48599;
AC
XX
DT 20-SEP-2001 (first entry)
XX
DE Human faecin associated primer SEQ ID 51.
XX
XX Faecin; regulatory sequence; human; dendritic cell; antiviral; tumor;
XX antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
XX immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
XX Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
XX autoimmune disease; transplant rejection; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200151631-A2.
PN
XX
PD 19-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-EP000362.
PF
XX 13-JAN-2000; 2000DE-01001169.
PR 02-MAR-2000; 2000DE-01010188.
XX
XX (RESK/) RESKE-KUNZ A.
PA (ROSS/) ROSS X.
PA (ROSS/) ROSS R.
PA (BROS/) BROS M.
XX
XX Reeske-Kunz A, Ross X, Ross R, Bros M;
XX WPI; 2001-451858/48.
XX

PT New regulatory sequences from the faecin gene, useful for providing
PT dendritic cell-specific expression of e.g. antigens, e.g. for vaccination
PT against tumors and infections.
XX
XX
XX Claim 2b; Page 108; 117pp; German.
XX
XX This invention describes novel regulatory sequences (A) derived from
CC human faecin that provide specific expression in dendritic cells (DC) and
CC which have antiviral, antibacterial, antifungal, antiparasitic, anti-
CC allergic, neurological, immunomodulatory and apoptotic activity. (A) are
CC used to regulate expression of antigens, immunoregulators, antisense
CC sequences etc. in DC-specific fashion. Recombinant DNA, vectors and host
CC cells that contain (A) are useful: (i) in vaccines against viruses,
CC bacteria, fungi, parasites, tumors, allergens and plaques in Creutzfeld-
CC Jakob and Alzheimer's disease; and (ii) for gene therapy of tumors, the
CC allergies, infections, autoimmune diseases and transplant rejection. They
CC can also be provide specific expression of antigens and immunoregulators
CC in DC, for isolation and identification of cell factors and cis-elements
CC from regulatory sequences that mediate DC-specific expression; to
CC determine the degree of maturity of DC and to block transcription
CC factors, by providing binding sites in DC. (A) provide DC-specific
CC expression of nucleic acid under their control, allowing a more specific
CC regulation of the immune response and eliminating the long and laborious
CC purification of DC (since a complete leucocyte population may be
CC transformed), including transformation in vitro. This sequence represents
CC a primer associated with the human faecin gene described in the invention
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 967 ATCTGGCTCACTGCA 982
DB 17 ATCTGGCTCACTGCA 2
RESULT 1697
AAS21754/C
ID AAS21754 standard; DNA; 20 BP.
XX
XX AAS21754;
AC
XX
DT 21-NOV-2001 (first entry)
XX
DE Mouse Survivin antisense oligonucleotide #56.
XX
XX Survivin; human; mouse; cytostatic; antisense oligonucleotide;
XX hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX
XX Mus musculus.
OS
XX
XX WO200157059-A1.
PN
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US002939.
PF
XX 02-FEB-2000; 2000US-00496694.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Ackermann EJ, Swayze EE, Cowseert LM;
XX WPI; 2001-488863/53.
XX
XX Novel antisense compounds for modulating the expression of Survivin and
XX treatment of cancer.
XX
XX Example 18; Page 62; 120pp; English.
XX

CC The invention relates to antisense oligonucleotides targeted to a nucleic
CC acid molecule encoding human Survivin, where the antisense
CC oligonucleotide inhibits the expression of human Survivin. These
CC antisense oligonucleotides are used in the treatment of an animal
CC suffering from a disease or condition associated with Survivin, e.g. a
CC hyperproliferative condition such as cancer, and comprises administering
CC a therapeutically or prophylactically effective amount of the antisense
CC oligonucleotide so that expression of Survivin is inhibited. The
CC oligonucleotides can also be used to treat a human suffering from a
CC disease or condition characterised by a reduction in apoptosis comprising
CC administering the antisense oligonucleotide to a human. In addition, the
CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.
CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the
CC cell cycle, or inhibit the proliferation in a cancer cell by contacting
CC the cell with the antisense oligonucleotide. AA521521-AA521768 represent
CC Survivin nucleic acids, and antisense oligonucleotides targeted to
CC Survivin, used in the method of the invention
SQ Sequence 20 BP; 2 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 884 CCACCCAGCCGCGCTT 899
DB 20 CCACCCAGCCGCGCTT 5
RESULT 1698
AAD25167
ID AAD25167 standard; DNA; 20 BP.
AC AAD25167;
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX
DE Human NOV7b gene expression assessing forward PCR primer.
XX
XX
XX Human; NOV7b; gene therapy; atherosclerosis; cardiomyopathy; leukaemia;
XX neurological; neurodegenerative disease; cell signalling; inflammation;
XX diabetes; seizure; muscular dystrophy; epilepsy; allergy; adenocarcinoma;
XX coagulation disorder; reproductive; respiratory; bone; nephrological;
XX multiple sclerosis; mental depression; gastro-intestinal disease; cancer;
XX urinary system disorder; Addison's disease; migraine; dermatomyositis;
XX bronchitis; PCR primer; ss.
XX
XX
XX Homo sapiens.
XX
XX PN WO200194416-A2.
XX
XX PD 13-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US018675.
XX
XX PR 07-JUN-2000; 2000US-0209927P.
XX PR 07-JUN-2000; 2000US-0209928P.
XX PR 07-JUN-2000; 2000US-0210091P.
XX PR 08-JUN-2000; 2000US-0210208P.
XX PR 08-JUN-2000; 2000US-0210425P.
XX PR 26-JUN-2000; 2000US-0214023P.
XX PR 26-JUN-2000; 2000US-0214150P.
XX PR 29-JUN-2000; 2000US-0215005P.
XX PR 20-FEB-2001; 2001US-0270060P.
XX PR 26-FEB-2001; 2001US-0271623P.
XX PR 26-MAR-2001; 2001US-0278915P.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX MAJUMDER K, SRYTEK KA, TCHERNEV VT, COLMAN SD, PADIGARU M,
PI ZERHUSEN B, GUSEV V, BURGESS C, LI L, MALYANKAR UM, GANGOLLI E,
PI Stone D, MacDougall J, Smithson G, Ellerman K,
XX

DR WPI; 2002-062612/08.
XX
XX Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
PT cardiomyopathy, atherosclerosis, neurological and neurodegenerative
PT diseases.
XX
XX Example 1; Page 168; 189pp; English.
XX
XX The invention relates to isolated nucleic acids encoding polypeptides,
CC designated NOVX polypeptides. The NOVX polypeptide and nucleic acid are
CC useful for treating cardiomyopathy, atherosclerosis, diabetes or a
CC disorder related to cell signal processing and metabolic pathway
CC modulation. The NOVX polypeptide, nucleic acid and antibody are useful
CC for treating or preventing a syndrome, e.g. various tissue/organ
CC inflammation, muscular dystrophy, neurological and neurodegenerative
CC diseases, cardiovascular diseases, coagulation disorders, cancers
CC (leukaemia, adenocarcinoma), multiple sclerosis, respiratory diseases,
CC reproductive disorders, allergy, seizures, mental depression, epilepsy,
CC gastro-intestinal diseases, bone disorders, nephrological disorders,
CC urinary system disorders, immunological disorders, Addison's disease,
CC migraine, dermatomyositis and bronchitis. The present sequence is a PCR
CC primer used for assessing human NOV7b gene expression. Note: The present
CC sequence is incorrectly referred as SEQ ID NO: 75 in page 168 of the
CC specification
SQ Sequence 20 BP; 5 A; 1 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 473 GGATGAGTGCAGTGG 488
DB 3 GGATGAGTGCAGTGG 18
RESULT 1699
ADD71348/C
ID ADD71348 standard; DNA; 20 BP.
XX
XX ADD71348;
XX
XX AC ADD71348;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE GFAT 1 gene intron 3 polymorphism PCR primer #13.
XX
XX
XX diabetes; haplotype; polymorphism; diagnosis; renopathy; intron;
XX KW glutamine:fructose-6-phosphate amide transferase 1; ss; primer.
XX
XX OS Homo sapiens.
XX
XX PN WO2003023063-A1.
XX
XX PD 20-MAR-2003.
XX
XX PF 06-SEP-2002; 2002WO-JP009093.
XX
XX PR 07-SEP-2001; 2001JP-00271870.
XX PR 28-MAR-2002; 2002JP-00090861.
XX
XX PA (SANY) SANKYO CO LTD.
XX
XX PI Itakura M, Yasuno H, Watanabe I;
XX
XX DR WPI; 2003-313261/30.
XX
XX Judging relative onset risk of diabetes including type I or II diabetes
PT and renopathy with or without type II diabetes accompanying, by detecting
PT haplotype with gene polymorphism from human genomic DNA.
XX
XX Example 2; SEQ ID NO 20; 157pp; Japanese.
XX

```
CC The invention relates to a method of judging the onset risk of diabetes
CC comprising detecting a haplotype consisting of gene polymorphism at 1 or
CC more positions selected from (a)-(h) from a specimen containing human
CC genomic DNA supplied by a patient: (a) the nucleotide located at position
CC 36 of the intron 1 on GFAT1 (glutamine:fructose-6-phosphate amidase
CC transferase 1) gene (nucleotide number 632 in sequence ADD71339; (b) the
CC nucleotide located at position 7 of the intron 11 on GFAT1 gene
CC (nucleotide number 266 in sequence ADD71330; (c) the nucleotide located
CC at position -147 of the intron 12 on GFAT1 gene (nucleotide number 338 in
CC sequence ADD71331; (d) the nucleotide located at positions 1853-1877 of
CC the intron 8 on GFAT1 gene (nucleotide numbers 336-360 in sequence
CC ADD71332; (e) the nucleotide located at positions 1988-2007 of the intron
CC 12 on GFAT1 gene (nucleotide numbers 328-347 in sequence ADD71333; (f)
CC the nucleotide located at position -11 to -22 of the intron 18 on GFAT1
CC gene (nucleotide numbers 253-264 in sequence ADD71334; (g) the nucleotide
CC located at positions 2632-2661 of the intron 3 on GFAT1 gene (nucleotide
CC numbers 237-266 in sequence ADD71335; and (h) the nucleotide located at
CC position 66 of the intron 18 on GFAT2 gene (nucleotide number 225 in
CC sequence ADD71351). The method is useful for judging relative onset risk
CC of diabetes including type I or II diabetes and renopathy with or without
CC type II diabetes accompanying. This sequence represents a PCR primer used
CC to amplify intron 3 of the GFAT1 gene in order to determine polymorphisms
CC in the sequence.
XX
SQ Sequence 20 BP; 8 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 20;
Best local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 778 TTTTGTAGAGATGGG 793
Db 16 TTTTGTAGAGATGGG 1
RESULT 1700
ADL24993/c
ID ADL24993 standard; DNA; 20 BP.
XX
AC ADL24993;
XX
DT 20-MAY-2004 (first entry)
XX
DE Intestinal epithelium/peyer's patch M cell-associated PCR primer #138.
XX
KW Intestinal epithelium cell development; peyer's patch M cell development;
KW inflammatory bowel disease; gluteenteropathy; infectious disease;
KW autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
KW immune system disorder; hypersensitivity; anaphylaxis;
KW blood group incompatibility; ss; human; PCR; primer.
XX
OS Homo sapiens.
XX
PN WO200208052-A2.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002MO-US010873.
XX
PR 04-APR-2001; 2001US-0281416P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
XX
DR WPI; 2003-075470/07.
XX
PT Novel isolated or purified polypeptide encoded by genes associated with
PT intestinal epithelium or M cell development, differentiation or function,
PT useful for treating autoimmune diseases and infectious diseases.
XX
PS Disclosure; SEQ ID NO 503; 15zbp; English.
```

```
XX
XX The invention comprises DNA sequences which are associated with
CC Intestinal epithelium and peyer's patch M cells. The DNA sequences of the
CC invention are useful for assessing, modifying, modulating or regulating
CC intestinal epithelium or M cell development. The DNA sequences of the
CC invention are also useful in the treatment of: inflammatory bowel
CC disease, gluteenteropathy, infectious diseases, autoimmune diseases
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
CC diseases or disorders of the immune system, hypersensitivity,
CC anaphylaxis, and blood group incompatibility. The present DNA sequence
CC represents a PCR primer in the treatment of intestinal
CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 16; DB 1; Length 20;
Best local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 393 TGCTGGGATTACAGGC 408
Db 20 TGCTGGGATTACAGGC 5
RESULT 1701
ADOB81026/c
ID ADOB81026 standard; DNA; 20 BP.
XX
AC ADOB81026;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human prion protein microsatellite locus primer #22.
XX
KW gene typing; polymorphic microsatellite loci; PMU;
KW disease predisposition; microsatellite marker; prion disease;
KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW milk protein; hormone; transcription factor; p7-blue-vector; human;
KW microsatellite; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN DE10236711-A1.
XX
PD 26-FEB-2004.
XX
PF 09-AUG-2002; 2002DE-01036711.
XX
PR 09-AUG-2002; 2002DE-01036711.
XX
PA (UYHO-) UNIV HOHENHEIM.
XX
PI Geldermann H, Preuss S, Han Y;
XX
DR WPI; 2004-215730/21.
XX
PT Typing genes that contain polymorphic microsatellite loci, useful for
PT identifying predisposition to disease, by amplification and determining
PT length of amplicons.
XX
PS Example 3; Page 34; 64pp; German.
XX
XX The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PMU). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PMU, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (MM) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PMU; and prediagnosis (M3) of diseases associated with gene that
CC include PMU. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
```

CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins,
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a primer used to genotype a region of the human prion
CC protein (PrP) comprising a polymorphic microsatellite locus.

CC Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 AATCTTGCTCACTGC 681
DB 16 AATCTTGCTCACTGC 1

RESULT 1702

ABV77328/C
ID ABV77328 standard; DNA; 41 BP.

XX AC ABV77328;

DT 07-FEB-2003 (first entry)

DE Human protein 10.01 related probe 1.

KM Human; 10.01; aminolase active site; arrhythmia; diabetes; probe; ss.

XX OS Homo sapiens.

XX PN CN1342770-A.

XX PD 03-APR-2002.

XX PF 12-SEP-2000; 2000CN-00125186.

XX PR 12-SEP-2000; 2000CN-00125186.

XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX PI Mao Y, Xie Y;

DR WPI; 2002-529811/57.

PT New human protein 10.01 containing Phe-His aminolase active site and
PT encoding polynucleotide, useful for treating arrhythmia and diabetes.

XX Example 7; Page 21 (disclosure); 33pp; Chinese.

CC The invention relates to a human protein designated 10.01, containing the
CC Phe-His aminolase active site. Also disclosed are the encoding
CC polynucleotide, and a method for preparing the polypeptide by DNA
CC recombination. The application of the polypeptide is in treating
CC arrhythmia and diabetes. Also disclosed are the antagonist against this
CC polypeptide and its therapeutic action, and the application of the
CC polynucleotide. The current sequence represents a human protein 10.01
CC related probe sequence

CC Sequence 41 BP; 6 A; 16 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 41;

Best Local Similarity 68.8%; Pred. No. 2.1e+03;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 651 GGAGTGCAGTGGCGCAATCTTGCTCACTGCA 682
DB 32 GGCTTGCACTGAACCAAGATGGCGCACTGCA 1

RESULT 1703

AA173524/C
ID AA173524 standard; DNA; 51 BP.

XX AC AA173524;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:465.

KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.

XX OS Homo sapiens.

XX PN WO200140521-A2.

XX PD 07-JUN-2001.

XX PF 30-NOV-2000; 2000WO-US032758.

XX PR 30-NOV-1999; 99US-0168138P.

XX PR 29-NOV-2000; 2000US-00726173.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.

XX Claim 1; Page 196; 263pp; English.

CC AA173060 to AA173867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

CC Sequence 51 BP; 10 A; 14 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 1.6%; Score 16; DB 1; Length 51;

Best Local Similarity 68.8%; Pred. No. 2e+03;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 817 TCTTGATCTCTGACCTTGATCTGCTGCC 848
DB 51 TCATGAGTGCAGAGATTGAGACGAGCCTGCC 20

RESULT 1704

AA082623/C
ID AA082623 standard; DNA; 19 BP.

XX AC AA082623;

DT 25-MAR-2003 (revised)

DT 14-SEP-1995 (first entry)
 XX Chromosome 11 (locus D11S964) STS primer UT544a.
 DE
 XX
 XX sequence sampled mapping; genomic analysis; complex genome mapping;
 KM cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9429486-A1.
 XX
 PD 22-DEC-1994.
 XX
 XX 15-JUN-1994; 94WO-US006810.
 PF
 XX 15-JUN-1993; 93US-00078471.
 PR
 PR 07-SEP-1993; 93US-00117952.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Evans GA, Smith MW;
 XX
 DR WPI; 1995-036508/05.
 XX
 XX Sequencing complex genomes, present as fragments in a cosmid library - by
 PT sequencing end-specific nucleotides of each clone then correlating with
 PT spatial relationship of cosmid, esp. for mammalian chromosomes.
 XX
 PS Example 4; Page 90; 128pp; English.
 XX
 CC Sequences were determined from the ends of chromosome 11-specific cosmids
 CC by automated sequencing without intermediate subcloning. A sample of 371
 CC DNA sequence fragments were determined and of these, 277 were suitable
 CC for STS primer prediction by computer analysis (using the "Primer"
 CC program available from E. Lander, MIT). The STSs and cosmids were mapped
 CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
 CC this method, 370 STSs specific for human chromosome 11 were generated and
 CC most of them were regionally mapped. This procedure illustrates a novel
 CC method for sequencing complex genomes, designated "sequence sampled
 CC mapping". The sequence sampled mapping method is useful for the
 CC completion of high density sequence-based maps, and ultimately, for the
 CC complete sequencing of genomic DNA directly from cosmid clones. See
 CC AA082001-082706 and AA091325-091358 for STS primers. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 1.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 637 CTGTCACCGAGCGTGAAGT 655
 DB 19 CTGTCACCGAGCGTGAAGT 1
 RESULT 1705
 AAQ75552
 ID AAQ75552 standard; DNA; 19 BP.
 XX
 AC AAQ75552;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PF
 XX 16-APR-1993; 93JP-00112515.
 PR
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESCO files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 429 TTTATTTTATTTTAA 447
 DB 1 TTTATTTTATTTTAA 19
 RESULT 1706
 AAQ95836
 ID AAQ95836 standard; DNA; 19 BP.
 XX
 AC AAQ95836;
 XX
 DT 20-FEB-1996 (first entry)
 XX
 DE Primer B (Group 10, set C) for marker D13S164, chromosome 13.
 XX
 KM primer; polymerase chain reaction; PCR; linkage study; locus;
 KM microsatellite marker sequence; automated genotyping; allele;
 KM polymorphism; detection; Homo sapiens; ss.
 XX
 OS Synthetic.
 XX
 PN WO9515400-A1.
 XX
 PD 08-JUN-1995.
 XX
 XX 05-DEC-1994; 94WO-US013945.
 PF
 XX 03-DEC-1993; 93US-00160837.
 PR
 XX (UJJO) UNIV JOHNS HOPKINS.
 PA
 XX
 PI Levitt RC;
 XX
 DR WPI; 1995-215278/28.
 XX
 XX Kit for automated genotyping contg. pairs of PCR primers - designed to
 PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
 PT with a characteristic fluorescence label, useful e.g. in detection of
 PT disease related genetic rearrangement.
 XX
 PS Disclosure; Fig 7J-3; 104pp; English.
 XX
 XX The method aims to provide a collection of highly reproducible

QY 657 CAGTGGCGCATCTTGCT 675
DB 19 CAGTGGCGCATCTTGCT 1
RESULT 1709
AAV85747/c
ID AAV85747 standard; DNA; 19 BP.
XX
XX AAV85747;
AC
XX 10-FEB-1999 (first entry)
XX
XX LRP5 exon primer 57-1 1r.
DE
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX insulin dependent diabetes mellitus; autoimmune disease;
XX glomerulonephritis; inflammation; viral infection; osteoporosis;
XX hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX PCR primer; ss.
OS Synthetic.
OS Homo sapiens.
XX WO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WEL) WELICOME TRUST LTD.
XX (MERI) MERCK & CO INC.
XX
XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
XX Phillips MS, Twells RCU;
XX WPI; 1998-594573/50.
XX
XX New isolated LDL-receptor related protein - used to develop products for
XX treating, e.g. elevated triglyceride levels, diabetes, autoimmune
XX disorders, inflammation or Alzheimer's disease.
XX
XX Claim 12; Page 105; 200pp; English.
XX
XX The present invention describes LRPS (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV85587 to
XX AAV85822 represent exon primers used for obtaining LRPS cDNA. Nucleic
XX acid molecules (NMs) encoding LRPS can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NMs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRPS may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 751 CACGACGCTGCTAATTT 769
DB 19 CACGACGCTGCTAATTT 1

QY 657 CAGTGGCGCATCTTGCT 675
DB 19 CAGTGGCGCATCTTGCT 1
RESULT 1710
AAV85825/c
ID AAV85825 standard; DNA; 19 BP.
XX
XX AAV85825;
AC
XX 10-FEB-1999 (first entry)
XX
XX LRP5 SNP primer 57-1 1r.
DE
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX insulin dependent diabetes mellitus; autoimmune disease;
XX glomerulonephritis; inflammation; viral infection; osteoporosis;
XX hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX PCR primer; ss.
OS Synthetic.
OS Homo sapiens.
XX WO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WEL) WELICOME TRUST LTD.
XX (MERI) MERCK & CO INC.
XX
XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
XX Phillips MS, Twells RCU;
XX WPI; 1998-594573/50.
XX
XX New isolated LDL-receptor related protein - used to develop products for
XX treating, e.g. elevated triglyceride levels, diabetes, autoimmune
XX disorders, inflammation or Alzheimer's disease.
XX
XX Claim 12; Page 110; 200pp; English.
XX
XX The present invention describes LRPS (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV85823 to
XX AAV85900 represent SNP primers used for obtaining LRPS cDNA. Nucleic acid
XX molecules (NMs) encoding LRPS can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NMs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRPS may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 751 CACGACGCTGCTAATTT 769
DB 19 CACGACGCTGCTAATTT 1
RESULT 1711
AAV85662/c

```
ID AAV85662 standard; DNA; 19 BP.
XX
XX AAV85662;
AC
XX 10-FEB-1999 (first entry)
DT
XX LRP5 exon primer Elx1 1f.
DE
XX LRP5 exon primer Elx1 1f.
DE
XX LRP5: LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KM insulin dependent diabetes mellitus; autoimmune disease;
KM glomerulonephritis; inflammation; viral infection; osteoporosis;
KM hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
KM PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9846743-A1.
PN
XX 22-OCT-1998.
PD
XX 15-APR-1998; 98WO-GB001102.
PF
XX 15-APR-1997; 97US-0043553P.
PR 05-JUN-1997; 97US-0048740P.
XX
XX (WELL ) WELLCOME TRUST LTD.
PA (MERI ) MERCK & CO INC.
XX
XX Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzger ML, Nakagawa Y;
PI Phillips MS, Twells RCJ;
XX
XX WPI; 1998-594573/50.
DR
XX New isolated LDL-receptor related protein - used to develop products for
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT disorders, inflammation or Alzheimer's disease.
XX
XX Claim 12; Page 102; 200pp; English.
PS
XX The present invention describes LRP5 (low density lipoprotein (LDL)
CC receptor related protein, previously designated LRP-3). AAV85587 to
CC AAV55822 represent exon primers used for obtaining LRP5 cDNA. Nucleic
CC acid molecules (NMs) encoding LRP5 can be used for determining if an
CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).
CC The NMs or proteins can be used for reducing triglyceride levels in the
CC serum of an individual. Therapies that affect LRP5 may also be useful in
CC the treatment of autoimmune diseases such as glomerulonephritis, diseases
CC and disorders involving disruption of endocytosis and/or antigen
CC presentation, cytokine clearance and/or inflammation, viral infection,
CC pathogenic bacterial toxin contamination, elevation of free fatty acids
CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
CC disease and cardiovascular disease. Products from the present invention
CC can also be used for detection, diagnosis and drug screening
XX
XX Sequence 19 BP; 6 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
DT 14-DEC-1998 (first entry)
XX
XX Aminoxy-modified oligonucleotide.
DE
XX phosphorochiote; ras gene; malignant cell growth; aminoxy-modified;
XX nuclease resistance; reporter group; ss.
KM
XX Synthetic.
OS
XX Key Location/Qualifiers
FH modified_base 15..18
FT /*tag= a
FT /note= "5-methyl, 2'-aminoxyethoxy-thymidine"
XX
XX WO9835978-A1.
PN
XX 20-AUG-1998.
PD
XX 13-FEB-1998; 98WO-US002405.
PF
XX 14-FEB-1997; 97US-0037143P.
PR 30-JAN-1998; 98US-00016520.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Cook PD, Manoharan M, Kawasaki AM;
PI WPI; 1998-568232/48.
XX
XX New aminoxy-modified oligonucleotides - which can show improved binding
PT to complementary strands and improved resistance to nuclease.
XX
XX Disclosure; Page 84; 131pp; English.
PS
XX The invention relates to aminoxy-modified(oligo)nucleotides or
CC nucleosides which are useful as therapeutics, diagnostics, and research
CC reagents. They may be used, e.g., for modulation of the ras gene and may
CC be able to modulate the process of transformation from normal to
CC malignant cell growth. They may be prepared using known methods.
CC Inclusion of the aminoxy moieties can improve binding of
CC oligonucleotides to complementary strands. The moieties can also provide
CC conjugation sites useful for conjugation of useful ligands (e.g. reporter
CC groups and groups for modifying uptake, distribution or other
CC pharmacodynamic properties) to oligonucleotides. The present sequence
CC represents an example of an aminoxy-modified oligonucleotide disclosed
CC in the specification
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 427 TTTTATTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTTATTTT 19
```

RESULT 1713
AAV06820
ID AAV06820 standard; DNA; 19 BP.
XX
XX AAV06820;
AC
XX 13-OCT-1998 (first entry)
DT
XX Oligonucleotide containing modified internucleotide linkage.
DE
XX oligonucleotide; ss.
KM
XX Synthetic.
OS
XX Key Location/Qualifiers
FH

```

FT modified_base 16..18 /+tag= a
FT /note= "these T residues are formed as part of a
FT conventional phosphoramidite oligonucleotide synthesis
FT process but using as the reactant a thymosine nucleoside
FT having at the 3'-position a group of formula -CH2-
FT P(OCH2CH2CN)-N(iPr)2"
XX
XX
XX WO9747636-A2.
XX
XX
XX 18-DEC-1997.
XX
XX PF 03-JUN-1997; 97WO-GB001490.
XX
XX PR 13-JUN-1996; 96GB-00012600.
XX
XX PA (NOVS ) NOVARTIS AG.
XX
XX PI Collingwood SP, Moser HE, Altmann K, Douglas ME;
XX WPI; 1998-052233/05.
XX
XX PT New tetrahydrofuran derivatives - useful in the synthesis of
XX oligo:nucleotide(s).
XX
XX PS Example 12; Page 29; 37pp; English.
XX
CC The invention relates, inter alia, to a method of preparing an
CC oligonucleotide by coupling (1) a new nucleoside having a protected 5' -
CC hydroxy group and at the 3'-position a group of formula -CH2-P(OR3) -
CC NRxR5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy
CC group, to give (3) a precursor having an internucleoside linkage of
CC formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-
CC P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific
CC example of an oligonucleotide so prepared
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0,
OY 427 TTTTATTATTTATTTTTTT 44S
DB 1 TTTTATTTTATTTTATTTT 19
RESULT 1714
AAxB1316
ID AAxB1316 standard; DNA; 19 BP.
XX
XX AC AAxB1316;
XX
XX DT 20-AUG-1999 (first entry)
XX
XX DE 5' amino oligonucleotide probe T-2.
XX
XX KW Microelectronic device; multi-step reaction; microscopic format;
XX ion-permeable permeation layer; electrode; electrical control; transport;
XX attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_feature 1
XX FT /+tag= a
XX FT /note= "amino group attached at 5' terminal"
XX
XX PN WO9929711-A1.
XX
XX PD 17-JUN-1999.
XX
XX XX 01-DEC-1998; 98WO-US025475.

```

```

XX 05-DEC-1997; 97US-00986065.
XX PR (NANO-) NANOGEN INC.
XX PA Sosnowski RG, Butler WF, Tu E, Nerenberg MT, Heller MJ, Edman CF,
XX PI WPI: 1999-385567/32.
XX DR
XX PT New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX PS Example 1, Page 90; 179pp; English.
XX CC The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this inventions is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific binding
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence represents a probe used to exemplify the invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 427 TTTTACTTTATTTTTTTT 445
XX 1 TTTTATTTTTTTTTTTT 19
XX
XX RESULT 1715
XX AAX36671/C
XX ID AAX36671 standard; DNA; 19 BP.
XX AC AAX36671;
XX XX
XX DT 13-JUL-1999 (first entry)
XX XX
XX PCR primer for marker D6S967.
XX XX
XX PCR primer; detection; glaucoma allele; haplotype analysis; human; GLC1B;
XX chromosome 2; chromosome 6; GLC6p25; haplotype profile;
XX KW presymptomatic glaucoma; symptomatic glaucoma; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9916899-A2.
XX XX
XX PD 08-APR-1999.
XX XX
XX PF 29-SEP-1998; 98WO-CA000924.
XX XX
XX PR 30-SEP-1997; 97CA-02217097.
XX XX
XX PA (UYLA-) UNIV LAVAL.
XX XX

```

PI Raymond V, Morissette J, Falardeau P, Cole G, Ancill J;
XX WPI; 1999-263704/22.
XX
XX Haplotype analyses for indirect detection of glaucoma.
XX
XX Claim 18; Page 28; 41pp; English.
XX
CC This sequence represents a PCR primer used in the method of the
CC invention. The method is for detecting the presence of alleles for
CC glaucoma comprising haplotype analysis of human chromosome 2 and 6
CC respectively, where the haplotypes are associated with loci GLC1B and
CC GLC6P25 respectively. The primers are used to amplify gene sequences to
CC generate information necessary to compile haplotype profiles. The
CC haplotype profiles can be used to detect presymptomatic and symptomatic
CC glaucoma. They can also be used to localise, isolate and identify the
CC GLC1B and GLC6P25 loci so that detection of individuals with glaucoma is
CC enhanced. The haplotype analyses also provide means for identification
CC and following of mutant alleles in pedigrees or populations.
CC Identification of presymptomatic individuals using the methods allows
CC intervention in the disease process and obviates the impact of inheriting
CC a mutant allele causing disease, by medically disrupting the initiation
CC or progression of the disease
CC
SQ Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 634 ACTCTGTACCCAGGCTGG 652
DB 19 ACTCTGTCCCAAGCTGG 1
RESULT 1716
AAZ01927
ID AAZ01927 strand; DNA; 19 BP.
XX
XX AAZ01927;
AC
XX
XX 07-SEP-1999 (first entry)
DT
XX
XX Polynucleotide strand with amino groups.
DE
XX
XX Enzyme-specific cleavable polynucleotide substrate;
XX quenched fluorescent moiety; biological assay; detection; identification;
XX microorganism; sterilization assurance; nuclease; ss.
XX
XX Synthetic.
OS
XX
XX Key
FH Location/Qualifiers
FT modified_base 7
FT /tag= a
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dT) "
FT modified_base 9
FT /tag= b
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dT) "
FT modified_base 11
FT /tag= c
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dT) "
FT modified_base 13
FT /tag= d
FT /note= "amine-modified C6 derivative of deoxythymidine
FT (dT) "
XX
XX WO9935288-A1.
XX
XX 15-JUL-1999.
XX

PF 20-AUG-1998; 98WO-US017311.
XX
XX
XX 09-JAN-1998; 98US-00005260.
XX
XX (MINN) MINNESOTA MINING & MFG CO.
XX
XX Wei A, Mach PA;
XX
XX WPI; 1999-419356/35.
XX
XX
XX An enzyme-specific cleavable polynucleotide substrate bearing quenched
XX fluorescent moieties.
XX
XX Example 2; Page 20; 34pp; English.
XX
XX The specification describes an enzyme-specific cleavable polynucleotide
XX substrate bearing quenched fluorescent moieties. The enzyme-specific
XX cleavable polynucleotide substrate is useful in biological assays for
XX detection and identification of microorganisms, sterilization assurance,
XX pharmaceutical discovery, enzyme assays, immunoassays and other
XX biological assays. The method provides a rapid and convenient approach
XX for detection and identification of microorganisms. It can be adapted to
XX sequence-dependent or sequence-independent tests. The invention provides
XX improved accuracy, faster detection, and overall lower cost in detection
XX and identification of microorganisms. The presence of nuclease is
XX measured more accurately and sensitively by red-shifting the emission
XX wavelength from far UV region (350-400 nm) to the 500-600 nm region of
XX the electromagnetic spectrum and reducing the effect of background signal
XX levels of intact reagents. The present sequence is used in the course of
XX the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19
RESULT 1717
AAZ01358
ID AAZ01358 strand; DNA; 19 BP.
XX
XX AAZ01358;
AC
XX
XX 27-SEP-1999 (first entry)
DT
XX
XX PCR primer for PGI biallelic marker 4-4-187.
DE
XX
XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
XX cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
XX PSA; human; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX
XX WO9932644-A2.
XX
XX 01-JUL-1999.
XX
XX 22-DEC-1998; 98WO-1B002133.
XX
XX 22-DEC-1997; 97US-00996306.
XX
XX 09-SEP-1998; 98US-0099658P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I, Bougueleret L,
XX
XX WPI; 1999-405178/34.
XX

XX Use of a prostate cancer associated gene and biallelic markers derived
PT from it.
XX
XX
PS Claim 4; Page 374; 385pp; English.
XX
CC The invention relates to a mammalian PGI gene and protein, and a set of
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
CC used in a hybridisation assay, a sequencing assay, or in an allele-
CC specific amplification assay for determining the identity of a nucleotide
CC at a PGI-related biallelic marker. The methods can be used to detect and
CC to assess the risk of developing cancer or prostate cancer. Early-stage
CC diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC dosage. However, the effectiveness of this is limited due to its
CC inability to discriminate between malignant and non-malignant affections
CC of the organ. A need exists for both a reliable diagnostic procedure
CC which would enable early-stage diagnosis, and for preventative and
CC curative treatments of the disease. The PGI gene can be used for
CC detection of prostate cancer, and the risk of developing it in the
CC future, and can also be used to determine therapies for the disease
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 19
RESULT 1718
AAZ61390
ID AAZ61390 standard; DNA; 19 BP.
XX
AC AAZ61390;
XX
DT 19-JUN-2000 (first entry)
XX
DE Uniform phosphodiester oligonucleotide.
XX
KM Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KM nuclease resistance; phosphodiester; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /note= "2'-modified T"
FT modified_base 17
FT /*tag= b
FT /note= "2'-modified T"
FT modified_base 18
FT /*tag= c
FT /note= "2'-modified T"
FT modified_base 19
FT /*tag= d
FT /note= "2'-modified T"
XX
XX WO300008044-A1.
XX PN 17-FEB-2000.
XX PD
XX PF 06-AUG-1999; 99WO-US017895.
XX PF
XX PR 07-AUG-1998; 98US-00130566.
XX PR
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD;
XX

DR WPI: 2000-205668/18.
XX Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT used in diagnostic, therapeutic and research reagents.
XX
XX
PS Disclosure; Page 44; 60pp; English.
XX
CC The present sequence represents an uniform phosphodiester
CC oligonucleotide. The specification describes oligomeric compounds
CC containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
CC nucleosides include ring structures that position the sugar moiety of the
CC nucleosides preferentially in 3' endo geometries. The modified oligomeric
CC compounds have increased binding affinity and increased nuclease
CC resistance. The oligomeric compounds can be used in diagnostic,
CC therapeutic and research reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 19
RESULT 1719
AAZ61404
ID AAZ61404 standard; DNA; 19 BP.
XX
AC AAZ61404;
XX
DT 19-JUN-2000 (first entry)
XX
DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
XX
KM Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KM nuclease resistance; phosphorothioate; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH misc_feature 1..19
FT /*tag= a
FT /note= "nucleosides linked by phosphodiester linkages"
FT modified_base 16..19
FT /*tag= b
FT /note= "2'-O-[2-N,N-dimethylaminoethyl]oxyethyl-5- methyl
FT uridine"
XX
XX WO300008044-A1.
XX PN 17-FEB-2000.
XX PD
XX PF 06-AUG-1999; 99WO-US017895.
XX PF
XX PR 07-AUG-1998; 98US-00130566.
XX PR
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD;
XX
XX WPI: 2000-205668/18.
XX DR
XX PT Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides
PT used in diagnostic, therapeutic and research reagents.
XX
XX
PS Disclosure; Page 51; 60pp; English.
XX
CC The present sequence represents an oligomeric compound containing 2'-O-
CC modified ribosyl nucleosides. The oligomeric compound contains
CC phosphodiester linkages. The 2'-O-modified nucleosides include ring

CC structures that position the sugar moiety of the nucleosides preferentially in 3' endo geometries. The modified oligomeric compounds CC have increased binding affinity and increased nuclease resistance. The CC oligomeric compounds can be used in diagnostic, therapeutic and research reagents

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTATTTT 445
Db 1 TTTTATTTATTTATTTT 19

RESULT 1720
AAC62422
ID AAC62422 standard; DNA; 19 BP.

XX AAC62422;

AC 07-FEB-2001 (first entry)

DT T19 diester for use in nuclease stability assay.

DE T19 diester; nuclease stability assay; polymerase chain reaction; PCR;
XX molecular cloning; disease diagnosis; disease treatment; ss.

KW Synthetic.

OS US6127124-A.

PN 03-OCT-2000.

PD 20-JAN-1999; 99US-00234237.

PF 20-JAN-1999; 99US-00234237.

XX 20-JAN-1999; 99US-00234237.

XX (ISIS-) ISIS PHARM INC.

PI Leeds JM, Cummins LJ;

DR WPI; 2000-637737/61.

XX Determining the nuclease stability and relative binding affinity of an
PT oligomeric compound comprises capillary gel electrophoresis using laser-
PT induced fluorescence.

XX Example 3; Col 19-20; 14pp; English.

CC The present invention is concerned with methods of determining the
CC nuclease stability of oligomeric compounds using capillary-gel
CC electrophoresis and laser-induced fluorescence. The methods are useful in
CC the polymerase chain reaction (PCR), molecular cloning and disease
CC diagnosis and treatment. The present sequence was used in a demonstration
CC of the methods of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTATTTT 445
Db 1 TTTTATTTATTTATTTT 19

RESULT 1721
AA295241
ID AA295241 standard; DNA; 19 BP.

XX AA295241;
AC 05-JUN-2000 (first entry)
XX Modified oligonucleotide #3 ISIS # 2211.

XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 2211;
XX research reagent; therapeutic; ss.

OS Synthetic.

XX Key Location/Qualifiers

FX misc_feature

FT /tag= a

FT /note= "Phosphorothioate internucleotide linkage"

FT misc_feature

FT /tag= d

FT /note= "Optionally all phosphorothioate internucleotide linkages"

FT modified_base

FT /tag= c

FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-(2-methoxyethyl)"

FT misc_RNA

FT /tag= d

XX WO200004189-A1.

XX 27-JAN-2000.

XX 13-JUL-1999; 99WO-US015886.

XX 14-JUL-1998; 98US-00115043.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Cook PD;

XX WPI; 2000-182445/16.

XX Novel modified oligonucleotides, useful in antisense methodologies,
PT diagnostics, therapeutics and as research reagents.

XX Example 54; Page 59; 75pp; English.

CC This sequence represents a modified oligonucleotide used in the course of
CC the invention. The invention relates to oligonucleotides comprising
CC nucleotides covalently linked together by internucleotide linkages where
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC can be used in gene therapy and are also useful in antisense
CC methodologies, diagnostics, therapeutics and as research reagents

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTATTTT 445
Db 1 TTTTATTTATTTATTTT 19

RESULT 1722
AA295240
ID AA295240 standard; DNA; 19 BP.

XX AA295240;
AC 05-JUN-2000 (first entry)

```

XX DE Modified oligonucleotide #3 ISIS # 22110.
XX XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
XX KM research reagent; therapeutic; ss.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX FH 1.15
XX FT /*tag= a
XX FT /note= "phosphorothioate internucleotide linkage"
XX FT misc_feature
XX FT 15.19
XX FT /*tag= d
XX FT /note= "Optionally all phosphorothioate internucleotide
XX FT linkages"
XX FT modified_base
XX FT 16.19
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
XX FT (2-methoxyethyl)"
XX PN
XX PD WO200004189-A1.
XX PD 27-JAN-2000.
XX XX
XX PF 13-JUL-1999; 99WO-US015886.
XX PR 14-JUL-1998; 98US-00115043.
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Manoharan M, Cook PD;
XX XX WPI; 2000-182445/16.
XX DR
XX XX
XX PT Novel modified oligonucleotides, useful in antisense methodologies,
XX PT diagnostics, therapeutics and as research reagents.
XX PS
XX PS Example 54; Page 59; 75pp; English.
XX CC This sequence represents a modified oligonucleotide used in the course of
XX CC the invention. The invention relates to oligonucleotides comprising
XX CC nucleotides covalently linked together by internucleotide linkages where
XX CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
XX CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX CC can be used in gene therapy and are also useful in antisense
XX CC methodologies, diagnostics, therapeutics and as research reagents
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. NO. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 427 TTTTATTATTATTTTTTT 445
XX Db 1 TTTTATTATTATTTTTTT 19
XX
XX RESULT 1723
XX ID AAA06839 standard; DNA; 19 BP.
XX AC AAA06839;
XX XX
XX DT 19-JUN-2000 (first entry)
XX XX
XX DE Modified T-containing oligonucleotide, SEQ ID NO:14.
XX XX
XX KM Modified nucleoside; aminoxy group;
XX KM 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
XX KM hybridisation; binding affinity; ss.

```

```

XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base
XX FT 16.19
XX FT /*tag= a
XX FT /note= "These nucleotides are substituted with 2'-O-(2-
XX FT [N-(2-amino)ethyl-N-(methyl)]aminoxyethyl) group"
XX XX
XX PN WO200008042-A1.
XX PD 17-FEB-2000.
XX XX
XX PF 09-AUG-1999; 99WO-US017988.
XX PR 07-AUG-1998; 98US-00130973.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;
XX XX WPI; 2000-224020/19.
XX DR
XX XX
XX PT Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,
XX PT therapeutic and research reagents and for modulating the expression of
XX PT protein in organisms.
XX PS
XX PS Example 99; Page 120; 195pp; English.
XX CC
XX CC The invention relates to aminoxy-modified nucleosides and
XX CC oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
XX CC in a complementary nucleic acid strand. It also relates to
XX CC oligonucleotides wherein at least some of the nucleotides are
XX CC functionalised to be nuclease resistant, at least some of the nucleotides
XX CC include a substituent that potentiates hybridisation of the
XX CC oligonucleotide to a complementary strand, and at least some of the
XX CC nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
XX CC inclusion of one or more aminoxy moieties in such oligonucleotides
XX CC provides for improved binding of such oligonucleotides to a complementary
XX CC strand. The oligonucleotides of the invention are used as diagnostic,
XX CC therapeutic or research reagents, and can be used to modulate gene
XX CC expression in organisms. The oligonucleotides containing the modified
XX CC nucleosides have increased nuclease resistance and increased binding
XX CC affinity to a complementary strand. The present sequence represents an
XX CC oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-
XX CC amino)ethyl-N-(methyl)]aminoxyethyl) group
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. NO. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 427 TTTTATTATTATTTTTTT 445
XX Db 1 TTTTATTATTATTTTTTT 19
XX
XX RESULT 1724
XX ID AAA88952 standard; DNA; 19 BP.
XX AC AAA88952;
XX XX
XX DT 05-MAR-2001 (first entry)
XX XX
XX DE Oligonucleotide ISIS 22115.
XX XX
XX KM Oligonucleotide; nuclease resistance; psoriasis; anti-psoriatic;
XX KM dermatological; cytostatic; virocid; antibacterial; fungicide; therapy;
XX KM diagnosis; DNA-RNA hybrid; ss.
XX OS Synthetic.

```

```
XX Key Location/Qualifiers
FH modified_base 1.15
FT /*tag= f
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT misc_RNA 19
FT /*tag= e
FT /label= RNA
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) uridine"
FT WO2006609-A1.
PN 09-NOV-2000.
XX 03-MAY-2000; 2000WO-US011913.
XX 03-MAY-1999; 99US-00303586.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX Example 54; Page 69; 132pp; English.
XX Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
CC phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
CC used in experiments to determine the effects of snake venom
CC phosphodiesterase and liver homogenate on the stability of
CC oligonucleotides. Novel oligonucleotides of the invention have both A-
CC and B-form conformational geometry. The A-form geometry modulates the
CC binding affinity and nuclease resistance of the oligonucleotide. The B-
CC form geometry allows the oligonucleotide to serve as substrate for RNase-
CC H when bound to a target nucleic acid strand. The oligonucleotides can be
CC used to treat psoriasis and other inflammatory skin conditions, skin
CC cancers and viral, bacterial and fungal infections, and in various
CC diagnostic applications
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
XX ||||| ||||| ||||| |||||
XX 1 TTTTATTTTATTTT 19
XX
XX RESULT 1725
XX ID AAA88965 standard; DNA; 19 BP.
XX
```

```
AC AAA88965;
XX 05-MAR-2001 (first entry)
XX 2'-Modified chimeric oligonucleotide.
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT WO2006609-A1.
PN 09-NOV-2000.
XX 03-MAY-2000; 2000WO-US011913.
XX 03-MAY-1999; 99US-00303586.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX Example 86; Page 102; 132pp; English.
XX This sequence represents 2'-modified chimeric oligonucleotides containing
CC 2'-modified T. The nucleotides were used to examine the effects of the
CC modifications on nuclease resistance. Novel oligonucleotides of the
CC invention have both A- and B-form conformational geometry. The A-form
CC geometry modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
XX ||||| ||||| ||||| |||||
```


Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 1726
ID AAA88949 standard; DNA; 19 BP.
AC AAA88949;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22112.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KM dermatological; cyostatic; virucide; antibacterial; fungicide; therapy;
KM diagnosis; ss.
XX
XX Synthetic.
OS

Key Location/Qualifiers
FH 1. .19
FT modified_base /tag= e
FT /note= "phosphorothioate linkage"
FT 16
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 17
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 18
FT modified_base /tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 19
FT modified_base /tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX W0200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has
CC 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC the effects of snake venom phosphodiesterase and liver homogenate on the
CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX
XX Sequence: 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

427 TTTT TTTT TTTT TTTT TTTT 445
||||| ||||| ||||| ||||| |||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 1727
ID AAA88950 standard; DNA; 19 BP.
AC AAA88950;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22113.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KM dermatological; cyostatic; virucide; antibacterial; fungicide; therapy;
KM diagnosis; DNA-RNA hybrid; ss.
XX
XX Synthetic.
OS

Key Location/Qualifiers
FH 1. .19
FT modified_base /tag= f
FT /note= "phosphorothioate linkage"
FT 16
FT modified_base /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT 17
FT modified_base /tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT 18
FT modified_base /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT 19
FT m1sc_RNA /tag= e
FT /label= RNA
FT modified_base /tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
XX
XX W0200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has
CC 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
CC the effects of snake venom phosphodiesterase and liver homogenate on the

CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
QY Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 427 TTTTATTATTATTATT 445
1 TTTTATTATTATTATT 19
RESULT 1728
ID AAA88951 standard; DNA; 19 BP.
AC AAA88951;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22114.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1.15
FT /*tag= e
FT /note= "phosphorothioate linkage"
FT 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
PN WO200066609-A1.
XX
XX 09-NOV-2000.
PD
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Manoharan M, Mohan V;
PI
XX WPI; 2000-672833/65.
DR
XX
XX
PT New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and

PT bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
PS
XX Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
CC phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
CC used in experiments to determine the effects of snake venom
CC phosphodiesterase and liver homogenate on the stability of
CC oligonucleotides. Novel oligonucleotides of the invention have both A-
CC and B-form conformational geometry. The A-form geometry modulates the
CC binding affinity and nuclease resistance of the oligonucleotide. The B-
CC form geometry allows the oligonucleotide to serve as substrate for RNase-
CC H when bound to a target nucleic acid strand. The oligonucleotides can be
CC used to treat psoriasis and other inflammatory skin conditions, skin
CC cancers and viral, bacterial and fungal infections, and in various
CC diagnostic applications
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
QY Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 427 TTTTATTATTATTATT 445
1 TTTTATTATTATTATT 19
RESULT 1729
ID AAA88947 standard; DNA; 19 BP.
AC AAA88947;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22110.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
PN WO200066609-A1.
XX
XX 09-NOV-2000.
PD
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Manoharan M, Mohan V;
PI
XX

```
XX DR WPI; 2000-672833/65.
XX
XX PT New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX PS Example 54; Page 69; 132pp; English.
XX
CC CC Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 3'-
CC O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC effects of snake venom phosphodiesterase and liver homogenate on the
CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 19
RESULT 1730
AA88948
ID AAA88948 standard; DNA; 19 BP.
XX
XX AC AAA88948;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22111.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; DNA-RNA hybrid; ss.
XX
XX OS Synthetic.
XX
XX FH Key
XX modified_base
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methoxyethyl)thymidine"
XX FT modified_base
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methoxyethyl)thymidine"
XX FT modified_base
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methoxyethyl)thymidine"
XX FT misc_RNA
XX FT /*tag= e
XX FT /label= RNA
XX FT modified_base
XX FT /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methoxyethyl)uridine"
XX
XX PN WO200066609-A1.
XX
XX PD 09-NOV-2000.
XX
```

```
PF 03-MAY-2000; 2000WO-US011913.
XX
XX XX 03-MAY-1999; 99US-00303586.
XX
XX PR (ISIS-) ISIS PHARM INC.
XX
XX PA Manoharan M, Mohan V;
XX
XX PI WPI; 2000-672833/65.
XX
XX DR New oligonucleotides containing sequences with A and B geometry, used to
XX PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX PT bacterial infections, bind to single stranded RNA or DNA.
XX
XX PS Example 54; Page 69; 132pp; English.
XX
XX XX Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-
XX O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 19
RESULT 1731
AA71630
ID AAA71630 standard; DNA; 19 BP.
XX
XX AC AAA71630;
XX
XX DT 14-DEC-2000 (first entry)
XX
XX DE Phosphorothioate 20-mer primer DNA #1.
XX
XX KW Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX
XX OS Synthetic.
XX
XX FH Key
XX modified_base
XX FT 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkage"
XX
XX PN EP1028124-A2.
XX
XX PD 16-AUG-2000.
XX
XX PP 06-SEP-1999; 99EP-00307066.
XX
XX PR 04-FEB-1999; 99US-0118564P.
XX PR 09-APR-1999; 99US-00288679.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL;
XX Guzaev A;
XX
```

DR WPI; 2000-500332/45.
XX Novel method for the production of oligomers with reduced exocyclic
PT adducts comprises treatment with deprotecting and cleaving reagents.
XX
XX Example 2; Page 17; 33pp; English.
XX
CC This invention describes a novel synthetic method (M) comprising: (a)
CC providing a sample comprising a number of oligomers of formula (I); (b)
CC contacting the sample with a deprotecting agent to remove R_t groups from
CC the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC method is used to produce oligomeric compounds for use in antisense and
CC oligonucleotide therapies. The method enables the synthesis of oligomers
CC with a reduction in the number acrylonitrile groups attached.
CC Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC This sequence represents a phosphorothioate 20-mer primer which is used
CC in the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19
Db

RESULT 1732
AAC62454
ID AAC62454 standard; DNA; 19 BP.
XX
AC AAC62454;
XX
DT 07-FEB-2001 (first entry)
XX
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
KM Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 10
FT misc_RNA /*tag= a
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Example 3; Page 34; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-

CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19
Db

RESULT 1733
AAF31458
ID AAF31458 standard; DNA; 19 BP.
XX
AC AAF31458;
XX
DT 10-APR-2001 (first entry)
XX
DE Oligonucleotide ISIS 109989.
XX
KM Gene expression; gene therapy; diagnosis; ss.
KW
OS Synthetic.
XX
PN WO200102423-A2.
XX
PD 11-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018609.
XX
PR 07-JUL-1999; 99US-00349040.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Prakash TP, Mohan V;
DR WPI; 2001-138119/14.
XX
PT Guanidinium functionalized oligomers prepared from corresponding monomer
PT units, are hybridizable with a specific RNA or DNA sequence, useful for
PT diagnostic and therapeutic purposes.
XX
PS Example 26; Page 54; 108pp; English.
XX
CC The present invention relates to nucleotide oligomers comprising monomer
CC units. Oligomers modulate gene expression when hybridized by a single- or
CC double-stranded nucleic acid. They are useful for gene therapy,
CC diagnostic and investigative purposes
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19
Db

RESULT 1734
AAF31564
ID AAF31564 standard; DNA; 19 BP.
XX
AC AAF31564;
XX
DT 09-APR-2001 (first entry)
XX

DE ISIS sequence 32327.
XX DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;
KM atherosclerosis; ss.
XX Synthetic.
OS
PN WO200102419-A1.
XX 11-JAN-2001.
PD
XX 05-JUL-2000; 2000WO-US040304.
PF
XX 07-JUL-1999; 99US-00349033.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Cook PD, Manoharan M, Maier M, An H;
PI WPI; 2001-138117/14.
DR
XX New oligomers for use as research reagent, for treating disease caused by
PT undesired production of proteins, and for diagnosing and treating AIDS,
PT atherosclerosis.
XX
PS Example 46; Page 74; 110pp; English.
XX
CC The present invention relates to C3' methylene hydrogen phosphate
CC oligomers. The oligomers may be used as research reagents, for treating
CC disease caused by undesired production of proteins and for diagnosing and
CC treating AIDS and atherosclerosis
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.7e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTATTTT 445
DB 1 TTTTATTTTUUUU 19
RESULT 1735
AAH56776
ID AAH56776 standard; DNA; 19 BP.
XX
AC AAH56776;
XX
DT 06-SEP-2001 (first entry)
XX
DE S. aureus groE operon antisense oligonucleotide SEQ ID NO:424.
XX
XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
KM microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
KM Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
KM antibacterial; antiviral; antiproliferative; antisense therapy;
KM microbial infection; ss.
XX
OS Staphylococcus aureus.
XX
PN WO200136625-A2.
XX
PD 25-MAY-2001.
XX
XX 20-NOV-2000; 2000WO-CA001347.
PF
XX 18-NOV-1999; 99US-0166249P.
PR
XX (GENE-) GENESENSE TECHNOLOGIES INC.
PA
XX Wright JA, Young AH, Dugourd D;
PI
XX

DR WPI; 2001-355633/37.
XX
XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
PT gene of microorganism, which hybridize with and inhibit expression of the
PT genes, useful to inhibit growth of microorganism having the genes.
XX
PS Claim 3; Page 52; 110pp; English.
XX
XX The present invention specifically claims AAH56368 to AAH56832 which are
CC antisense oligonucleotides to nucleotide sequences encoding groE. More
CC generally, antisense compounds (I) comprising antisense oligonucleotides
CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
CC microorganism, where the antisense compound is complementary to GL or GS
CC of a microorganism and specifically hybridizes with and inhibits the
CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
CC antiproliferative activities, and can be used in antisense therapy and
CC for inhibition of expression of groES or groEL. (I) are useful for
CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
CC also useful for inhibiting the growth of a microorganism, or inhibiting
CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
CC virus) having a GL or GS gene which involves administering to the
CC microorganism or to a cell infected with the microorganism, (I). (I) are
CC also useful for treating a mammalian pathological condition mediated by
CC the microorganisms which involves identifying a eukaryotic organism
CC having a pathological condition mediated by microorganisms having a GL or
CC GS gene and administering (I) such that the growth of microorganisms
CC is inhibited. The antisense compounds are utilized for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
CC prevent or delay microbial infections in humans. They are also useful as
CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
CC represent PCR primers for groE sequences which are used in the
CC exemplification of the present invention. AAH56855 to AAH56870 represent
CC groE nucleotide sequence given in the present invention
XX
SQ Sequence 19 BP; 4 A; 2 C; 2 G; 11 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 604 TTTTATTTATTTTGAG 622
DB 1 TTTTTCACACTTTTGAG 19
RESULT 1736
AAH38442
ID AAH38442 standard; DNA; 19 BP.
XX
AC AAH38442;
XX
DT 14-AUG-2001 (first entry)
XX
XX SNP specific lower PCR primer SEQ ID 1238.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
PF
XX 15-OCT-1999; 99US-016096P.
PR
XX

PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI, 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
PS Claim 1; Page 56; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 248 CTCGGCCTCCCAAGTCT 266
DB 1 CTTGGCCTCCCAAGTCT 19
XX
RESULT 1737
AAH39785/c
ID AAH39785 standard; DNA; 19 BP.
XX
AC AAH39785;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 2581.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000MO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P..

XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI, 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
PS Claim 1; Page 63; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1089 GGCGGGTTTCACCATATT 1107
DB 19 GACGGGGTTTCACCATGTT 1
XX
RESULT 1738
AAH40317/c
ID AAH40317 standard; DNA; 19 BP.
XX
AC AAH40317;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific upper PCR primer SEQ ID 3113.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000MO-US028436.
XX
PR

PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX Picoult-Newburg L, Pohl M;
PI
XX WPI; 2001-290930/30.
DR
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 65; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNP) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leach-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
XX
SQ Sequence 19 BP; 5 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 674 CTCACGCAACCTCGCT 692
DB 19 CTTACTGCACCTCGCT 1
RESULT 1739
AAH46460
ID AAH46460 standard; DNA; 19 BP.
XX
XX AAH46460;
AC
XX
XX 14-SEP-2001 (first entry)
DT
XX
XX Oligonucleotide #8.
DE
XX
XX Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
KM
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1.19
FT modified_base
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All bases are phosphorothioate"
FT modified_base
FT 1
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Modified with 2'-O-methoxyethyl"

PN US6242591-B1.
XX \$
XX 05-JUN-2001.
PD
XX
XX 11-JAN-2000; 2000US-00481486.
PF
XX
XX 15-OCT-1997; 97US-00950779.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Cole DL, Ravikumar VT, Chervuallach ZS;
PI
XX WPI; 2001-407218/43.
DR
XX
XX
XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
PT useful in biological research, comprises phosphorylating the 5'-hydroxyl
PT of a nucleic acid having a nucleoside with a 2' modification.
XX
XX Example 12; Col 7, 7pp; English.
XX
XX The present invention relates to a method for preparing phosphorothioate
CC oligonucleotides having at least one nucleoside with a 2' modification.
CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
CC group having at least one nucleoside with a 2' modification in an
CC acetonitrile. The present sequence was used to illustrate the method of
CC the present invention. The method is useful for synthesizing sulphurised
CC 2' substituted phosphorothioate oligonucleotides, which may be used in
CC molecular biological research, in applications such as anti-viral
CC therapy, and for determining the stereochemical pathways of certain
CC enzymes which recognise nucleic acids
XX
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTATTTT 445
DB 1 TTTTATTTT 19
RESULT 1740
AAH25737
ID AAH25737 standard; DNA; 19 BP.
XX
XX AAH25737;
AC
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX Human type II RNase H substrate oligonucleotide #4.
DE
XX
XX Human RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KM gene therapy; primer; phosphorothioate backbone; ss.
RW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1.19
FT modified_base
FT /*tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base
FT 16.19
FT /*tag= b
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT methoxyethyl)"
XX
XX WO200123613-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-US026729.
PF

```

XX 30-SEP-1999; 99US-00409926.
XX (ISIS-) ISIS PHARM INC.
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI, 2001-343164/36.
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies.
XX Example 54; Page 88; 178pp; English.
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase HI (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1741
AAH25738
ID AAH25738 standard; DNA; 19 BP.
XX AAH25738;
AC
XX
XX 14-AUG-2001 (first entry)
XX
XX Human type II RNase H substrate oligonucleotide #5.
XX
XX Human; RNase H type II; RNase HI cleavage substrate; antisense therapy;
XX gene therapy; primer; phosphorochioate backbone; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1.19
XX modified_base /*tag= a
XX FT /mod_base= OTHER
XX FT /note="optionally phosphorochioate backbone"
XX modified_base 16.19
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note="optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
XX methoxyethyl)"
XX FT misc_RNA 19
XX FT /*tag= c
XX
XX WO200123613-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-US026729.
XX
XX 30-SEP-1999; 99US-00409926.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX

```

```

DR WPI; 2001-343164/36.
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies.
XX Example 54; Page 88; 178pp; English.
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase HI (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1742
AAC62164/C
ID AAC62164 standard; DNA; 19 BP.
XX AAC62164;
AC
XX
XX 06-MAR-2001 (first entry)
XX
XX PCR primer used to amplify a human APOC1 allele fragment.
XX
XX Human; apolipoprotein CI; APOC1; Alzheimer's disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6136530-A.
XX
XX 24-OCT-2000.
XX
XX 27-NOV-1996; 96US-00757223.
XX
XX 29-NOV-1995; 95US-0007738P.
XX
XX (UYTE-) UNIV TEXAS TECH HEALTH SCI CENT.
XX
XX Poduslo SE;
XX
XX WPI; 2001-030938/04.
XX
XX Screening for a genetic factor for having an enhanced risk of developing
XX Alzheimer's disease (AD), useful for identifying and monitoring the
XX presence or development of AD, by amplifying the DNA encoding an
XX apolipoprotein CI region.
XX
XX Example 8; Col 18; 21pp; English.
XX
XX PCR primers AAC62163-64 were used to amplify a human apolipoprotein CI
XX (APOC1) allele. The primers are used in the method of the invention. The
XX specification describes a method for screening for a genetic factor for
XX having an enhanced risk of developing Alzheimer's disease. The method
XX comprises amplifying the genomic DNA encoding an APOC1 region in a
XX patient sample. The method is useful for early screening or
XX identification of Alzheimer's disease, and for monitoring the presence or
XX development of the disease
XX
SQ Sequence 19 BP; 4 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

```


Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 AAAGTCTGGGATTACAGG 407
Db 19 AAAGTGTGGGATTACAGG 1

RESULT 1743

AAC62165/c
ID AAC62165 standard; DNA; 19 BP.

AAC62165;

06-MAR-2001 (first entry)

PCR primer used to amplify a human APOC1 allele fragment.

Human; apolipoprotein CI; APOC1; Alzheimer's disease; PCR primer; ss.

Homo sapiens.

US6136530-A.

24-OCT-2000.

27-NOV-1996; 96US-00757223.

29-NOV-1995; 95US-0007738P.

(UYTE-) UNIV TEXAS TECH HEALTH SCI CENT.

Poduslo SE;

WPI; 2001-030938/04.

Screening for a genetic factor for having an enhanced risk of developing

Alzheimer's disease (AD), useful for identifying and monitoring the

presence or development of AD, by amplifying the DNA encoding an

apolipoprotein CI region.

Example 8; Col 18; 21pp; English.

PCR primers AAC62165-66 were used to amplify a human apolipoprotein CI

(APOC1) allele. The primers are used in the method of the invention. The

specification describes a method for screening for a genetic factor for

having an enhanced risk of developing Alzheimer's disease. The method

comprises amplifying the genomic DNA encoding an APOC1 region in a

patient sample. The method is useful for early screening or

identification of Alzheimer's disease, and for monitoring the presence or

development of the disease

Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 697 GGTTCAAGTTATCTCTCTG 715
Db 19 GGTTCAAGCCATCTCTCTG 1

RESULT 1744
AAF91128
ID AAF91128 standard; DNA; 19 BP.

AAF91128;

04-MAY-2001 (first entry)

Human multi drug resistance-1 gene related sequence SEQ ID NO: 215.

KW Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;
KW inflammatory disease; neuronal disease; CNS disease;
KW cardiovascular disease; PCR primer; ss.

Homo sapiens.

WO200109183-A2.

08-FEB-2001.

28-JUL-2000; 2000WO-EP007314.

30-JUL-1999; 99EP-00114938.

22-FEB-2000; 2000EP-00103361.

(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;

WPI; 2001-159855/16.

New polynucleotide encoding a molecular variant Multi Drug Resistance

(MDR)-1 polypeptide is useful for diagnosing and treating diseases

associated with abnormal MDR-1 expression or function, e.g. cancer.

Claim 1; Page 121; 154pp; English.

The present invention provides nucleotides encoding molecular variants of

the human multi drug resistance-1 (MDR-1) protein. These can be used to

identify compounds capable of treating multidrug resistance and

sensitively interfering resulting from polymorphisms in MDR-1, which can

lead to difficulties in treating cancer, cardiovascular, neuronal,

inflammatory and CNS diseases

Sequence 19 BP; 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 832 CTTGTGATCTGCCGCTC 850
Db 1 CTTGTGATCTGCCGCTC 19

RESULT 1745
AAF91127/c

AAF91127 standard; DNA; 19 BP.

AAF91127;

04-MAY-2001 (first entry)

Human multi drug resistance-1 gene related sequence SEQ ID NO: 214.

Human; MDR-1; multi drug resistance-1; drug uptake; disease; cancer;

inflammatory disease; neuronal disease; CNS disease;

cardiovascular disease; PCR primer; ss.

Homo sapiens.

WO200109183-A2.

08-FEB-2001.

28-JUL-2000; 2000WO-EP007314.

30-JUL-1999; 99EP-00114938.

22-FEB-2000; 2000EP-00103361.

(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;

```
XX
DR   WPI; 2001-159855/16.
XX
PT   New polynucleotide encoding a molecular variant Multi Drug Resistance
PT   (MDR)-1 polypeptide is useful for diagnosing and treating diseases
XX   associated with abnormal MDR-1 expression or function, e.g. cancer.
XX
PS   Claim 1, Page 121, 154pp; English.
XX
CC   The present invention provides nucleotides encoding molecular variants of
CC   the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC   identify compounds capable of treating multidrug resistance and
CC   sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC   lead to difficulties in treating cancer, cardiovascular, neuronal,
CC   inflammatory and CNS diseases
XX
SQ   Sequence 19 BP; 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
      Query Match      1.6%; Score 15.8; DB 1; Length 19;
      Best Local Similarity 89.5%; Pred. No. 1.7e+03;
      Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY   832 CTTGATCTGCCTGCTC 850
      |||||
DB   19 CTCGTGATCTGCCGCTC 1

RESULT 1746
AAC83664
ID   AAC83664 standard; DNA; 19 BP.
XX
AC   AAC83664;
XX
DT   02-MAR-2001 (first entry)
XX
DE   2'-O-N-(2-(dimethylamino)ethylacetamido)-modified oligo ISIS #32335.
XX
KW   2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
XX   tumour formation; cancer; protein kinase C expression;
XX   cell adhesion molecule expression; multidrug resistance; ss.
XX
OS   Synthetic.
XX
FH   Key      Location/Qualifiers
FT   modified_base 16..19
FT   :             /*tag= a
FT   FT           /mod_base= OTHER
FT   FT           /note= "2'-O-N-(2-(dimethylamino)ethylacetamido) 5Meu"
XX
PN   US6147200-A.
XX
PD   14-NOV-2000.
XX
PF   19-AUG-1999; 99US-00378568.
XX
PR   19-AUG-1999; 99US-00378568.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M, Cook PD, Frazer AS, Prakash TP, Kawaseki AM;
XX   WPI; 2001-069824/08.
XX
DR   WPI; 2001-069824/08.
XX
PT   New 2'-O-acetamido modified nucleosides (1) used to produce
PT   oligonucleotides which have enhanced nuclease resistance and superior
PT   hybridization properties than prior art.
XX
PS   Example 12; Col 28; 29pp; English.
XX
CC   The present sequence is a modified oligonucleotide. 2'-O-acetamido-
CC   modified nucleosides were used to produce oligonucleotides which have
CC   enhanced nuclease resistance and superior hybridisation properties than
CC   prior art. The oligomeric compounds are useful for identification or
```

```
CC   quantification of ribonucleic acid and deoxyribonucleic acid or for
CC   modulating the activity of an ribonucleic acid or deoxyribonucleic acid
CC   molecule. They have a modified nucleoside monomer and are specifically
CC   hybridisable with a preselected nucleotide sequence of a single-stranded
CC   or double-stranded target deoxyribonucleic acid or ribonucleic acid
CC   molecule. The oligomers are further useful in a ras-luciferase fusion
CC   system using ras-luciferase transactivation. They are useful in abnormal
CC   cell proliferation and tumour formation and modulation of expression of
CC   protein kinase C and cell adhesion molecules such as ICAM. They are
CC   useful in the modulation of proteins related to multidrug resistance and
CC   viral genomic nucleic acids such as HIV, herpes viruses, Epstein-Barr
CC   virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
XX
SQ   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
      Query Match      1.6%; Score 15.8; DB 1; Length 19;
      Best Local Similarity 89.5%; Pred. No. 1.7e+03;
      Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY   427 TTTTATTTTATTTT 445
      |||||
DB   1 TTTTATTTTATTTT 19

RESULT 1747
AAK98526
ID   AAK98526 standard; DNA; 19 BP.
XX
AC   AAK98526;
XX
DT   16-APR-2002 (first entry)
XX
DE   Nucleic acid quantitative analysis related oligonucleotide #1.
XX
KW   Target detection; quantitative analysis; probe; medical diagnosis;
XX   forensics; bacterial screening; tissue typing; gene expression analysis;
XX   genotyping; ss.
XX
OS   Synthetic.
XX
FH   Key      Location/Qualifiers
FT   modified_base 1
FT   :             /*tag= a
FT   FT           /mod_base= OTHER
FT   FT           /note= "modified by thiol"
XX
PN   WO200202810-A2.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-BP007575.
XX
PR   01-JUL-2000; 2000DE-01033334.
XX
PA   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI   Bickel R, Ehrlich R, Ellinger T, Ermentraut E, Kaiser T;
XX   Schulz T, Wagner G;
XX   WPI; 2002-154760/20.
XX
DR   WPI; 2002-154760/20.
XX
PT   Determining targets by interaction with probe array, useful e.g. for
PT   diagnosis, based on detecting formation of precipitate at specific probe
PT   sites.
XX
PS   Example 5; Page 47; 92pp; German.
XX
CC   The present invention relates to a method for the qualitative and
CC   quantitative detection of targets in a sample by molecular interaction
CC   between the target and probes in an array. The method can be used to
CC   detect interactions between nucleic acids, antigens and antibodies or
CC   receptor and ligands, particularly in applications such as medical
```

CC diagnosis, forensic science, bacterial screening, tissue typing for
CC transplantation, monitoring gene expression, and genotyping. The present
CC sequence is a modifying oligonucleotide used in the exemplification of
CC the invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTATTTT 445
Db 1 TTTTATTTATTTATTTT 19

RESULT 1748
AAD31455/c
ID AAD31455 standard; DNA; 19 BP.

XX AC AAD31455;

XX DT 31-MAY-2002 (first entry)

XX DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt2R.

XX KW Human: Van Buchem's disease; genomic deletion; craniofacial dysmorphism;
XX KW autosomal recessive disorder; chromosome 17; chromosome 17q21;
XX KW bone dysplasia; 92kb gene fragment; PCR primer; 88.

XX OS Homo sapiens.

XX PN WO200210455-A2.

XX PD 07-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US023968.

XX PR 28-JUL-2000; 2000US-0221855P.
XX PR 06-JUL-2001; 2001US-030386P.

XX PA (CELL-) CELTECH R & D INC.
XX PA (STRA/) STRAHLING HAMPTON K.

XX PI Brunkow ME, Proll S, Paepfer B;

XX DR WPI; 2002-227089/28.

XX PT Methods for identifying subjects who are afflicted with or carriers of
XX PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,
XX PT by determining the presence of a deletion in the 92 kb region of human
XX PT chromosome 17 at 17q21.

XX PS Example 3; Page 26; 109pp; English.

XX CC The present invention relates to methods for distinguishing between
XX CC individuals homozygous for and therefore afflicted with Van Buchem's
XX CC disease, individuals heterozygous for and therefore carriers of Van
XX CC Buchem's disease and individuals who are not afflicted with Van Buchem's
XX CC disease comprise identifying a large genomic deletion in chromosome 17 at
XX CC 17q21. The method is useful for identifying individuals who are afflicted
XX CC with or carriers of diseases associated with one or more genomic
XX CC deletion, particularly Van Buchem's disease, which is a rare autosomal
XX CC recessive disorder that results in a bone dysplasia referred to a
XX CC craniofacial dysmorphism. The present sequence is a PCR primer used to
XX CC amplify 92kb gene fragment in human chromosome 17 at 17q21

XX SQ Sequence 19 BP; 5 A; 1 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1056 CCACACCCGCTATTTT 1074
Db 19 CCACACCCGCTATTTT 1

RESULT 1749

ID ABA91949 standard; DNA; 19 BP.

XX AC ABA91949;

XX DT 23-MAY-2002 (first entry)

XX DE Methyl thioethyl modified oligonucleotide.

XX KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; 88.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 16

XX FT /*tag= a /mod_base= OTHER /note= "2'-methyl thioethyl thymidine"

XX FT modified_base 17

XX FT /*tag= b /mod_base= OTHER /note= "2'-methyl thioethyl thymidine"

XX FT modified_base 18

XX FT /*tag= c /mod_base= OTHER /note= "2'-methyl thioethyl thymidine"

XX FT modified_base 19

XX FT /*tag= d /mod_base= OTHER /note= "2'-methyl thioethyl thymidine"

XX PN US6277982-B1.

XX PD 21-AUG-2001.

XX PF 20-AUG-1999; 99US-00378665.

XX PR 20-AUG-1999; 99US-00378665.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;

XX DR WPI; 2002-235143/29.

XX PT Alkylation of alcohols, amines, or thiols, useful for preparing
XX PT nucleosides that are precursors for preparation of oligomeric compounds
XX PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.

XX PS Example 15; Col 35; 45pp; English.

XX CC The present sequence is that of a chimeric oligonucleotide having some 2'
XX CC methyl thioethyl modifications. This was compared with oligonucleotides
XX CC with methoxyethoxy (see ABA91950) and dimethylaminoethyl (see ABA91951)
XX CC modifications for resistance to snake venom phosphodiesterase. The assay
XX CC revealed the nuclease resistance of the modified oligomers. The invention
XX CC provides methods for the alkylation of alcohols, amines, thiols and their
XX CC derivatives by cyclic sulfate intermediates. In particular, methods for
XX CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
XX CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
XX CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or
XX CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
XX CC nucleosides and their analogues. The methods are especially useful for
XX CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
XX CC surrogates that are precursors for the preparation of oligomeric
XX CC compounds useful as therapeutics, diagnostics and research reagents

```
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 19
DB

RESULT 1750
ABA91951
ID ABA91951 standard; DNA; 19 BP.
AC ABA91951;
XX
XX 23-MAY-2002 (first entry)
XX
XX Dimethylaminopropyl modified oligonucleotide.
XX
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH modified_base 16 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-dimethylaminopropyl thymidine"
XX FT modified_base 17 /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-dimethylaminopropyl thymidine"
XX FT modified_base 18 /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-dimethylaminopropyl thymidine"
XX FT modified_base 19 /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "2'-dimethylaminopropyl thymidine"
XX
XX US627982-B1.
XX
XX 21-AUG-2001.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Frazer AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
XX WPI; 2002-235143/29.
XX
XX Alkylation of alcohols, amines, or thiols, useful for preparing
XX nucleosides that are precursors for preparation of oligomeric compounds
XX beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
XX Example 15; Col 35; 45pp; English.
XX
XX The present sequence is that of a chimeric oligonucleotide having some 2'
XX -dimethylaminopropyl modifications. This was compared with
XX oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
XX (see ABA91950) modifications for resistance to snake venom
XX phosphodiesterase. The assay revealed the nuclease resistance of the
XX modified oligomers. The invention provides methods for the alkylation of
XX alcohols, amines, thiols and their derivatives by cyclic sulfate
XX intermediates. In particular, methods for the alkylation of the 2', 3' or
XX 5'-hydroxy position of nucleosides and their analogues with cyclic
XX sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
```

```
CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
CC methods are especially useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates that are precursors
CC for the preparation of oligomeric compounds useful as therapeutics,
CC diagnostics and research reagents
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 19
DB

RESULT 1751
ABA91950
ID ABA91950 standard; DNA; 19 BP.
AC ABA91950;
XX
XX 23-MAY-2002 (first entry)
XX
XX Methoxyethoxy modified oligonucleotide.
XX
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH modified_base 16 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethoxy thymidine"
XX FT modified_base 17 /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethoxy thymidine"
XX FT modified_base 18 /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethoxy thymidine"
XX FT modified_base 19 /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethoxy thymidine"
XX
XX US627982-B1.
XX
XX 21-AUG-2001.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX 20-AUG-1999; 99US-00378665.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Frazer AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
XX WPI; 2002-235143/29.
XX
XX Alkylation of alcohols, amines, or thiols, useful for preparing
XX nucleosides that are precursors for preparation of oligomeric compounds
XX beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
XX Example 15; Col 35; 45pp; English.
XX
XX The present sequence is that of a chimeric oligonucleotide having some 2'
XX -methoxyethoxy modifications. This was compared with oligonucleotides
XX with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see
```

CC ABA9195L modifications for resistance to snake venom phosphodiesterase.
CC The assay revealed the nuclease resistance of the modified oligomers. The
CC invention provides methods for the alkylation of alcohols, amines, thiols
CC and their derivatives by cyclic sulfate intermediates. In particular,
CC methods for the alkylation of the 2', 3' or 5'-hydroxy position of
CC nucleosides and their analogues with cyclic sulfates to form the 2', 3'
CC or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of
CC the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-
CC modified nucleosides and their analogues. The methods are especially
CC useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and
CC nucleoside surrogates that are precursors for the preparation of
CC oligomeric compounds useful as therapeutics, diagnostics and research
CC reagents

CC SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Qy Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 427 TTTTATTTTTATTTTTTT 445
|||||
1 TTTTATTTTTTTTTTTTTT 19

RESULT 1752
ABK94423
ID ABK94423 standard; DNA; 19 BP.

XX ABK94423;
XX
XX 27-AUG-2002 (first entry)
XX
XX DE Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
XX
XX KM hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
XX breast and ovarian cancer susceptibility gene; TGDS; human;
XX two-dimensional DNA electrophoresis; tumour suppressor gene;
XX breast cancer; ovarian cancer; tumour.
XX OS Homo sapiens.
XX PN WO200236819-A1.
XX PD 10-MAY-2002.
XX PF 06-NOV-2000; 200OWO-IB001607.
XX PR 06-NOV-2000; 200OWO-IB001607.
XX PA (SCGC-) ACAD APPLIED SCI.
XX PJ Vijg J;
XX PI
XX DR WPI; 2002-471507/50.
XX PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce a
PT characteristic spot pattern for a specific mutation in either the BRCA1
PT or the hMLH1 gene.
XX
XX PS Claim 6; Page 21; 57pp; English.
XX
CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC comprising subjecting a set of amplification products to two-dimensional
CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC detecting mutations in the BRCA1 (breast and ovarian cancer
CC susceptibility gene), a tumour suppressor gene) and hMLH1 gene (a DNA
CC mismatch repair gene). The present sequence is a PCR primer specific to

```

CC hmlh1 used in the method of the invention
XX Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 433 TTTTATTTTTTTTAAGACA 451
DB 1 TTTTATTTTTTTTAATACA 19
RESULT 1753
ABL51520
ID ABL51520 standard; DNA; 19 BP.
XX
AC ABL51520;
DT 01-JUL-2002 (first entry)
XX
DE Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.
XX
KM Tailing reaction; tailed primer; primer; probe; identification;
KM detection; linear amplification scheme; chain extending enzyme;
KM telomerase; ss.
XX
OS Synthetic.
FH
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "biotinylated"
FT misc_RNA 19
FT /*tag= b
XX
XX US2002031776-A1.
XX
XX 14-MAR-2002.
XX
XX 26-JUL-2001; 2001US-00917138.
XX
XX 28-MAY-1999; 99US-0136545P.
XX
XX 25-MAY-2000; 2000US-00580358.
XX
XX (TULL/) TULLIS R H.
XX (STRE/) STREIFEL J A.
XX
XX Tullis RH, Streifel JA;
XX
XX WPI; 2002-361176/39.
XX
XX Identifying and detecting nucleic acids; particularly DNA hybridization
XX probes, involves employing chain extending enzymes (e.g. telomerase) to
XX elongate probes to render them readily detectable.
XX
XX Example 1; Page 5; 10pp; English.
XX
XX The present invention describes a method for detecting a nucleic acid
XX probe, which comprises using chain extending enzymes to elongate probes.
XX The method comprises: (a) treating the sample with a chain terminating
XX reagent to prevent polynucleotide chain growth from the nucleic acid in
XX the sample; (b) contacting the sample with the probe containing a
XX terminus capable of elongation by a chain extending enzyme, where the
XX probe hybridises to the nucleic acid in the sample; (c) contacting the
XX sample with a chain extending enzyme and its substrates, which elongates
XX the probe; and (d) detecting the elongated hybridised probe. Also
XX described is a method comprising: (a) treating nucleic acid molecules or
XX modified nucleic acids in a sample with a reagent or reagents that render
XX the nucleic acid chains unextendable by a non-templeate-dependent enzyme;
XX (b) hybridising the treated molecules with a nucleic acid probe that
XX includes an extendable terminus, under conditions where hybrids form; and

```

CC (c) treating any hybrids formed with a non-template dependent chain
CC elongating enzyme and its substrates, where any hybridised probe is
CC extended. The method is useful for identifying and detecting nucleic
CC acids, particularly DNA hybridisation probes. The present sequence
CC represents a tailing reaction exemplary primer, which is used in an
CC example from the present invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 1.7e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19

RESULT 1754

ABA91970 standard; DNA; 19 BP.

ABA91970;

23-MAY-2002 (first entry)

Single nucleotide polymorphism PCR primer MPO-R.

Single nucleotide polymorphism; SNP; detection; Taqman; assay; quencher;

hybridisation; human; PCR; primer; ss.

Homo sapiens.

US6348596-B1.

19-FEB-2002.

20-JUL-1999; 99US-00357740.

23-JAN-1998; 98US-00012525.

(PEKE) PE CORP NY.

Lee LG, Graham RJ, Mullah KB, Haxo FT;

WPI; 2002-225175/28.

New non-fluorescent asymmetric cyanide dye compounds, useful for
quenching reporter dyes in nucleic acid hybridization assays employing
fluorescence energy transfer as means of detection.

Example 4; Col 66; 62pp; English.

The present sequence is that of single nucleotide polymorphism (SNP)
primer MPO-R. This primer was used in a multiplex endpoint SNP analysis
as an example of the use of novel non-fluorescent asymmetric cyanide dye
compounds of the invention as quenching reporter dyes. A 7-colour
homogeneous detection of multiple PCR products was performed as an
extension of the fluorogenic PCR 5'-nuclease, or Taqman, assay. The test
system was a set of 3 SNPs, denoted MPO, BAK and LIG. Each SNP system
consisted of 2 primers (see ABA91969-74) and 2 sequence-specific probes
(see ABA91975-80) consisting of a novel non-fluorescent quencher,
nitrothiazole blue, at the 3' end, and 6 different reporter dyes (6-FAM,
dr110, dR6G, dTMR, DRX and JAZ) at the 5' end. The 7th colour was from
aluminium pthalocyanine tetrakisulfonate, used as a passive reference.
Following PCR, the reactions were measured on a luminescence spectrometer
in synchronous scanning mode. The spectral overlap in the set was
evaluated by calculation of the conditioning number of the 7x7 matrix
(dye fluorescence versus wavelength). The small value of the condition
number (1.5) proved that crosstalk between the dyes was minimal. SNP
analyses of known, synthetic target DNA sequences (see ABA91961-90) and
genomic DNA (from human blood samples and Raji (ATCC CCL-86) cells) were
plotted as normalised, subtracted spectra and as data points in dot

CC plots. The multiplex PCR system provides increased sample throughput and
CC potential cost savings

XX Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

204 GGTCAGCTGCTCGAAC 222
1 GGCCAGCTGCTTGAAAC 19

RESULT 1755

AAD42000 standard; DNA; 19 BP.

AAD42000;

04-NOV-2002 (first entry)

Oligonucleotide #3 used to illustrate the method of the invention.

dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;

nuclear resistance; alkylation; therapeutic; diagnostic; ss.

Unidentified.

Key Location/Qualifiers

modified_base 15..18

/tag= a

/mod_base= OTHER

/note= "2'-methoxyethoxy (MOE) residues"

US6403779-B1.

11-JUN-2002.

08-JAN-1999; 99US-00227782.

08-JAN-1999; 99US-00227782.

(ISIS-) ISIS PHARM INC.

Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;

WPI; 2002-546338/58.

Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
for preparation of 2'-O-alkylated compounds comprises dissolving
nucleoside in aprotic solvent, cooling, treating with base, warming,
cooling and reacting with ester.

Example 46; Col 31; 24pp; English.

The present invention relates to a novel method of selective alkylation
of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
The method involves dissolving the nucleoside in at least one aprotic
solvent, cooling, treating with base, warming, cooling and reacting with
a reactive ester. The method is useful for the preparation of 2'-O-alkyl
nucleosides, nucleosides and nucleoside surrogates used for preparation
of oligomeric compounds having improved hybridisation affinity and
nuclear resistance, which are useful as therapeutics, diagnostics and
research reagents. The present sequence is a modified oligonucleotide
used to illustrate the method of the invention

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 427 TTTTATTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1756
AAD42002
ID AAD42002 standard; DNA; 19 BP.
XX
AC AAD42002;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #5 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-methoxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2',-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1757
AAD42004
ID AAD42004 standard; DNA; 19 BP.
XX
```

```
AC AAD42004;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #7 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethyl residue"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2',-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1758
AAD42010
ID AAD42010 standard; DNA; 19 BP.
XX
AC AAD42010;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #13 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
```



```
PR 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2',3'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleosides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1761
AADD2011
ID AAD42011 standard; DNA; 19 BP.
XX
XX AAD42011;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #14 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
```

```
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
XX Example 46; Col 37; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleosides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1762
AADD2005
ID AAD42005 standard; DNA; 19 BP.
XX
XX AAD42005;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #8 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 18
XX /*tag= a
XX /mod_base= OTHER
XX /note= "5-methyl, 2'-methoxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 33; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2',3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
```

CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention

SO Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1763

AAD42003
ID AAD42003 standard; DNA; 19 BP.

AC AAD42003;

DT 04-NOV-2002 (first entry)

DE Oligonucleotide #6 used to illustrate the method of the invention.

KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;

KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.

XX Unidentified.

FT Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-O-propyl residues"

PN US6403779-B1.

PD 11-JUN-2002.

PR 08-JAN-1999; 99US-00227782.

PR 08-JAN-1999; 99US-00227782.

PR 08-JAN-1999; 99US-00227782.

PA (ISIS-) ISIS PHARM INC.

PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;

DR WPI; 2002-546338/58.

PT Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving

PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.

XX Example 46; Col 33; 24pp; English.

CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.

CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with

CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates used for preparation

CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and

CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention

SO Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

RESULT 1764

AAD41998
ID AAD41998 standard; DNA; 19 BP.

AC AAD41998;

DT 04-NOV-2002 (first entry)

DE Oligonucleotide #1 used to illustrate the method of the invention.

KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;

KM nuclear resistance; alkylation; therapeutic; diagnostic; ss.

XX Unidentified.

FT Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"

PN US6403779-B1.

PD 11-JUN-2002.

PR 08-JAN-1999; 99US-00227782.

PR 08-JAN-1999; 99US-00227782.

PR 08-JAN-1999; 99US-00227782.

PA (ISIS-) ISIS PHARM INC.

PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;

DR WPI; 2002-546338/58.

PT Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving

PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.

XX Example 46; Col 31; 24pp; English.

CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.

CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with

CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleosides, nucleosides and nucleoside surrogates used for preparation

CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and

CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention

SO Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

```
RESULT 1765
AAD41999
ID AAD41999 standard; DNA; 19 BP.
XX
AC AAD41999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KM Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethoxy (2'-DMAOE)
FT residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawaasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent; cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19
XX
RESULT 1766
AAD42009
ID AAD42009 standard; DNA; 19 BP.
XX
AC AAD42009;
XX
DT 04-NOV-2002 (first entry)
XX
```

```
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminoxyethyl thymidine (T'-2'DMAOE)"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawaasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent; cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 35; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19
XX
RESULT 1767
ACF62693
ID ACF62693 standard; DNA; 19 BP.
XX
AC ACF62693;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:522.
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
XX cytochrome p450; subfamily IIA; nifedipine oxidase; polypeptide 5;
XX cytosolic; PCR primer; ss.
XX
XX Synthetic.
XX
```

PN WO2003013534-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-268144/26.
DR
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily I1IA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; Page 46; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily I1IA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCGCTGCTC 850
DB 1 CTCGTGATCTGCGCGCTC 19
RESULT 1768
ACF62692/c
ID ACF62692 standard; DNA; 19 BP.
XX
XX ACF62692;
AC
XX
XX 08-OCT-2003 (first entry)
DT
XX
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:521.
DE
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KW cytochrome p450; subfamily I1IA; nifedipine oxidase; polypeptide 5;
KW cytochrome p450; subfamily I1IA; nifedipine oxidase; polypeptide 5;
XX
XX Synthetic.
OS
XX
XX WO2003013534-A2.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008219.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-268144/26.
DR
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily I1IA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; Page 46; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily I1IA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCGCTGCTC 850
DB 19 CTCGTGATCTGCGCGCTC 1
RESULT 1769
ADB21364
ID ADB21364 standard; DNA; 19 BP.
XX
XX ADB21364;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX MRP1 based cancer related nucleic acid SEQ ID NO:522.
DE
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
XX
XX ds.
XX
XX Unidentified.
OS
XX
XX WO2003013533-A2.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008200.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-354397/33.
DR
XX
XX Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a

PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX Disclosure; Page 55; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytosolic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 832 CTTGTGATCGCTGCCTC 850
DB 1 CTCGTGATCGCCGCGCTC 19

RESULT 1770
ADB21363/c
ID ADB21363 standard; DNA; 19 BP.
XX
XX ADB21363;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:521.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
XX ds.
XX
XX Unidentified.
XX
XX WO2003013533-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008200.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX WPI; 2003-354397/33.
XX
XX
XX Use of irinotecan or its derivative for preparation of a pharmaceutical
XX composition for treating cancer in a subject having a genome with a
XX variant allele comprising a multidrug resistance protein 1
XX polynucleotide.
XX
XX Disclosure; Page 55; 100pp; English.
XX
XX The present invention describes a method for the use of irinotecan (I) or
XX its derivative for the preparation of a pharmaceutical composition for
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic
XX cancer, or malignant glioma in a subject having a genome with a variant
XX allele which comprises a multidrug resistance protein 1 (MRP1)
XX polynucleotide (II). (I) has cytosolic activity. (I) or its derivative

CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 832 CTTGTGATCGCTGCCTC 850
DB 19 CTCGTGATCGCCGCGCTC 1

RESULT 1771
AB258336
ID AB258336 standard; DNA; 19 BP.
XX
XX AB258336;
XX
DT 28-APR-2003 (first entry)
XX
XX Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
XX
XX Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;
XX DNA-RNA hybrid; ss.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX 16
XX modified_base /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX modified_base 17
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX modified_base 18
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX modified_base 19
XX /tag= d
XX /mod_base= OTHER
XX /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX WO200304603-A2.
XX
XX 16-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020940.
XX
XX 03-JUL-2001; 2001US-0302683P.
XX
XX 28-JAN-2002; 2002US-00058740.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Prakash TP, Manoharan M;
XX WPI; 2003-239204/23.
XX
XX
XX Increasing binding of oligomeric compound to proteins useful in
XX preparation of antisense therapeutics, involves use of modified
XX oligomeric compound having oligonucleotide group.
XX
XX Example 27; Page 72; 122pp; English.
XX
XX The present sequence is an example of an oligonucleotide of the invention
XX containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTB)-5-

CC methyluridine) modifications. In examples of the invention, 2'-O-MTE was
 CC incorporated into oligonucleotides and evaluated for antisense properties
 CC in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)
 CC modification. The 2'-O-MTE modified oligonucleotides exhibited similar
 CC binding affinity to target RNA as their 2'-O-MOE equivalent while binding
 CC to human serum albumin was improved. The modification can be used to
 CC modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
 CC therapy

XX Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

XX
 XX

Query Match 1.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 68.4%; Pred. No. 1.7e+03;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTATTTT 445
 |||||
 Db 1 TTTTATTTTUUU 19

RESULT 1772
 ACC62369/c
 ID ACC62369 standard; DNA; 19 BP.

AC ACC62369;
 XX
 XX

DT 23-JUN-2003 (first entry)
 XX
 XX

DE Human NOV9 reverse PCR primer SEQ ID NO:244.
 XX
 XX

KM Human; NOV9; antiatherosclerotic; hypotensive; cardiac; dermatological;
 KM anorectic; immunosuppressive; cytostatic; antidiabetic; antifertility;
 KM haemostatic; antiinflammatory; antiparkinsonian; metabolic; cancer;
 KM neuroprotective; noctropic; antiparkinsonian; metaplastic; scleroderma;
 KM gene therapy; cardiomyopathy; atherosclerosis; hypertension; diabetes;
 KM congenital heart defect; aortic stenosis; valve disease; transplantation;
 KM tuberculous sclerosis; obesity; congenital adrenal hyperplasia; diabetes;
 KM prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer;
 KM fertility; haemophilia; hypercoagulation; graft versus host disease;
 KM idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia;
 KM Crohn's disease; multiple sclerosis; infectious disease; cancer;
 KM cancer-associated cachexia; Alzheimer's disease; Parkinson's disease;
 KM immune disorder; haematopoietic disorder; dyslipidaemia;
 KM metabolic syndrome X; PCR primer; ss.

XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX

PN WO2003023001-A2.
 XX
 XX

PD 20-MAR-2003.
 XX
 XX

PF 09-SEP-2002; 2002MO-US028538.
 XX
 XX

PR 07-SEP-2001; 2001US-0118120P.
 PR 07-SEP-2001; 2001US-0318184P.
 PR 10-SEP-2001; 2001US-0318430P.
 PR 17-SEP-2001; 2001US-0322636P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 17-SEP-2001; 2001US-0322816P.
 PR 17-SEP-2001; 2001US-0322817P.
 PR 19-SEP-2001; 2001US-0323519P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 20-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324596P.
 PR 25-SEP-2001; 2001US-0325091P.
 PR 26-SEP-2001; 2001US-0324590P.
 PR 14-DEC-2001; 2001US-0341144P.
 PR 26-FEB-2002; 2002US-0359599P.
 PR 05-MAR-2002; 2002US-0361663P.
 PR 03-MAY-2002; 2002US-037908P.
 PR 17-MAY-2002; 2002US-0381483P.
 PR 29-MAY-2002; 2002US-0383863P.

PR 02-JUL-2002; 2002US-0393332P.
 PR 17-JUL-2002; 2002US-0396412P.
 PR 13-AUG-2002; 2002US-0403517P.
 PR 06-SEP-2002; 2002US-00236417.
 XX
 XX

PA (CURA-) CURAGEN CORP.
 XX
 XX

PI Agee ML, Alsbrook JP, Anderson DW, Berghs C, Boldog FL;
 PI Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
 PI Crabtree U, DiPippo VA, Edinger SR, Eisen AJ, Ellerman K;
 PI Gangoli EA, Getlach VL, Gioc L, Gorman U, Guo X, Gusev VY, Ji W;
 PI Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
 PI Malvankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patuzzian M;
 PI Pena CB, Rieger DK, Rothenberg ME, Shenoy SG, Shinkens RA;
 PI Spaderna SK, Spytek KA, Taupier RJ, Twonlow N, Vernet CM, Voos EZ;
 PI Zernusen BD, Zhong M;
 DR WPI; 2003-313241/30.
 XX
 XX

PT Novel human proteins and nucleic acid encoding the proteins, useful for
 PT diagnosis, treatment and prevention of disorders involving the human
 PT protein or nucleic acid e.g. cardiac and neurological disorders.

XX
 XX

PS Example C; Page 308; 460P; English.
 XX
 XX

CC The present invention describes isolated human NOVX proteins, where X is
 CC 1 to 42. ACC6236 to ACC62345 encode the human NOVX proteins given in
 CC ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiac,
 CC hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
 CC antidiabetic, antifertility, haemostatic, antiinflammatory, anti-HIV,
 CC antiparkinsonian and antipapillary activities, and can be used in gene
 CC therapy. NOVX proteins are useful for treating or preventing a pathology
 CC associated with a NOVX protein in humans and for treating a syndrome
 CC associated with the human disease. NOVX nucleic acids, proteins and
 CC antibodies can be used in the treatment and diagnosis of cardiomyopathy,
 CC atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
 CC valve disease, tuberculous sclerosis, scleroderma, obesity, transplantation,
 CC congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
 CC disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
 CC hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
 CC disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorder, dyslipidaemia, and metabolic syndrome X.
 CC ACC62346 to ACC62465 represent PCR primers and probes for human NOVX
 CC sequences, which are used in examples from the present invention.
 CC ABR54277 represents a human trypsinogen protein given in comparison with
 CC the human NOV35b protein in the exemplification of the present invention

XX
 XX

SO Sequence 19 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 653 AGTGCAGTGGCCGATCTT 671
 |||||
 Db 19 AGTGCAGTGGCCGATCTT 1

RESULT 1773
 ADB88452/c
 ID ADB88452 standard; DNA; 19 BP.
 XX
 XX

AC ADB88452;
 XX
 XX

DT 04-DEC-2003 (first entry)
 XX
 XX

DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:521.
 XX
 XX

KM ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
 KM colorectal cancer; cervical cancer; gastric cancer; lung cancer;

KW ovarian cancer; pancreatic cancer; malignant glioma;
KM uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008217.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-289896/28.
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
PS Disclosure; Page 60; 107pp; English.
XX
CC The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
CY 832 CTTGTGATCTGCGCGCTC 850
DB 19 CTCGTGATCTGCGCGCTC 1
XX
RESULT 1774
ADB88453
ID ADB88453 standard; DNA; 19 BP.
XX
AC ADB88453;
XX
DE 04-DEC-2003 (first entry)
XX
XX Human UGT1A1 variant allele sequence fragment SEQ ID NO:522.
XX
XX ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KM colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KM ovarian cancer; pancreatic cancer; malignant glioma;
KM uridine diphosphate glycosyltransferase1 member A1.
XX
OS Homo sapiens.
XX
PN WO2003013536-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008217.
XX

PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-289896/28.
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
PS Disclosure; Page 60; 107pp; English.
XX
CC The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
CY 832 CTTGTGATCTGCGCGCTC 850
DB 1 CTCGTGATCTGCGCGCTC 19
XX
RESULT 1775
ADB97435/C
ID ADB97435 standard; DNA; 19 BP.
XX
AC ADB97435;
XX
DE 04-DEC-2003 (first entry)
XX
XX Human MDRI variant allele sequence fragment SEQ ID NO:521.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDRI; cytostatic; human; ds; CYP3A5; MRP1; MDRI;
KM TOP1.
XX
OS Homo sapiens.
XX
PN WO2003013537-A2.
XX
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
PF 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-268145/26.
XX
PF New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.
XX
XX
PS Claim 1; Page 84; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 19 BP, 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 832 CTGTGATCTGCGCTC 850
DB 19 CTCGTGATCTGCGCGCTC 1
RESULT 1776
ADB97436
ID ADB97436 standard; DNA; 19 BP.
XX
AC ADB97436;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 variant allele sequence fragment SEQ ID NO:522.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; human; de; CYP3A5; MRP1; MDR1;
KM TOP1.
XX
XX Homo sapiens.
OS
XX
XX MO2003013537-A2.
PN
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002MO-EP008218.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
PI WPI; 2003-268145/26.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Claim 1; Page 84; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 19 BP, 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 832 CTGTGATCTGCGCTC 850
DB 1 CTCGTGATCTGCGCGCTC 19
RESULT 1777
ADB92627
ID ADB92627 standard; DNA; 19 BP.
XX
AC ADB92627;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 variant allele sequence fragment SEQ ID NO:522.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; de; human; UGT1A1; MRP1; TOP1.
XX
OS Homo sapiens.
XX
XX MO2003013535-A2.
PN
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002MO-EP008220.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
PI WPI; 2003-342400/32.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Claim 8; Page 55; 104pp; English.
XX
CC The invention relates to a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 19 BP, 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 832 CTGTGATCTGCGCTC 850
DB 1 CTCGTGATCTGCGCGCTC 19
RESULT 1778
ADB92626/c

ID ADB92626 standard; DNA; 19 BP.
XX
AC ADB92626;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 variant allele sequence fragment SEQ ID NO:521.
XX
KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDR1; cytosolic; ds; human; UG11A1; MRP1, TOP1.
XX
XX Homo sapiens.
OS
PN MO2003013535-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002MO-EP008220.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PI Heinrich G, Kerb R;
XX WPI; 2003-342400/32.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
XX multidrug resistance 1 polynucleotide.
XX
PS Claim 8; Page 55; 104pp; English.
XX
CC The invention relates to a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 19 BP; 5 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCGCTCC 850
DB 19 CTCGTGATCTGCCGCCCTC 1
XX
RESULT 1779
ADE14131/c
ID ADE14131 standard; DNA; 19 BP.
XX
AC ADE14131;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #240.
XX
KM Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KM SNF; glaucoma; progressive ocular hypertensive disorder;
KM glaucoma related disorder; motif; repeat element; regulatory region.
XX
OS Homo sapiens.
XX
PN US2003190617-A1.
XX
PD 09-OCT-2003.

XX
PF 06-MAR-2002; 2002US-00091281.
XX
PR 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
PI Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX
DR
XX
PT New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.
XX
PS Claim 11; SEQ ID NO 242; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing
CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
SQ Sequence 19 BP; 4 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 370 CCACCTGCTCAGCCTCC 388
DB 19 CCACCTGCTCGCCTTCC 1
XX
RESULT 1780
ADE99245
ID ADE99245 standard; DNA; 19 BP.
XX
AC ADE99245;
XX
DT 12-FEB-2004 (first entry)
XX
DE Modified oligomeric compound #5.
XX
KM Oligomeric compound; hepatitis C virus; 2'-O-modification;
KM nuclease resistance; hepatotropic; virucide; antiinflammatory; ss.
XX
OS Synthetic.
XX
PN US6600032-B1.
XX

PD 29-JUL-2003.
XX 06-AUG-1999; 99US-00370625.
XX 07-AUG-1998; 98US-00130566.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cook PD;
XX WPI; 2003-895259/82.
XX
XX New oligomeric compound having at least one nucleoside useful for
PT therapeutic and investigative purposes e.g. for treating hepatitis C
PT virus infection.
XX
XX Disclosure; SEQ ID NO 5; 26pp; English.
XX
XX The invention relates to oligomeric compounds having at least one
CC nucleoside. The compounds are useful for therapeutic and investigative
CC purposes and for treating hepatitis C virus infection. The compounds
CC having 2'-O-modifications increases their affinity and nuclease
CC resistance. This sequence represents an oligomeric compound of the
CC invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19
RESULT 1781
ADE9265
ID ADE9265 standard; DNA; 19 BP.
XX
XX ADE9265;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX Modified oligomeric compound #26.
DE
XX
XX Oligomeric compound; hepatitis C virus; 2'-O-modification;
KW nuclease resistance; hepatotropic; virucide; antiinflammatory; ss.
XX
XX Synthetic.
OS
XX
XX US660032-B1.
PN
XX
XX 29-JUL-2003.
PD
XX
XX 06-AUG-1999; 99US-00370625.
PF
XX
XX 07-AUG-1998; 98US-00130566.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD;
PI
XX
XX WPI; 2003-895259/82.
DR
XX
XX New oligomeric compound having at least one nucleoside useful for
PT therapeutic and investigative purposes e.g. for treating hepatitis C
PT virus infection.
XX
XX Disclosure; SEQ ID NO 26; 26pp; English.
XX
XX The invention relates to oligomeric compounds having at least one
CC nucleoside. The compounds are useful for therapeutic and investigative

CC purposes and for treating hepatitis C virus infection. The compounds
CC having 2'-O-modifications increases their affinity and nuclease
CC resistance. This sequence represents an oligomeric compound of the
CC invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19
RESULT 1782
ADH97218
ID ADH97218 standard; DNA; 19 BP.
XX
XX ADH97218;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Synthetically modified nuclease resistant oligomer #7.
DE
XX
XX Nuclease resistance; hybrid binding; antisense technology; ss.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX US6534639-B1.
PN
XX
XX 18-MAR-2003.
PD
XX
XX 07-JUL-2000; 2000US-00612531.
PF
XX
XX 07-JUL-1999; 99US-00349040.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
PI
XX
XX WPI; 2003-644179/61.
DR
XX
XX Guanidinium functionalized oligonucleotides used for diagnostic,
PT therapeutic or investigative purposes comprises a number of nucleotide
PT units.
XX
XX Example 26; SEQ ID NO 7; 51pp; English.
PS
XX
XX This invention relates to novel synthetically modified oligomers that
CC have increased nuclease resistance and have enhanced hybrid binding. Such
CC oligomers are useful for diagnostic and therapeutic uses such as
CC antisense technologies. The invention also discloses a method for the
CC preparation of the oligomers with modifications as fully defined in the
CC specification. The present sequence represents a synthetically modified
CC oligonucleotide of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 19

```
RESULT 1783
ADH97214
ID ADH97214 standard; DNA; 19 BP.
AC ADH97214;
XX
XX
XX 15-APR-2004 (first entry)
DE Synthetically modified nuclease resistant oligomer #3.
XX
XX
XX Nuclease resistance; hybrid binding; antisense technology; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX
XX US6534639-B1.
XX
XX 18-MAR-2003.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2003-644179/61.
XX
XX
XX Guanidinium functionalized oligonucleotides used for diagnostic,
XX therapeutic or investigative purposes comprises a number of nucleotide
XX units.
XX
XX Example 26; SEQ ID NO 3; 51pp; English.
XX
XX
XX This invention relates to novel synthetically modified oligomers that
XX have increased nuclease resistance and have enhanced hybrid binding. Such
XX oligomers are useful for diagnostic and therapeutic uses such as
XX antisense technologies. The invention also discloses a method for the
XX preparation of the oligomers with modifications as fully defined in the
XX specification. The present sequence represents a synthetically modified
XX oligonucleotide of the invention.
XX
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTATTTT 445
XX |||||
DB 1 TTTTATTTT 19
```

```
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 17
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX
XX modified_base 19
XX /*tag= b
XX /mod_base= OTHER
XX /note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX
XX US6534639-B1.
XX
XX 18-MAR-2003.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2003-644179/61.
XX
XX
XX Guanidinium functionalized oligonucleotides used for diagnostic,
XX therapeutic or investigative purposes comprises a number of nucleotide
XX units.
XX
XX Example 26; SEQ ID NO 13; 51pp; English.
XX
XX
XX This invention relates to novel synthetically modified oligomers that
XX have increased nuclease resistance and have enhanced hybrid binding. Such
XX oligomers are useful for diagnostic and therapeutic uses such as
XX antisense technologies. The invention also discloses a method for the
XX preparation of the oligomers with modifications as fully defined in the
XX specification. The present sequence represents a synthetically modified
XX oligonucleotide of the invention.
XX
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 427 TTTTATTTATTTT 445
XX |||||
DB 1 TTTTATTTT 19
```

```
RESULT 1785
ABZ97252
ID ABZ97252 standard; DNA; 19 BP.
AC ABZ97252;
XX
XX
XX 17-OCT-2003 (first entry)
DE Human nucleic acid sequence.
XX
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
```

XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI, 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAe, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 12494; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 885 CACCACGCCGCGCTATT 903
Db 1 CACCACGCCGCGCTCTCT 19
RESULT 1786
AB297253
ID AB297253 standard; DNA; 19 BP.
XX
XX
AC AB297253;
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human nucleic acid sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD

XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI, 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 12495; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 839 TCTGCTGCTCGGCTCC 857
Db 1 TCTGCTGCTCGGCTCC 19
RESULT 1787
AB297333
ID AB297333 standard; DNA; 19 BP.
XX
XX
AC AB297333;
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human IL4-R oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD

```
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIGENESIS PHARM INC.
XX PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12575; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 885 CACCACGCGCGCTTATT 903
Db 1 CACCACGCGCGCTTCTCT 19
RESULT 1788
AB297334
ID AB297334 standard; DNA; 19 BP.
XX AC
XX AB297334;
XX DT 17-OCT-2003 (first entry)
XX DE Human IL4-R oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
```

```
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIC-) EPIGENESIS PHARM INC.
XX PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX PT respiration, has oligo(s) antisense to specific gene(s) or its
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX PT ubiquinone.
XX PS Disclosure; SEQ ID NO 12576; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 839 TCTGCGCTGCGGCTCC 857
Db 1 TCTGCGCGCTTCAGCCTCC 19
RESULT 1789
ACA88902/c
ID ACA88902 standard; DNA; 19 BP.
XX AC
XX ACA88902;
XX DT 08-JUL-2003 (first entry)
XX DE Selection and amplification of genetic markers PCR related primer #13.
XX
XX Genetic marker selection; multiplex PCR amplification;
XX prenatal diagnostic testing; foetal sex determination;
XX genetic identification; DNA profiling; DNA fingerprinting;
XX forensic analysis; PCR; primer; ss.
XX OS Homo sapiens.
XX PN WO2003031646-A1.
XX PD 17-APR-2003.
XX PF 14-OCT-2002; 2002WO-AU001388.
```


XX PS Claim 24, Page 57, 74pp; English.
 XX CC The invention describes a method of determining the ethnic origin of a
 CC male comprising obtaining a nucleic acid sample from the male, and
 CC identifying at least two polymorphic markers in the nucleic acid sample
 CC indicative of the ethnic origin of the male, using at least one primer
 CC pair from the ethnic origin of the male in the specification. Also described is
 CC a method of: identifying polymorphic sites in a nucleic acid; a kit for
 CC determining the ethnic origin of an individual; determining the ethnic
 CC origin of a human male individual; an isolated nucleic acid segment of a
 CC human Y chromosome comprising at least 10 contiguous bases including at
 CC least one of the polymorphic sites given in the specification; nucleic
 CC acid primer pairs for amplifying polymorphic regions of the Y chromosome
 CC given in the specification; and determining the paternity of a human male
 CC individual. The method is useful for determining the ethnic origin of a
 CC male, for paternity testing, for forensic studies or for diagnosis. This
 CC sequence represents a primer used to detect polymorphisms in the non-
 CC recombining region of the human Y chromosome (NRY).
 XX SQ Sequence 19 BP; 4 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 1.64; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1056 CCACACCCCGCTAATTTT 1074
 Db 1 CCACACCCCGCTAATTTT 19
 RESULT 1792
 ADO14381/c
 ID ADO14381 standard; RNA; 19 BP.
 XX AC ADO14381;
 XX DT 01-JUL-2004 (first entry)
 XX DE Human interleukin-2-targeted siNA upper strand SEQ ID NO:116.
 KW cyrostatic; vasotropic; nephrotropic; cancer; restenosis;
 KW polycystic kidney disease; RNA interference;
 KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
 KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
 KW expression modulation; gene therapy; drug screening; diagnosis;
 KW therapeutic target identification; pharmacogenomics;
 KW gene function analysis; gene mapping; human; interleukin-2; ss.
 XX OS Homo sapiens.
 XX PN WO2003070744-A1.
 XX PD 28-AUG-2003.
 XX PF 11-FEB-2003; 2003WO-US004566.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J, Beigelman J, Thompson J;
 XX DR WPI, 2003-731546/69.
 XX PT New short interfering nucleic acid, useful e.g. for treatment and
 diagnosis of cancer, downregulates expression of an interleukin gene.

XX PS Example 3; SEQ ID NO 116; 138pp; English.
 XX CC The invention relates to short interfering nucleic acids (siNA) which
 CC downregulate expression of the human interleukin-2 gene by RNA
 CC interference. The siNA may or may not comprise ribonucleotides and may
 CC be double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siNA include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
 CC hairpin RNA (shRNA). The siNA can be unmodified or chemically modified,
 CC can contain deoxyribonucleotides, and can be chemically synthesised,
 CC expressed from a vector or enzymatically synthesised. The invention also
 CC relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
 CC and/or complexes of siRNA; and vectors that express siNA. The siNA are
 CC used to modulate expression of the interleukin-2 gene in cells, tissue
 CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
 CC transplants for the treatment of a variety of conditions. They may be
 CC used for treating cancer, restenosis and polycystic kidney disease. The
 CC siNA are also useful for drug screening, diagnosis, therapeutic target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function, and gene mapping (e.g., of single nucleotide
 CC polymorphisms). The present sequence represents the upper strand of a
 CC human interleukin-2-targeted double-stranded siNA, which is identical to
 CC the interleukin-2 transcript target sequence.
 XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 0 T; 5 U; 0 Other;
 Query Match 1.64; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1121 TCAACTCTGACCTCAGG 1139
 Db 19 TCAACTCTGACCTCAGG 1
 RESULT 1793
 ADO14386/c
 ID ADO14386 standard; RNA; 19 BP.
 XX AC ADO14386;
 XX DT 01-JUL-2004 (first entry)
 XX DE Human interleukin-2-targeted siNA upper strand SEQ ID NO:121.
 KW cyrostatic; vasotropic; nephrotropic; cancer; restenosis;
 KW polycystic kidney disease; RNA interference;
 KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
 KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
 KW expression modulation; gene therapy; drug screening; diagnosis;
 KW therapeutic target identification; pharmacogenomics;
 KW gene function analysis; gene mapping; human; interleukin-2; ss.
 XX OS Homo sapiens.
 XX PN WO2003070744-A1.
 XX PD 28-AUG-2003.
 XX PF 11-FEB-2003; 2003WO-US004566.
 XX PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX PA (RIBO-) RIBOZYME PHARM INC.

PI Mcswigen J, Beigelman L, Thompson J;
DR WPI; 2003-731546/69.
XX
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Example 3; SEQ ID NO 121; 138bp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
downregulate expression of the human interleukin-2 gene by RNA
interference. The siNAs may or may not comprise ribonucleotides and may
be double or single stranded. They further comprise sense and antisense
regions, or alternatively are assembled from a sense oligonucleotide and
an antisense oligonucleotide. Specifically, the siNAs include short
interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
can contain deoxyribonucleotides, and can be chemically synthesised,
expressed from a vector or enzymatically synthesised. The invention also
relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
and/or complexes of siRNA; and vectors that express siNA. The siNAs are
used to modulate expression of the interleukin-2 gene in cells, tissue
explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
transplants for the treatment of a variety of conditions. They may be
used for treating cancer, restenosis and polycystic kidney disease. The
siNAs are also useful for drug screening, diagnosis, therapeutic target
identification and validation, genetic engineering, pharmacogenomics,
studying gene function, and gene mapping (e.g., of single nucleotide
polymorphisms). The present sequence represents the upper strand of a
human interleukin-2-targeted double-stranded siNA, which is identical to
the interleukin-2 transcript target sequence.
SQ Sequence 19 BP; 3 A; 7 C; 4 G; 0 T; 5 U; 0 Other;
QY
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 729 AGTACTGGAGCTACAGGC 747
19 AGTGGCTAGGACTACAGGC 1
RESULT 1794
AD014514
ID AD014514 standard; RNA; 19 BP.
XX
AC AD014514;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human interleukin-2-targeted siNA lower strand SEQ ID NO:249.
XX
KW cytosolic; vasotropic; nephrotropic; cancer; restenosis;
KW polycystic kidney disease; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human; interleukin-2; ss.
XX
XX Homo sapiens.
XX
PN WO2003070744-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004566.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX
PR 11-MAR-2002; 2002US-0363124P.
XX
PR 06-JUN-2002; 2002US-0386782P.
XX
PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswigen J, Beigelman L, Thompson J;
XX
XX WPI; 2003-731546/69.
DR
XX
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Example 3; SEQ ID NO 249; 138bp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
downregulate expression of the human interleukin-2 gene by RNA
interference. The siNAs may or may not comprise ribonucleotides and may
be double or single stranded. They further comprise sense and antisense
regions, or alternatively are assembled from a sense oligonucleotide and
an antisense oligonucleotide. Specifically, the siNAs include short
interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
can contain deoxyribonucleotides, and can be chemically synthesised,
expressed from a vector or enzymatically synthesised. The invention also
relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
and/or complexes of siRNA; and vectors that express siNA. The siNAs are
used to modulate expression of the interleukin-2 gene in cells, tissue
explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
transplants for the treatment of a variety of conditions. They may be
used for treating cancer, restenosis and polycystic kidney disease. The
siNAs are also useful for drug screening, diagnosis, therapeutic target
identification and validation, genetic engineering, pharmacogenomics,
studying gene function, and gene mapping (e.g., of single nucleotide
polymorphisms). The present sequence represents the lower strand of a
human interleukin-2-targeted double-stranded siNA.
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 0 T; 3 U; 0 Other;
QY
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 1.7e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Db 729 AGTACTGGAGCTACAGGC 747
1 AGTGGCTAGGACTACAGGC 19
RESULT 1795
AD014509
ID AD014509 standard; RNA; 19 BP.
XX
AC AD014509;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human interleukin-2-targeted siNA lower strand SEQ ID NO:244.
XX
KW cytosolic; vasotropic; nephrotropic; cancer; restenosis;
KW polycystic kidney disease; RNA interference;
KW short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KW double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
KW expression modulation; gene therapy; drug screening; diagnosis;
KW therapeutic target identification; pharmacogenomics;
KW gene function analysis; gene mapping; human; interleukin-2; ss.
XX
XX Homo sapiens.
XX
PN WO2003070744-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004566.

XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Thompson J;
PI
DR WPI; 2003-731546/69.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of an interleukin gene.
XX
PS Example 3; SEQ ID NO 244; 138pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human interleukin-2 gene by RNA
CC interference. The siNA may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNA include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNA can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siRNA; conjugates
CC and/or complexes of siRNA; and vectors that express siNA. The siNA are
CC used to modulate expression of the interleukin-2 gene in cells, tissue
CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
CC transplants for the treatment of a variety of conditions. They may be
CC used for treating cancer, restenosis and polycystic kidney disease. The
CC siNA are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the lower strand of a
CC human interleukin-2-targeted double-stranded siNA.
XX
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.7e+03;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1121 TCNAACCTCTGACCTCAAG 1139
1 UCANAACUCUGGCCUCACAG 19
XX
RESULT 1796
ABD30364
ID ABD30364 standard; DNA; 19 BP.
XX
AC ABD30364;
XX
DT 29-JUL-2004 (first entry)
XX
XX Human IL4-R derived oligonucleotide SEQ ID 12575.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenoma sensitivity; lung cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiaesthetic;
KW analgesic; hypotensive; immunosuppressive; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.

XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002MO-US011143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
DR WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 12575; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiaesthetic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 885 CACCAAGCCCGGCTTATT 903
1 CACCAAGCCCGGCTTCT 19
XX
RESULT 1797
ABD30365
ID ABD30365 standard; DNA; 19 BP.
XX
AC ABD30365;
XX
DT 29-JUL-2004 (first entry)
XX

DE Human IL4-R derived oligonucleotide SEQ ID 12576.
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.
XX Homo sapiens.
XX
XX MO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002MO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahbuddin S;
XX MPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 12576; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it.
XX
XX Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

839 TCTGCTGCTGCTGCTCC 857

DB 1 TCTGCTGCTGCTGCTCC 19
|||||
RESULT 1798
ADG28485
ID ADG28485 standard; DNA; 19 BP.
XX
XX ADG28485;
AC
XX 26-FEB-2004 (first entry)
XX
XX Modified oligonucleotide seq id 6.
XX
XX antibacterial; protozoacide; antialgal; fungicide;
XX internucleotide linkage; 2',5'-internucleotide linkage; 3'-substituent;
XX antisense; pharmaceutical; RNA-DNA transcription;
XX RNA-protein translation; infection; diagnostic; therapeutic;
XX nuclease resistance; ss.
XX
XX Synthetic.
XX
XX US6653458-B1.
XX
XX 25-NOV-2003.
XX
XX 08-NOV-1999; 99US-00435806.
XX
XX 03-SEP-1993; 93US-00117363.
XX 02-SEP-1994; 94WO-US010131.
XX 28-FEB-1996; 96US-00602862.
XX 14-JUL-1998; 98US-00115043.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Guinasso CJ;
XX MPI; 2004-079586/08.
XX
XX New oligonucleotide comprising at least one 2',5'-internucleotide linkage
XX useful for treating organisms having disease caused by undesired
XX production of protein e.g. bacteria, yeast, protozoa and algae.
XX
XX Example 54; SEQ ID NO 6; 30pp; English.
XX
XX The invention describes an oligonucleotide comprising several nucleotides
XX covalently linked together by internucleotide linkages. At least one of
XX the nucleotides is linked to an adjacent nucleotide by 2',5'-
XX internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX are useful as antisense oligonucleotides; in pharmaceutical compositions
XX for treating organisms having disease caused by undesired production of
XX protein e.g. organism that utilizes RNA-DNA transcription or RNA-protein
XX translation, bacteria, yeast, protozoa, algae and warm-blooded animals;
XX for developing diagnostic and therapeutic agents. The modified
XX oligonucleotide exhibits improved properties of nuclease resistance and
XX binding affinity. The oligonucleotides are easy to synthesize and exhibit
XX good properties of nuclease resistance and hybridisation to target
XX nucleic acids. The oligonucleotide is potent antisense agent with longer
XX duration of action. This sequence represents an oligonucleotide of the
XX invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 1798

```
ADG47994
ID ADG47994 standard; DNA; 19 BP.
XX
AC ADG47994;
XX
DT 11-MAR-2004 (first entry)
XX
DE Oligonucleotide #3 used in the exemplification of the invention.
XX
KM Hybridisation; diagnosis; therapeutic; investigation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX US2003092046-A1.
XX
XX 15-MAY-2003.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX
XX (COOK/) COOK P D.
XX
XX (PRAK/) PRAKASH T P.
XX
XX (MOHA/) MOHAN V.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-031184/03.
XX
XX New oligomers containing guanidinium groups, useful for modulating gene
XX
XX expression by hybridizing oligomer with single- or double-stranded
XX
XX nucleic acids.
XX
XX Example 26; SEQ ID NO 3; 54pp; English.
XX
XX The present invention relates to novel oligonucleotides comprising
XX
XX several nucleotide units which are specifically hybridisable with a
XX
XX selected sequence of RNA or DNA wherein at least one of the nucleotide
XX
XX moieties of the oligomer is modified to include a guanidinium group.
XX
XX These oligonucleotides are useful for diagnostic, therapeutic and
XX
XX investigative purposes. The present sequence is an oligonucleotide used
XX
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 427 TTTTATTTATTTT 445
XX
XX 1 TTTTATTTT 19
XX
XX Db
XX
XX RESULT 1800
XX
XX ADG48004
XX
XX ID ADG48004 standard; DNA; 19 BP.
XX
XX AC ADG48004;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Oligonucleotide #11 used in the exemplification of the invention.
XX
XX Hybridisation; diagnosis; therapeutic; investigation; ss.
XX
XX KW
```

```
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX
XX modified_base 17
XX
XX /*tag= a
XX
XX /mod_base= OTHER
XX
XX /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX modified_base 19
XX
XX /*tag= b
XX
XX /mod_base= OTHER
XX
XX /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX EN US2003092046-A1.
XX
XX 15-MAY-2003.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX
XX (COOK/) COOK P D.
XX
XX (PRAK/) PRAKASH T P.
XX
XX (MOHA/) MOHAN V.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-031184/03.
XX
XX New oligomers containing guanidinium groups, useful for modulating gene
XX
XX expression by hybridizing oligomer with single- or double-stranded
XX
XX nucleic acids.
XX
XX Example 26; SEQ ID NO 13; 54pp; English.
XX
XX The present invention relates to novel oligonucleotides comprising
XX
XX several nucleotide units which are specifically hybridisable with a
XX
XX selected sequence of RNA or DNA wherein at least one of the nucleotide
XX
XX moieties of the oligomer is modified to include a guanidinium group.
XX
XX These oligonucleotides are useful for diagnostic, therapeutic and
XX
XX investigative purposes. The present sequence is an oligonucleotide used
XX
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX
XX Best Local Similarity 89.5%; Pred. No. 1.7e+03;
XX
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 427 TTTTATTTATTTT 445
XX
XX 1 TTTTATTTT 19
XX
XX Db
XX
XX RESULT 1801
XX
XX ADG47998
XX
XX ID ADG47998 standard; DNA; 19 BP.
XX
XX AC ADG47998;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Oligonucleotide #5 used in the exemplification of the invention.
XX
XX Hybridisation; diagnosis; therapeutic; investigation; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX
XX modified_base 19
XX
XX /*tag= a
XX
XX
```

```
FT /mod_base= OTHER
FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX
XX US2003092046-A1.
XX
XX 15-MAY-2003.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX (COOK/) COOK P D.
XX (PRAK/) PRAKASH T P.
XX (MOHA/) MOHAN V.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-031184/03.
XX
XX New oligomers containing guanidinium groups, useful for modulating gene
XX expression by hybridizing oligomer with single- or double-stranded
XX nucleic acids.
XX
XX Example 26; SEQ ID NO 7; 54pp; English.
XX
XX The present invention relates to novel oligonucleotides comprising
XX several nucleotide units which are specifically hybridisable with a
XX selected sequence of RNA or DNA wherein at least one of the nucleotide
XX moieties of the oligomer is modified to include a guanidinium group.
XX These oligonucleotides are useful for diagnostic, therapeutic and
XX investigative purposes. The present sequence is an oligonucleotide used
XX in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No.1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 427 TTTTATTTTATTTT 445
XX 1 TTTTATTTTATTTT 19
XX
XX
XX RESULT 1802
XX ADH42933
XX ID ADH42933 standard; DNA; 19 BP.
XX
XX ADH42933;
XX
XX 25-MAR-2004 (first entry)
XX
XX Guanidinium functionalised oligonucleotide ISIS #109973.
XX
XX ss; guanidinium functionalised nucleotide; guanidinium;
XX 2-O-guanidinium ethyl; increased binding affinity.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 19
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER = 2-O-[2-(guanidinium)-ethyl] modified"
XX
XX US6593466-B1.
XX
XX 15-JUL-2003.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX
```

```
PR 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-118052/12.
XX
XX New guanidinium functionalized nucleotide compounds useful for preparing
XX oligomers used for diagnostic, therapeutic and investigative
XX applications.
XX
XX Example 26; SEQ ID NO 5; 40pp; English.
XX
XX The invention relates to a guanidinium functionalised nucleotide
XX compounds. The guanidinium functionalised nucleotide compounds are used
XX for preparation of oligomers useful for diagnostic, therapeutic and
XX investigative applications. The 2-O-guanidinium ethyl modification
XX increases binding affinity to a target. The present sequence represents a
XX guanidinium functionalised oligonucleotide.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.6%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No.1.7e+03;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 427 TTTTATTTTATTTT 445
XX 1 TTTTATTTTATTTT 19
XX
XX
XX RESULT 1803
XX ADH42931
XX ID ADH42931 standard; DNA; 19 BP.
XX
XX ADH42931;
XX
XX 25-MAR-2004 (first entry)
XX
XX Guanidinium functionalised oligonucleotide ISIS #109990.
XX
XX ss; guanidinium functionalised nucleotide; guanidinium;
XX 2-O-guanidinium ethyl; increased binding affinity.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 16.19
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER = 2-O-[2-(guanidinium)-ethyl] modified"
XX
XX US6593466-B1.
XX
XX 15-JUL-2003.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-118052/12.
XX
XX New guanidinium functionalized nucleotide compounds useful for preparing
XX oligomers used for diagnostic, therapeutic and investigative
XX applications.
XX
XX Example 26; SEQ ID NO 3; 40pp; English.
XX
```

CC The invention relates to a guanidinium functionalised nucleotide
CC compounds. The guanidinium functionalised nucleotide compounds are used
CC for preparation of oligomers useful for diagnostic, therapeutic and
CC investigative applications. The 2-O-guanidinium ethyl modification
CC increases binding affinity to a target. The present sequence represents a
CC guanidinium functionalised oligonucleotide.
XX

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19

Db

RESULT 1804

ID ADH42932 standard; DNA; 19 BP.

ADH42932;

25-MAR-2004 (first entry)

Guanidinium functionalised oligonucleotide ISIS #109989.

ss; guanidinium functionalised nucleotide; guanidinium;

2-O-guanidinium ethyl; increased binding affinity.

Synthetic.

Location/Qualifiers

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

modified_base

Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

427 TTTTATTTATTTATTTT 445
1 TTTTATTTATTTATTTT 19

Db

RESULT 1805

ID ADH76758 standard; DNA; 19 BP.

ADH76758;

22-APR-2004 (first entry)

MCHR1 genomic sequence analysis primer #67.

melanin-concentrating hormone receptor 1; MCHR1; anorectic; gene therapy;

Obesity; primer; ss.

Unidentified.

WO2003104489-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-EP005917.

05-JUN-2002; 2002EP-00012569.

(UYPH-) UNIV PHILIPPS MARBURG.

Platzter M, Platzter C, Gudermann T, Hebebrand J, Hinney A;

Reichwald K;

WPI; 2004-062377/06.

New diagnostic composition, useful for diagnosing obesity related to the

presence of a molecular variant of the MCHR1 gene or a susceptibility to

the disorder.

Example 2; Page 43; 76pp; English.

The invention relates to a novel diagnostic polynucleotide composition.

The polynucleotide composition comprises: a sequence encoding a

polypeptide with defined sequences given in the specification; a sequence

capable of hybridizing to a melanin-concentrating hormone receptor 1

(MCHR1) gene; a polynucleotide encoding an MCHR1 polypeptide; or a

sequence comprising one or more of the nucleotide exchanges (SNP's) given

in the specification and at least 8 bases of surrounding sequence of the

MCHR1 gene. The composition has anorectic activity. The polynucleotide

composition may be used in gene therapy to treat the disorders of the

invention. The composition is useful for diagnosing obesity related to

the presence of a molecular variant of the MCHR1 gene or a susceptibility

to the disorder. The MCHR1 protein or polynucleotide is useful for

preparing a medicament for treating or preventing obesity related to the

presence of a molecular variant of the MCHR1 gene. This polynucleotide

represents an MCHR1 primer of the invention.

Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

797 CACCATGTTCGCCGATG 815
19 CACCATGTTCGCCGATG 1

Db

RESULT 1806

AD12546/c

ID ADI12546 standard; DNA; 19 BP.
XX
AC ADI12546;
XX
DT 22-APR-2004 (first entry)
XX
DE Mutant human BRCA1 genomic DNA resulting from deletion 4 Segid 29.
XX
KM ds; cancer; human; tumour suppressor;
KM breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
KM ovarian cancer; recombination; mutant.
XX
OS Homo sapiens.
XX
PN MO2003104474-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-US018098.
XX
PR 07-JUN-2002; 2002US-0387132P.
XX
PR 09-AUG-2002; 2002US-0402430P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Scholl T, Hendrickson BC, Ward B, Pruss D;
XX
XX WPI; 2004-062369/06.
XX
PT Predicting a predisposition to cancer in a patient comprising detecting a
PT deletion in the BRCA1 gene that results from the unequal crossover
PT between a pair of repetitive sequences in the BRCA1 gene.
XX
XX Disclosure; SEQ ID NO 29; 59pp; English.
XX
XX This invention relates to a novel method for predicting a predisposition
XX to cancer in a patient by detecting large deletions in the human tumour
XX suppressor gene identified as the breast cancer susceptibility gene 1
XX (BRCA1). Specifically, it refers to deletions that result from the
XX unequal crossover between a pair of repetitive Alu sequences in the BRCA1
XX gene, such that the recombinant nucleotide sequence containing the
XX deletion indicates a predisposition to breast and ovarian cancer. The
XX present invention describes newly discovered deletion mutations that are
XX believed to be deleterious and cause significant alterations in the
XX structure or biochemical function of BRCA1. Accordingly, it provides
XX methods for detecting such mutants, as well as identifying and screening
XX for cytostatic compounds useful for treating or preventing cancers
XX associated with a BRCA1 genetic variant. This polynucleotide is a mutant
XX human BRCA1 genomic DNA fragment that arises as a result of a
XX recombination event (deletion 4), which causes the omission of exons 16
XX and 17, given in an exemplification of the invention.
SQ
SQ Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 671 TGGCTACTGCAACTCTG 689
DB 19 TGGCTACTGCAACTCTG 1
RESULT 1807
ADJ59152
ID ADJ59152 standard; DNA; 19 BP.
XX
AC ADJ59152;
XX
DT 06-MAY-2004 (first entry)
XX
XX Oligonucleotide associated to IL 4R #7.
DE

KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KM airway inflammation; allergy; asthma; impeded respiration;
KM cystic fibrosis; acute respiratory distress syndrome;
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KM ss.
XX
XX Homo sapiens.
XX
OS
XX
PN MO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Myce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahbuddin S, Lu H, Cong H;
XX
XX WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX PT initiation codons and introns of respiratory disease-relevant genes e.g.,
XX PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX PT disease e.g., asthma.
PS
PS Claim 2; SEQ ID NO 8; 85pp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
XX CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
XX CC end of nucleic acid target comprising gene(s) chosen from e.g.,
XX CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
XX CC oligonucleotide and optionally surfactant operatively linked to the
XX CC oligonucleotide. The method is useful for preventing or treating a
XX CC respiratory or lung disease, which involves administering to the airways
XX CC of a subject an effective amount of an inhibitor. The oligonucleotide is
XX CC useful for production of a medicament for the prevention and/or treatment
XX CC of a respiratory or lung disease. The respiratory or lung disease is
XX CC chosen from airway inflammation, allergy/asthma, impeded
XX CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
XX CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
XX CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
XX CC obstruction. The present sequence represents an oligonucleotide of the
XX CC invention.
SQ
SQ Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 885 CACCAAGCCCGGCTTATT 903
DB 1 CACCAAGCCCGGCTTATT 19
RESULT 1808
ADJ59153
ID ADJ59153 standard; DNA; 19 BP.
XX
AC ADJ59153;
XX
DT 06-MAY-2004 (first entry)
XX
XX Oligonucleotide associated to IL 4R #8.
DE
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX KM airway inflammation; allergy; asthma; impeded respiration;
XX KM cystic fibrosis; acute respiratory distress syndrome;
XX KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX KM ss.

XX Homo sapiens.
OS
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
XX Claim 2; SEQ ID NO 9; 85pp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 839 TCTGCGCTGCTCGGCTCC 857
DB 1 TCTGCGCGCTCGGCTCC 19
XX
RESULT 1809
ADJ61646
ID ADJ61646 standard; DNA; 19 BP.
XX
XX AC ADJ61646;
XX
DT 06-MAY-2004 (first entry)
XX
XX IL-4Ra receptor #3.
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
XX Synthetic.
XX
XX WO2004011613-A2.
XX
XX

PD 05-FEB-2004.
XX
XX 25-JUL-2003; 2003WO-US023509.
XX
XX 29-JUL-2002; 2002US-0399076P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-203534/19.
XX
XX Example 5; SEQ ID NO 2502; 85pp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents a receptor of the invention.
XX
SQ Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 839 TCTGCGCTGCTCGGCTCC 857
DB 1 TCTGCGCGCTCGGCTCC 19
XX
RESULT 1810
ADJ61645
ID ADJ61645 standard; DNA; 19 BP.
XX
XX AC ADJ61645;
XX
DT 06-MAY-2004 (first entry)
XX
XX IL-4Ra receptor #2.
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
XX Synthetic.
XX
XX WO2004011613-A2.
XX
XX PD 05-FEB-2004.
XX
XX 25-JUL-2003; 2003WO-US023509.
XX
XX 29-JUL-2002; 2002US-0399076P.
XX
XX

PA (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JM, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT Initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
XX Example 5; SEQ ID NO 2501; 85bp; English.
XX
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC Initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the always
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from allergy inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents a receptor of the invention.
XX
XX Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 885 CACCACGCCGCGCTTATTT 903
DB 1 CACCACGCCGCGCTTCTCT 19
RESULT 1811
ADJ77769 standard; DNA; 19 BP.
XX
XX ADJ77769;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Modified antisense oligonucleotide #5.
DE
XX
XX 2'-O-aminoethylthioethyl-modified ribosyl nucleoside;
KW antisense oligonucleotide; ss.
XX
XX Synthetic.
OS
XX
XX US6673912-B1.
PN
XX
XX 06-JAN-2004.
PD
XX
XX 11-APR-2002; 2002US-00121135.
PF
XX
XX 07-AUG-1998; 98US-00130566.
PR
XX
XX 06-AUG-1999; 99US-00370625.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD;
PI
XX
XX WPI; 2004-106293/11.
DR
XX
XX New 2'-O-aminoethylthioethyl-modified ribosyl nucleosides useful as
PT monomer for the synthesis of modified anti-sense oligonucleotides.

XX
XX Disclosure; SEQ ID NO 5; 26bp; English.
PS
XX
XX The invention relates to 2'-O-aminoethylthioethyl-modified ribosyl
CC nucleosides. The modified ribosyl nucleosides are used as monomers for
CC the synthesis of modified antisense oligonucleotides, which are useful in
CC diagnosis and therapeutics (e.g. in gene therapy, for treating organisms
CC having a disease associated by the undesired production of proteins) and
CC as research reagents. The oligonucleotides obtained from the monomers
CC show enhanced hybrid binding affinity towards targeted DNA or RNA and
CC resistance towards nucleases. This sequence represents a modified
CC antisense oligonucleotide of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTTATTTT 19
RESULT 1812
ADJ77789 standard; DNA; 19 BP.
XX
XX ADJ77789;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Modified antisense oligonucleotide #25.
DE
XX
XX 2'-O-aminoethylthioethyl-modified ribosyl nucleoside;
KW antisense oligonucleotide; ss.
XX
XX Synthetic.
OS
XX
XX US6673912-B1.
PN
XX
XX 06-JAN-2004.
PD
XX
XX 11-APR-2002; 2002US-00121135.
PF
XX
XX 07-AUG-1998; 98US-00130566.
PR
XX
XX 06-AUG-1999; 99US-00370625.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Manoharan M, Cook PD;
PI
XX
XX WPI; 2004-106293/11.
DR
XX
XX New 2'-O-aminoethylthioethyl-modified ribosyl nucleosides useful as
PT monomer for the synthesis of modified anti-sense oligonucleotides.
PS
XX
XX Disclosure; SEQ ID NO 26; 26bp; English.
XX
XX The invention relates to 2'-O-aminoethylthioethyl-modified ribosyl
CC nucleosides. The modified ribosyl nucleosides are used as monomers for
CC the synthesis of modified antisense oligonucleotides, which are useful in
CC diagnosis and therapeutics (e.g. in gene therapy, for treating organisms
CC having a disease associated by the undesired production of proteins) and
CC as research reagents. The oligonucleotides obtained from the monomers
CC show enhanced hybrid binding affinity towards targeted DNA or RNA and
CC resistance towards nucleases. This sequence represents a modified
CC antisense oligonucleotide of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 445
|||||
1 TTTTATTTTATTTT 19

RESULT 1813
ADM42087
ADM42087 standard; DNA; 19 BP.

ADM42087;

03-JUN-2004 (first entry)

Exemplary DNA molecule.

nanotube; nucleic acid sensor; DNA array; conductor; nanoparticle;
biosensor; detection; screening; bacterial; viral; pharmaceutical;
agricultural; food control; hygiene; environmental; forensic;
nano-scale conductor; semiconductor; nano-electronic; prostatic nerve;
bio-electronic interface; transistor; gated device; ss.

Synthetic.

MO2004020450-A1.

11-MAR-2004.

29-AUG-2003; 2003WO-AU001118.

30-AUG-2002; 2002AU-00951274.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Mccall M, Moghaddam M;

WPI; 2004-269207/25.

Carbon nanotube attached with one or more nucleic acid molecules, useful
as biosensor for screening presence of bacterial or viral nucleic acid in
clinical samples.

Example 6; Page 91; 147pp; English.

The present invention describes a nanotube (I) attached with one or more
nucleic acid molecule(s). Also described: (1) chemically modifying (M1) a
nanotube; (2) physically modifying (M2) a nanotube; (3) linking (M3)
nanotubes; (4) a several linked nanotubes (II) produced by (M3); (5)
directing (M4) nanotubes to specific targets; (6) a nucleic acid sensor
(III) comprising (I), where the base sequence of the attached nucleic
acid molecule is substantially complementary to all or a portion of the
base sequence of the nucleic acid molecules being detected; (7) a DNA
array consisting of an array of groups of one or more nanotubes, each
group having one or more nucleic acid molecules of the same base sequence
attached to each nanotubes in the group, and where the base sequence of
the nucleic acid molecules, attached to the nanotubes in one group
differs from those in other groups so that a number of different target
DNA molecules may be detected; (8) an actuator comprising (I) and a
membrane support to which the DNA-modified nanotubes are attached; and
(9) a conductor (IV) comprising (I). (I) is useful in coating one or more
nanotubes with nanoparticles, which involves exposing (I) to
nanoparticles comprising several attached complementary nucleic acid
molecules, where the nanoparticles hybridize to the nucleic acid
molecules on the surface of the nanotube(s) as well as self-assembling to
other nanoparticles, forming one or more coated nanotubes. (I) can be
used as a biosensor for detecting complementary nucleic acid strands,
useful in clinical application for screening presence of bacterial
viral nucleic acid, in pharmaceutical applications, agricultural
applications, food control, hygiene and environmental monitoring and
forensic applications. (II) is useful as a nano-scale conductor or
semiconductor, more specifically as a component in nano-electronic
applications, as a replacement for damaged nerves in prostatic

* applications, or as the bio-electronic interface in bio-electronic
devices. (III) can also be used as a transistor or gated device. The
CC present sequence represents an oligonucleotide which is used in an
CC example from the present invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 445
|||||
1 TTTTATTTTATTTT 19

RESULT 1814

ADM47150
ADM47150 standard; DNA; 19 BP.

ADM47150;

03-JUN-2004 (first entry)

2'-O-MOE-2-thio modified oligonucleotide #3.
ss; antisense; infection; inflammation; tumour;
enhanced binding affinity.

Synthetic.

Key Location/Qualifiers
modified_base 16..19
/*tag= a
/mod_base= OTHER
/note= "OTHER = 2'-O-[2-(methoxy-ethyl)-2-thio-5-
methyluridine"]

US2004033973-A1.

19-FEB-2004.

16-AUG-2002; 2002US-00222588.

16-AUG-2002; 2002US-00222588.

(MANO/) MANOHARAN M.

(PRAK/) PRAKASH T P.

(RAJE/) RAJEEV K G.

Manoharan M, Prakash TP, Rajeev KG;

WPI; 2004-256363/24.

New nucleoside compounds useful as antisense compounds to prevent or
delay e.g. infection, inflammation or tumor formation.

Example 211; SEQ ID NO 17; 96pp; English.

The invention relates to nucleoside compounds. The nucleoside compounds
are useful as antisense compounds in diagnostics, therapeutics, and
prophylaxis, and as research reagents and kits, and to prevent or delay
infection, inflammation or tumour formation. The compounds have enhanced
binding affinity properties. The present sequence represents a 2'-O-MOE-2
-thio modified oligonucleotide.

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 445

AC AD058942 ;

lung disease; hyper-responsiveness; adenosine; adenosine A receptor

KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
OS Homo sapiens.
PN US2004049022-A1.
PD 11-MAR-2004.
PF 25-JUL-2003; 2003US-00627930.
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUHH/) LU H.
XX (CONG/) CONG H.
PI NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
DR WPI; 2004-293804/27.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX Example 5; Page 163; 174pp; English.
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC triptase a, triptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, triptase a,
CC triptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hyperextension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
SO Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 885 CACGACGCGCGCTATT 903
1 CACGACGCGCGCTTCTCT 19

RESULT 1818
AD044643
ID. AD044643 standard; DNA; 19 BP.
XX
AC AD044643;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #9.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; triptase a;
KW triptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease; cystic fibrosis; CF;
KW airway inflammation; allergy; impeded respiration; allergic rhinitis;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
OS Homo sapiens.
PN US2004049022-A1.
PD 11-MAR-2004.
PF 25-JUL-2003; 2003US-00627930.
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUHH/) LU H.
XX (CONG/) CONG H.
PI NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
DR WPI; 2004-293804/27.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX Claim 2; SEQ ID NO 9; 174pp; English.
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC triptase a, triptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, triptase a,
CC triptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary

CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
QY
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 TCTGCCCGCTCAGCCTCC 19
RESULT 1819
AD047037
AD047037 standard; DNA; 19 BP.
AC
AD047037;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #2403.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KM trypsinase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KM lung disease; hyper-responsiveness; adenosis; adenosis A receptor;
KM asthma; lung allergy; inflammation; inflammatory disease;
KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KM acute respiratory distress syndrome; pulmonary hypertension;
KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI, 2004-293804/27.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
PS Example 5; Page 163; 174pp; English.
XX
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, trypsinase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention

CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC trypsinase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosis and/or levels of adenosis A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 19 BP; 1 A; 11 C; 3 G; 4 T; 0 U; 0 Other;
QY
Query Match 1.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 TCTGCCCGCTCAGCCTCC 19
RESULT 1820
AD044642
AD044642 standard; DNA; 19 BP.
AC
AD044642;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #8.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KM trypsinase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KM lung disease; hyper-responsiveness; adenosis; adenosis A receptor;
KM asthma; lung allergy; inflammation; inflammatory disease;
KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KM acute respiratory distress syndrome; pulmonary hypertension;
KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
OS Homo sapiens.
XX
PN US2004049022-A1.
XX
PD 11-MAR-2004.
XX
PF 25-JUL-2003; 2003US-00627930.
XX
PR 23-APR-2002; 2002WO-US013135.
PR 23-APR-2002; 2002WO-US013143.
XX
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX

DR WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT Initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.

PS Claim 2; SEQ ID NO 8; 174bp; English.

XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-
CC 5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tyrosinase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tyrosinase a,
CC tyrosinase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.

XX
SQ Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 885 CACCAAGCGCGCTTATT 903

DB 1 CACCAAGCGCGCTTCTCT 19

RESULT 1821

ID ADP08673/C

ID ADP08673 standard; DNA; 19 BP.

AC ADP08673;

DT 26-AUG-2004 (first entry)

DE Extend primer 10 used to genotype human glycoprotein VI polymorphism.

XX breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;

KM GP6; GPVI; chromosome 19q13.4; ss; PCR; primer; SNP;

KW single nucleotide polymorphism.

XX Homo sapiens.

OS WO2004047767-A2.

PN 10-JUN-2004.

PD 25-NOV-2003; 2003WO-US037966.

PR 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX
DR WPI; 2004-441082/41.

XX Identifying a subject at risk of breast cancer by detecting the presence
PT of one or more nucleotide polymorphic variations, useful for
PT diagnosing, preventing and/or treating breast cancer.

PS Example 3; Page 82; 286pp; English.

XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of an extend primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
CC GPVI/GPVI) DNA which is located at chromosomal position 19q13.4.

XX
SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 870 ATTACAGCGTGAAGCCACC 888

DB 19 ATTACAGGTGTGAGCGGCC 1

RESULT 1822

ID ADO59136

ID ADO59136 standard; DNA; 19 BP.

AC ADO59136;

DT 09-SEP-2004 (first entry)

DE Tobacco cytochrome P450 PCR primer #6.

XX ss; primer; PCR; cytochrome P450; transgenic; tobacco; plant.

XX Nicotiana sp.

PN US2004117869-A1.

PD 17-JUN-2004.

PF 12-MAR-2003; 2003US-00387346.

PR 11-JAN-2002; 2002US-0347444P.

PR 12-MAR-2002; 2002US-0363684P.

PR 10-JAN-2003; 2003US-00340861.

PA (USSM-) US SMOKELESS TOBACCO CO.

XX Xu D;

PI WPI; 2004-449487/42.

XX An isolated nucleic acid molecule, comprising nucleic acid sequence of
PT Nicotiana derived cytochrome P450 enzyme fragments, useful for producing
PT transgenic plants.

PS Disclosure; SEQ ID NO 154; 82pp; English.

XX The invention relates to an isolated nucleic acid molecule (I),
CC comprising a nucleic acid sequence chosen from 75 Nicotiana-derived
CC cytochrome P450 enzyme fragment sequences. (I) is useful for producing a
CC transgenic tobacco plant, which involves operably linking (I) with a
CC promoter functional in the plant to create a plant transformation vector,
CC and transforming the plant with the plant transformation vector.

CC selecting a plant cell transformed with the transformation vector, and
CC regenerating a plant from the selected plant cell. The nucleic acid
CC molecule is in an antisense orientation, sense orientation or is in a RNA
CC interference orientation. The present sequence represents a PCR primer
CC used to clone DNA encoding tobacco cyclochrome P450 enzyme fragments of
CC the invention.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 427 TTTTATTTATTTT 445

Db 1 TTTTATTTATTTT 19

RESULT 1823

AD120573/c

ID AD120573 standard; DNA; 60 BP.

XX AD120573;

DT 15-APR-2004 (first entry)

XX Oligonucleotide sequence enquiry #60.

XX human; ds; eRNA.

XX Homo sapiens.

XX MO2003025229-A1.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-AU001286.

XX 19-SEP-2001; 2001US-0324127P.

XX (UYOU) UNIV QUEENSLAND.

XX Matlick J, Gagen M, Stanley S;

XX WPI; 2003-371830/35.

XX Identifying an eRNA or a DNA sequence comprising an eRNA-encoding

PT sequence in the nucleome of a eukaryotic cell, comprising identifying non

PT -protein-encoding nucleotide sequences within an mRNA transcript or a DNA

PT sequence.

XX Example 12; SEQ ID NO 63; 137pp; English.

CC The present invention relates to identifying an eRNA or a DNA sequence
CC comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell
CC comprising identifying non-protein-encoding nucleotide sequences within an
CC mRNA transcript or a DNA sequence encoding same in the nucleome. The
CC methods are useful for identifying an eRNA or DNA for modifying a genetic
CC network in cell to alter the cells phenotype. The present sequence
CC represents human oligonucleotide sequence enquiry.

XX Sequence 60 BP; 8 A; 22 C; 16 G; 14 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.8; DB 1; Length 60;

Best Local Similarity 60.5%; Pred. No. 1.8e+03;

Matches 26; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 619 TGAGACAGAGTCACTGTCTGACCCAGGCTGAGTGCAGTG 661

Db 43 TGAGCCAGATGCGACACCTGCACTCCAGCTGGGTGACAGAG 1

RESULT 1824

AD056744

ID AD056744 standard; DNA; 18 BP.

XX AD056744;

DT 12-AUG-2004 (first entry)

XX Human presynaptic cytomatrix protein, PCLO, proximal SNP probe #56.

XX gene therapy; human; ss; melanoma;

XX melanoma associated polymorphic variation;

XX presynaptic cytomatrix protein; PCLO; SNP;

XX single nucleotide polymorphism; probe.

XX Homo sapiens.

XX WO2004044164-A2.

XX 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035879.

XX 06-NOV-2002; 2002US-0424475P.

XX 23-JUL-2003; 2003US-0489703P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM;

XX WPI; 2004-411721/38.

XX Identifying a subject at risk of melanoma, useful for treating melanoma,
XX comprises detecting the presence or absence of one or more polymorphic
XX variations associated with melanoma in a nucleic acid sample from a
XX subject.

XX Example 6; Page 105; 295pp; English.

CC The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human presynaptic cytomatrix protein, PCLO, proximal probe.

XX Sequence 18 BP; 1 A; 7 C; 3 G; 6 T; 0 U; 1 Other;

Query Match 1.6%; Score 15.6; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.7e+03;

Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 686 TCTGCTCCCGGCTTCAA 703

Db 1 TCTGCTCCCTGCTTCAH 18

RESULT 1825

AAH38408

ID AAH38408 standard; DNA; 51 BP.

XX AAH38408;

DT 14-AUG-2001 (first entry)

XX Human SNP flanking oligonucleotide SEQ ID 1204.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;

KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Leisch-Myan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polyostotic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
OS Homo sapiens.
XX WO200129262-A2.
XX 26-APR-2001.
XX 13-OCT-2000; 2000WO-US028436.
XX 15-OCT-1999; 99US-0160096P.
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX Picoult-Newburg L, Pohl M;
XX WPI; 2001-290930/30.
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX Claim 1; Page 56; 83pp; English.
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leisch-Myan syndrome, muscular
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism
XX
SQ Sequence 51 BP; 12 A; 11 C; 17 G; 10 T; 0 U; 1 Other;
Query Match 1.6%; Score 15.6; DB 1; Length 51;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 24; Conservative 1; Mismatches 15; Indels 0; Gaps 0;
QY 1032 AGCTGGGATTAACGGGACCTGACACACACCCCGCTAATT 1071
DB 8 AGCCGGCGCTGTGCGACAGTGTCTTAATCCAGCTACTY 47
RESULT 1826
AAAX10256/c
ID AAAX10256 standard; DNA; 17 BP.
XX
AC AAAX10256;
XX
DT 24-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic marker downstream primer #562.
XX

KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; primer; ss.
OS Synthetic.
XX Homo sapiens.
XX WO9820165-A2.
XX 14-MAY-1998.
XX 05-NOV-1997; 97WO-US020313.
XX 06-NOV-1996; 96US-0030455P.
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX Lander ES, Wang D, Hudson T;
XX WPI; 1998-286974/25.
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX Claim 16; Page 220; 310pp; English.
XX AAH09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AAH10269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Leisch-Myan syndrome, muscular
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberosus sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 673 GCTCAGTCGCAACCTCTG 689
DB 17 GCTCAGTCGCAACCTCG 1
RESULT 1827
AAAX22858
ID AAAX22858 standard; RNA; 17 BP.
XX
AC AAAX22858;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6084.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW

KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
OS Homo sapiens.
PN MO9950403-A2.
XX 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
PR (RIBO-) RIBOZYME PHARM INC.
PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
PI WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS Claim 54; Page 246; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA1167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA2422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodioma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX

SO Sequence 17 BP; 0 A; 9 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 842 GCCTGCTGGGCTCC 858
DB 1 GCCUGCCUUGGCCUCC 17

RESULT 1828

AAA22737 standard; RNA; 17 BP.

AAA22737;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SSO ID NO:5963.

XX

KW Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairy ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
PN MO9950403-A2.
XX 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
PR (RIBO-) RIBOZYME PHARM INC.
PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
PI WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS Claim 54; Page 239; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA2422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodioma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX

SO Sequence 17 BP; 3 A; 5 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.6e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 734 CCGGAGCTACAGGCGC 750
DB 1 CUGGAGUUDACAGCGCC 17

RESULT 1829

AAA22829 standard; RNA; 17 BP.

AAA22829;

AC


```
XX 19-JUN-2000 (first entry)
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6055.
XX
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, TIE-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS
XX MO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99MO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 245; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAL16775 to
XX AAL17167 and AAL17561 to AAL17622 represent ribozyme sequences for ARNT,
XX and AAL17623 to AAL17684 represent their
XX corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to
XX AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086
XX and AAL19155 to AAL19222 represent their corresponding target sequences;
XX AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and
XX AAL21596 to AAL21688 represent their corresponding target sequences;
XX AAL21689 to AAL22475 and AAL23263 to AAL23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to
XX AAL23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
SO
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. NO. 1.6e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
0y 1002 AAGCATCTCTCTGCT 1018
Db 1 AAGCGAUUUCUCUCUCU 17
```

```
RESULT 1830
AA22832
ID AAA22832 standard; RNA; 17 BP.
XX
XX AAA22832;
AC
XX
XX 19-JUN-2000 (first entry)
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6058.
XX
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, TIE-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS
XX MO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99MO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 245; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAL16775 to
XX AAL17167 and AAL17561 to AAL17622 represent ribozyme sequences for ARNT,
XX and AAL17623 to AAL17684 represent their
XX corresponding target sequences; AAL17685 to AAL18385 and AAL19087 to
XX AAL19154 represent ribozyme sequences for Tie-2, and AAL18386 to AAL19086
XX and AAL19155 to AAL19222 represent their corresponding target sequences;
XX AAL19223 to AAL20361 and AAL21501 to AAL21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAL20362 to AAL21500 and
XX AAL21596 to AAL21688 represent their corresponding target sequences;
XX AAL21689 to AAL22475 and AAL23263 to AAL23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAL22476 to AAL23262, AAL23343 to
XX AAL23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;
SO
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. NO. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 542 CTCAGCTCCCAAGTAG 558
|:|||||:|:|:|:|:
Db 1 CUCAGCCTCCCAAGTAG 17

RESULT 1831
AAA22828
ID AAA22828 standard; RNA; 17 BP.

AAA22828;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6054.

Human; aryl hydrocarbon nuclear transport; ARNT, TIE-2; angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
Klippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US006507.

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability
of an mRNA encoding an angiogenic factors.

Claim 54; Page 245; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
cleaving activity, which specifically cleave RNA encoded by an aryl
hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
and AAA19155 to AAA19222 represent their corresponding target sequences;
AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
AAA21596 to AAA21688 represent their corresponding target sequences;
AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
AAA23422 represent their corresponding target sequences. The ribozymes of
the invention are used for modulating the synthesis, expression and/or
stability of an mRNA encoding angiogenic factor, especially ARNT,
integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
especially used to treat cancer, diabetic retinopathy, age related
macular degeneration (ARMD), inflammation, and arthritis, as well as
neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
and other syndromes and diseases related to the levels of ARNT, Tie-2,
integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1001 CAAGCATTCCTGCTC 1017
|:|||||:|:|:|:|:
Db 1 CAAGCATTCCTGCTC 17

RESULT 1832
AAA22847
ID AAA22847 standard; RNA; 17 BP.

AAA22847;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6073.

Human; aryl hydrocarbon nuclear transport; ARNT, TIE-2; angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
Klippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US006507.

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability
of an mRNA encoding an angiogenic factors.

Claim 54; Page 246; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
cleaving activity, which specifically cleave RNA encoded by an aryl
hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
and AAA19155 to AAA19222 represent their corresponding target sequences;
AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
AAA21596 to AAA21688 represent their corresponding target sequences;
AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
AAA23422 represent their corresponding target sequences. The ribozymes of
the invention are used for modulating the synthesis, expression and/or
stability of an mRNA encoding angiogenic factor, especially ARNT,
integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
especially used to treat cancer, diabetic retinopathy, age related
macular degeneration (ARMD), inflammation, and arthritis, as well as
neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber

CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 1 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 777 TTTTGTAGATGCGG 793
Db 1 UUUUAGUAGACGCGG 17

RESULT 1833
AAA22827
ID AAA22827 standard; RNA; 17 BP.

XX AAA22827;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6053.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KM ophthalmologic; antiinflammatory; antirheumatic; antipsoriatic; AMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

PN MO9950403-A2.

PD 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability

PT of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 245; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA1685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,

CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiobroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 993 CCCGGCTCAAGCGATT 1009
Db 1 CCCGGUUCAGCGAUAU 17

RESULT 1834
AAA22830
ID AAA22830 standard; RNA; 17 BP.

XX AAA22830;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6056.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KM ophthalmologic; antiinflammatory; antirheumatic; antipsoriatic; AMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

PN MO9950403-A2.

PD 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability

PT of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 245; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA1685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;

CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT.
CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1004 GCGATTCTCTCTCTCA 1020
DB 1 GCGAUUCCUCCUCCUCA 17
XX
RESULT 1835
AAA22739
ID AAA22739 standard; RNA; 17 BP. }
XX
AC AAA22739;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5965.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO950403-A2.
XX
PD 07-OCT-1999.
XX
PP 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA1167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to

CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18366 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA1556 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT.
CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 3 A; 2 C; 3 G; 0 T; 9 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.6e+03;
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1063 CCGCTAATTTTGTATT 1079
DB 1 CCGCUAUAUUUUUGUAUU 17
XX
RESULT 1836
AAA22734
ID AAA22734 standard; RNA; 17 BP.
XX
AC AAA22734;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5960.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO950403-A2.
XX
PD 07-OCT-1999.
XX
PP 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 542 CTCAGCCTCCCAAGTAG 558
Db 1 CTCAGCCTCCCAAGTAG 17

RESULT 1837
AAA22826
ID AAA22826 standard; RNA; 17 BP.

XX
AC AAA22826;

XX
DT 19-JUN-2000 (first entry)

XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6052.

XX
DE Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX
OS Homo sapiens.

XX
EN WO950403-A2.

XX
PD 07-OCT-1999.

XX
PF 24-MAR-1999; 99WO-US006507.

XX
PR 27-MAR-1998; 98US-0079678P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX
DR WPI, 1999-591315/50.

XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
of an mRNA encoding an angiogenic factors.

XX
PS Claim 54; Page 244; 305pp; English.

XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 992 TCCCGGCTCAGCGAT 1008
Db 1 TCCCGGCTCAGCGAT 17

RESULT 1838
AAA22859
ID AAA22859 standard; RNA; 17 BP.

XX
AC AAA22859;

XX
DT 19-JUN-2000 (first entry)

XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6085.

XX
DE Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX
OS Homo sapiens.

XX
EN WO950403-A2.

XX
PD 07-OCT-1999.

XX
PF 24-MAR-1999; 99WO-US006507.

XX
PR 27-MAR-1998; 98US-0079678P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX DR WPI; 1999-591315/50.
XX XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX PS Claim 54; Page 247; 305pp; English.
XX CC The present invention describes enzymatic cleavage of nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences. AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA2422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiobroma of tuberculous scleriosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 1.6e+03;
XX Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 248 CTCGGCCTCCCAAGTG 264
DB 1 CUGGCGCCUCCCAAGUG 17
RESULT 1839
AAA22760
ID AAA22760 standard; RNA; 17 BP.
XX
XX AAA22760;
AC
XX
DT 19-JUN-2000 (first entry)
DE
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5986.
XX
XX Human: aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antitumor; antiparasitic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
XX tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX OS
XX MO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX PD
XX PF 24-MAR-1999; 99WO-US006507.
XX

PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcwigen JA;
XX WPI; 1999-591315/50.
XX DR
XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX PS Claim 54; Page 240; 305pp; English.
XX
XX CC The present invention describes enzymatic cleavage of nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences. AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA2422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (AMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiobroma of tuberculous scleriosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX SQ Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 1.6e+03;
XX Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 395 CTCGGATTACAGCGTG 411
DB 1 CUGGGAUACAGCGCGUG 17
RESULT 1840
AAA22834
ID AAA22834 standard; RNA; 17 BP.
XX
XX AAA22834;
AC
XX
DT 19-JUN-2000 (first entry)
DE
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6060.
XX
XX Human: aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antitumor; antiparasitic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
XX tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX OS
XX MO9950403-A2.
XX

```

XX 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
XX (RIBO-) RIBOZYME PHARM INC.
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
DR WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 245; 305pp; English.
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidioma of tubercous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 4 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1033 GCTGGGATTACGGGCAC 1049
DB 1 GCTGGGATUUCAGGCAC 17

```

```

RESULT 1841
AAA22723
ID AAA22723 standard; RNA; 17 BP.
XX
AC AAA22723;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5949.
XX
KW Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angioidioma;
KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;

```

```

KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS MO9950403-A2.
XX 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
XX (RIBO-) RIBOZYME PHARM INC.
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
DR WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 238; 305pp; English.
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidioma of tubercous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 678 CTGCACCTCTGCTCC 694
DB 1 CTGCACCTCTGCTCC 17

```

```

RESULT 1842
AAA22966/c
ID AAA22966 standard; RNA; 17 BP.
XX
AC AAA22966;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6192.
XX
KW Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;

```


KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
 XX WPI; 1999-591315/50.
 DR
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 54; Page 253; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA1751 to
 CC AAA1767 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA1768 to AAA17660 and AAA17623 to AAA17664 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA24222 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiodioma of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 0 T; 2 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 211 CTGGTCTCGAAGTCCCG 227
 Db 17 CTGGTCTCGAAGTCTG 1
 XX
 RESULT 1843
 ID AAA25179
 AC AAA25179 standard; DNA; 17 BP.
 AC AAA25179;
 XX
 DT 19-JUL-2000 (first entry)
 XX

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1677.
 XX
 XX Oestrogen receptor; c-rai; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Belgelman L, Mcswigen JA, Karpelky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
 PI Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 DR
 PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX
 PS Claim 77; Page 71; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium), or
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 594 ATTGTTATTTATTTATTT 610
 Db 1 ATTGTTATTTATTTATTT 17
 XX
 RESULT 1844
 ID AAA25553/c
 AC AAA25553 standard; DNA; 17 BP.
 AC AAA25553;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2051.
 XX

KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
OS Homo sapiens.
XX MO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US008547.
XX
XX 20-APR-1998; 98US-0082404P.
XX 23-JUN-1998; 98US-00103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Metulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PS Claim 77; Page 83; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 14 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 429 TTTATTTTATTTT 445
DB 17 TTTATTTTAAATTTT 1
RESULT 1845
AAA2554/c
ID AAA25554 standard; DNA; 17 BP.
XX AAA25554;
AC
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2052.
DE
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW anticancer; breast cancer; endometrium cancer; ss.

KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
OS Homo sapiens.
XX MO9954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US008547.
XX
XX 20-APR-1998; 98US-0082404P.
XX 23-JUN-1998; 98US-00103636.
XX (RIBO-) RIBOZYME PHARM INC.
XX Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Metulic-Adamic J;
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PS Claim 77; Page 83; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 14 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 428 TTTATTTTATTTT 444
DB 17 TTTATTTTAAATTTT 1
RESULT 1846
AAA25180
ID AAA25180 standard; DNA; 17 BP.
XX AAA25180;
AC
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678.
DE
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.

```
XX OS Homo sapiens.
XX PN WO954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US008547.
XX PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L,
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX PT New nucleic acids that interact, and optionally cleave, target sequences,
XX PS used to treat cancer.
XX PS Claim 77; Page 71; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
XX CC with a target sequence and contain at least one phosphorodithioate
XX CC link, having endonuclease activity. (A), and more generally any catalytic
XX CC nucleic acid (A') that modulates expression of the oestrogen receptor
XX CC gene, are used to treat cancer (particularly of breast or endometrium),
XX CC in vivo or by transforming cells ex vivo and implanting treated cells, or
XX CC for other conditions associated with levels of oestrogen receptor.
XX CC Because of the high selectivity for targeted RNA, (A) can also be used to
XX CC correlate inhibition of gene expression with alterations in phenotype,
XX CC particularly for identification of therapeutic targets, and as research
XX CC reagents (for RNA, in the same way that restriction endonucleases are
XX CC used with DNA). The combination of modifications in (A) improves
XX CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX CC AAA24748 to AAA25992 represent their corresponding target sequences.
XX CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX CC sequences, and AAA26107 to AAA26218 represent their corresponding target
XX CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX CC antisense oligonucleotides used in the exemplification of the present
XX CC invention
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 595 TTTTATTATTTATTTT 611
XX DB 1 TTTTGTTTTATTTT 17
XX
XX RESULT 1847
XX AAF06150
XX ID AAF06150 standard; DNA; 17 BP.
XX AC AAF06150;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #2947.
XX XX
XX KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX OS interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
```

```
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, Mcswigen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PS Claim 42; Page 123; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
XX CC molecules that act as inhibitors of the expression of repressor genes
XX CC encoding the TR2 Orphan receptor, EAR3/CORP-TF-1, the GATA transcription
XX CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
XX CC consequently increases expression of) genes involved in the production of
XX CC erythropoietin, granulocyte colony stimulating factor protein and
XX CC interferon alpha
XX SQ Sequence 17 BP; 2 A; 0 C; 1 G; 0 T; 14 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 11.8%; Pred. No. 1.6e+03;
XX Matches 2; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 428 TTTTATTATTTATTTT 444
XX DB 1 UUGUUVUUUUUUUUUU 17
XX
XX RESULT 1848
XX AAF06149
XX ID AAF06149 standard; DNA; 17 BP.
XX AC AAF06149;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #2946.
XX KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX KM interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, Mcswigen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX PT interferon alpha and erythropoietin.
XX PS Claim 42; Page 123; 164pp; English.
```

XX CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TP2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP, 2 A; 0 C; 1 G; 0 T; 14 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 11.8%; Pred. No. 1.6e+03;
Matches 2; Conservative 14; Mismatches 1; Indels 0; Gaps 0;
QY 427 TTTTATTATTATTATT 443
DB 1 UUGUAAUUUUUUUUUU 17
XX
RESULT 1849
ABT39409/C
ID ABT39409 standard; DNA; 17 BP.
XX
AC ABT39409;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5046.
XX
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 623; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC degeneration, specifically cancer but also Alzheimer's disease and

CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP, 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 479 AGTGCAGTGTGTGATC 495
DB 17 AGTGCAGTGTGTGATC 1
XX
RESULT 1850
ABT38882
ID ABT38882 standard; DNA; 17 BP.
XX
AC ABT38882;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4519.
XX
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 562; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SEQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGGC 853

Db 1 GATCTGCTGCTCGGC 17

RESULT 1851

ABT38151

ID ABT38151 standard; DNA; 17 BP.

XX ABT38151;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 3788.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

XX anti-sense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrenia; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; Page 476; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX given in the specification, a sequence containing at least 15 consecutive

XX nucleotides from the 17 mer sequence, a sequence with, after optimal

XX alignment, at least 80 % identity to the 17 mer sequence, or the complement

XX of any of them, or the corresponding RNA. The novel isolated nucleic

XX acids of the invention are useful as probes and primers for detecting,

XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX component of a gene chip, in vitro as (anti)sense reagents, and for

XX production of recombinant polypeptides. Any of the nucleic acids,

XX polypeptides, vectors containing the nucleic acids, cells containing the

XX vector or antibodies directed against the polypeptides are useful for

XX preparation of pharmaceuticals for prevention and/or treatment of viral

XX diseases that are characterised by development of tumours or cell

XX degeneration, specifically cancer but also Alzheimer's disease and

XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

XX patient samples is useful for diagnosis and/or prognosis of these

XX diseases. The polypeptides can also be used to generate antibodies, and

XX both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SEQ Sequence 17 BP; 1 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGGC 853

Db 1 GATCTGCTGCTCGGC 17

RESULT 1852

ABT38720/c

ID ABT38720 standard; DNA; 17 BP.

XX ABT38720;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 4357.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;

XX anti-sense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrenia; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; Page 543; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX given in the specification, a sequence containing at least 15 consecutive

XX nucleotides from the 17 mer sequence, a sequence with, after optimal

XX alignment, at least 80 % identity to the 17 mer sequence, or the complement

XX of any of them, or the corresponding RNA. The novel isolated nucleic

XX acids of the invention are useful as probes and primers for detecting,

XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX component of a gene chip, in vitro as (anti)sense reagents, and for

XX production of recombinant polypeptides. Any of the nucleic acids,

XX polypeptides, vectors containing the nucleic acids, cells containing the

XX vector or antibodies directed against the polypeptides are useful for

XX preparation of pharmaceuticals for prevention and/or treatment of viral

XX diseases that are characterised by development of tumours or cell

XX degeneration, specifically cancer but also Alzheimer's disease and

XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in

XX patient samples is useful for diagnosis and/or prognosis of these

XX diseases. The polypeptides can also be used to generate antibodies, and

XX both the polypeptide and antibodies are useful as components of protein

XX chips. The nucleic acid sequences of the invention can be used in gene

XX therapy. This polynucleotide sequence represents a tumour suppression

The invention relates to a novel isolated 17 mer nucleic acid sequence, nucleotides from the 17 mer sequence, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, or a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acid of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukulin oligonucleotide of the invention

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, or the complement hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention


```
RESULT 1859
ABT40194/C
ID ABT40194 standard; DNA; 17 BP.
XX
XX
AC ABT40194;
XX
XX
DT 13-JUN-2003 (first entry)
XX
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5831.
XX
XX
KW Cytostatic; virocid; neuroprotective; nootropic; neuroleptic; gene chip;
KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025175-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313353/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; Page 715; 720pp; French.
XX
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 653 AGTCAGTGGCGGCATC 669
DB 17 AGTCAGTGGCGGCATC 1
RESULT 1860
```

```
ABT35639
ID ABT35639 standard; DNA; 17 BP.
XX
XX
AC ABT35639;
XX
XX
DT 12-JUN-2003 (first entry)
XX
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 1276.
XX
XX
KW Cytostatic; virocid; neuroprotective; nootropic; neuroleptic; gene chip;
KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025175-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313353/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; Page 182; 720pp; French.
XX
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 869 GATTACAGCGCGTGAGCC 885
DB 1 GATCACAGCGCGTGAGCC 17
RESULT 1861
ABT40150/C
ID ABT40150 standard; DNA; 17 BP.
```


XX AC ABT40150;
 XX XX
 DT 13-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 5787.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
 XX KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN MO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002MO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-313353/30.
 XX PT New isolated nucleic acid, useful for treating viral diseases associated
 XX PT with tumors and cell degeneration, also related polypeptides, antibodies
 XX PT and transfected cells.
 XX PS Disclosure; Page 710; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX CC given in the specification, a sequence containing at least 15 consecutive
 XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 XX CC hybridizes to them under highly stringent conditions, or the complement
 XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
 XX CC acids of the invention are useful as probes and primers for detecting,
 XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
 XX CC production of recombinant polypeptides. Any of the nucleic acids,
 XX CC polypeptides, vectors containing the nucleic acids, cells containing the
 XX CC vector or antibodies directed against the polypeptides are useful for
 XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
 XX CC diseases that are characterised by development of tumours or cell
 XX CC degeneration, specifically cancer but also Alzheimer's disease and
 XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX CC patient samples is useful for diagnosis and/or prognosis of these
 XX CC diseases. The polypeptides can also be used to generate antibodies, and
 XX CC both the polypeptide and antibodies are useful as components of protein
 XX CC chips. The nucleic acid sequences of the invention can be used in gene
 XX CC therapy. This polynucleotide sequence represents a tumour suppression
 XX CC related human fukutin oligonucleotide of the invention
 XX XX
 SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 479 AGTCAGTGTGTGATC 495
 DB 17 AGTCAGTGTGTGATC 1
 RESULT 1862
 ABT35874/C
 ID ABT35874 standard; DNA; 17 BP.
 XX AC ABT35874;
 XX AC

XX. XX. 12-JUN-2003 (first entry)
 DT 12-JUN-2003 (first entry)
 XX DE Tumour suppression related human fukutin oligo SEQ ID No 1511.
 XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
 XX KW human fukutin; ds.
 XX OS Homo sapiens.
 XX PN MO2003025175-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002MO-IB004208.
 XX PR 17-SEP-2001; 2001FR-00011978.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-313353/30.
 XX PT New isolated nucleic acid, useful for treating viral diseases associated
 XX PT with tumors and cell degeneration, also related polypeptides, antibodies
 XX PT and transfected cells.
 XX PS Disclosure; Page 209; 720pp; French.
 XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 XX CC given in the specification, a sequence containing at least 15 consecutive
 XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 XX CC hybridizes to them under highly stringent conditions, or the complement
 XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
 XX CC acids of the invention are useful as probes and primers for detecting,
 XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
 XX CC production of recombinant polypeptides. Any of the nucleic acids,
 XX CC polypeptides, vectors containing the nucleic acids, cells containing the
 XX CC vector or antibodies directed against the polypeptides are useful for
 XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
 XX CC diseases that are characterised by development of tumours or cell
 XX CC degeneration, specifically cancer but also Alzheimer's disease and
 XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 XX CC patient samples is useful for diagnosis and/or prognosis of these
 XX CC diseases. The polypeptides can also be used to generate antibodies, and
 XX CC both the polypeptide and antibodies are useful as components of protein
 XX CC chips. The nucleic acid sequences of the invention can be used in gene
 XX CC therapy. This polynucleotide sequence represents a tumour suppression
 XX CC related human fukutin oligonucleotide of the invention
 XX XX
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 479 AGTCAGTGTGTGATC 495
 DB 17 AGTCAGTGTGTGATC 1
 RESULT 1863
 ABT39264
 ID ABT39264 standard; DNA; 17 BP.
 XX AC ABT39264;
 XX AC
 DT 12-JUN-2003 (first entry)

XX	Cytostatic; vincinide; neuroprotective; nocrotropic; neuroleptic; gene chip;
XX	antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM	schizophrenia; protein chip; gene therapy; tumour suppression;
KM	human fukutin; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO2003025175-A2.
XX	
PD	27-MAR-2003.
XX	
XX	17-SEP-2002; 2002WO-IB004208.
XX	
PR	17-SEP-2001; 2001FR-00011978.
XX	
PA	(MOLE-) MOLECULAR ENGINES LAB.
XX	
PI	Telerman A, Amson R, Tuijnder M,
DR	WPI; 2003-313353/30.
XX	
PT	New isolated nucleic acid, useful for treating viral diseases associated
PT	with tumors and cell degeneration, also related polypeptides, antibodies
PT	and transfected cells.
XX	
PS	Claim 1; Page 709; 720pp; French.
XX	
CC	The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC	given in the specification, a sequence containing at least 15 consecutive
CC	nucleotides from the 17 mer sequence, a sequence with, after optimal
CC	alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC	hybridizes to them under highly stringent conditions, or the complement
CC	of any of them, or the corresponding RNA. The novel isolated nucleic
CC	acids of the invention are useful as probes and primers for detecting,
CC	identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC	component of a gene chip, in vitro as (anti)sense reagents, and for
CC	production of recombinant polypeptides. Any of the nucleic acids,
CC	polypeptides, vectors containing the nucleic acids, cells containing the
CC	vector or antibodies directed against the polypeptides are useful for
CC	preparation of pharmaceuticals for prevention and/or treatment of viral
CC	diseases that are characterized by development of tumours or cell
CC	degeneration, specifically cancer but also Alzheimer's disease and
CC	schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC	patient samples is useful for diagnosis and/or prognosis of these
CC	diseases. The polypeptides can also be used to generate antibodies, and
CC	both the polypeptide and antibodies are useful as components of protein
CC	chips. The nucleic acid sequences of the invention can be used in gene
CC	therapy. This polynucleotide sequence represents a tumour suppression
CC	related human fukutin oligonucleotide of the invention
XX	
SO	Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX	
Query Match	1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity	94.1%; Pred. No. 1.6e+03;
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	224 CCCGACCTCAGATGATC 240
DB	17 CCCGACCTCAGTGATC 1
XX	
RESULT 1865	
ADB04318	
ID	ADB04318 standard; DNA; 17 BP.
XX	
AC	ADB04318;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Human MD27 scanning oligonucleotide SEQ ID 5304.
XX	
XX	Cycostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
OS Homo sapiens.
XX EPI281758-A2.
XX
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX MPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5304; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 651 GGAGTGCAGTGGCGCA 667
DB 1 GGAGTGCAGTGGCGCCA 17
RESULT 1866
ADB04317
ID ADB04317 standard; DNA; 17 BP.
XX
XX ADB04317;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5303.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX

PD 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX MPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5303; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 650 TGGAGTGCAGTGGCGCA 666
DB 1 TGGAGTGCAGTGGCGCCA 17
RESULT 1867
ADB04437
ID ADB04437 standard; DNA; 17 BP.
XX
XX ADB04437;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5423.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX

```
PI Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5423; 103bp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 17 BP; 3 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

Query Match      1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      768 TTTTGTATTCTTACT 784
      1 |||||
      1 TATTGTATTCTTACT 17

Db
RESULT 1868
ADB04446
ID ADB04446 standard; DNA; 17 BP.
XX
XX ADB04446;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5432.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX EPI281758-A2.
PD
XX
XX 05-FEB-2003.
PF
XX
XX 30-JUL-2002; 2002EP-00016874.
PR
XX
XX 02-AUG-2001; 2001US-00922181.
PA
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
```

```
XX
XX
XX Example 8; SEQ ID NO 5432; 103bp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 17 BP; 4 A; 1 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      777 TTTTGTAGAGATGCG 793
      |||||
      1 TTTTGTAGAGATGCG 17

Db
RESULT 1869
ADB04316
ID ADB04316 standard; DNA; 17 BP.
XX
XX ADB04316;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5302.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PR
XX
XX 02-AUG-2001; 2001US-00922181.
PA
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5302; 103bp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
```

or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.

Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 649 CTGGAGTGCAGTGGCGC 665
DB 1 CTGGAGTGCAGTGGCGC 17

RESULT 1870
ADB04447
ID ADB04447 standard; DNA; 17 BP.
XX ADB04447;
AC ADB04447;
XX 20-NOV-2003 (first entry)
DT
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5433.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.

XX Homo sapiens.

OS
XX
PN EP1281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

PI
XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5433; 103bp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 4 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 778 TTTTAGTAGAGATGGCG 794
DB 1 TTTTAGTAGAGATGGCG 17

RESULT 1871
ADB04444
ID ADB04444 standard; DNA; 17 BP.

XX ADB04444;
AC ADB04444;
XX 20-NOV-2003 (first entry)
DT
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5430.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.

XX Homo sapiens.

OS
XX
PN EP1281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

PI
XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5430; 103bp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 5 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 775 TATTTTAGTAGAG 791
 |||||
 DB 1 TATTTTAGTAGAGC 17

RESULT 1872
 ADB04445
 ID ADB04445 standard; DNA; 17 BP.
 AC ADB04445;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD27 scanning oligonucleotide SEQ ID 5431.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KM developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 5431; 103bp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 5 A; 1 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 776 ATTTTAGTAGAGTGG 792
 |||||
 DB 1 ATTTTAGTAGAGCG 17

RESULT 1873
 ABZ60575

ID ABZ60575 standard; RNA; 17 BP.
 XX
 AC ABZ60575;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNzyme substrate #687.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016840.
 XX
 PR 29-MAY-2001; 2001US-0294140P.
 XX
 PR 06-JUN-2001; 2001US-0296249P.
 XX
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswigen J;
 XX
 DR WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 56; Page 98; 185bp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytoskeletal, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ65524 -
 CC ABZ6530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention.
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 1.6e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 498 AGCTCACTGCAGCTTC 514
 |||||
 DB 1 AGCTCACTGCAGCTTC 17

RESULT 1874
 ABZ60585
 ID ABZ60585 standard; RNA; 17 BP.
 XX
 AC ABZ60585;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNzyme substrate #697.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.
 XX PN WO200297114-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-US016840.
 XX PR 29-MAY-2001; 2001US-0294140P.
 XX PR 06-JUN-2001; 2001US-0296249P.
 XX PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX DR WPI; 2003-140484/13.
 XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX PS Claim 58; Page 98; 185pp; English.
 XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ6531, ABZ66520 - ABZ6524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 CC
 SQ Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 1.6e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 725 CCTGAGTAGCTGGGACT 741
 Db 1 CCUGAGUGGCGUGGAGUU 17
 RESULT 1875
 ABZ60574
 ID ABZ60574 standard; RNA; 17 BP.
 XX AC ABZ60574;
 XX DT 21-MAR-2003 (first entry)
 XX DE Human K-Ras DNAzyme substrate #686.
 XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX OS Homo sapiens.
 XX PN WO200297114-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-US016840.
 XX PR 29-MAY-2001; 2001US-0294140P.
 XX PR 06-JUN-2001; 2001US-0296249P.
 XX PR 10-SEP-2001; 2001US-0318471P.

PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX DR WPI; 2003-140484/13.
 XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX PS Claim 58; Page 98; 185pp; English.
 XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ6531, ABZ66520 - ABZ6524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 CC
 SQ Sequence 17 BP; 4 A; 8 C; 2 G; 0 T; 3 U; 0 Other;
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 969 CTCGGCTCACTGCACAC 985
 Db 1 CUCAGCUCACUCGACAC 17
 RESULT 1876
 ABZ60568
 ID ABZ60568 standard; RNA; 17 BP.
 XX AC ABZ60568;
 XX DT 21-MAR-2003 (first entry)
 XX DE Human K-Ras DNAzyme substrate #680.
 XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX OS Homo sapiens.
 XX PN WO200297114-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-US016840.
 XX PR 29-MAY-2001; 2001US-0294140P.
 XX PR 06-JUN-2001; 2001US-0296249P.
 XX PR 10-SEP-2001; 2001US-0318471P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Mcswiggen J;
 XX DR WPI; 2003-140484/13.
 XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 98; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
XX ribozymes of the invention
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 648 GCTGAGTGCAGTGGCG 664
DB 1 GCTGGAUGCAGUGGCG 17
RESULT 1877
ABZ60586
ID ABZ60586 standard; RNA; 17 BP.
XX AC ABZ60586;
XX DT 21-MAR-2003 (first entry)
XX DE Human K-Ras DNAzyme substrate #698.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PN WO200297114-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US016840.
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PS Claim 58; Page 98; 185pp; English.
XX PI Mcswigen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX PS Claim 58; Page 98; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
CC ribozymes of the invention
SQ Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 731 TAGTGGAGTACAGGC 747
DB 1 UAGCTGGAGUACAGGC 17
RESULT 1878
ABZ60606
ID ABZ60606 standard; RNA; 17 BP.
XX AC ABZ60606;
XX DT 21-MAR-2003 (first entry)
XX DE Human K-Ras DNAzyme substrate #718.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PN WO200297114-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US016840.
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PS Claim 58; Page 98; 185pp; English.
XX PI Mcswigen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX PS Claim 58; Page 98; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
XX ribozymes of the invention
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 213 GGTCTCGAAGCTCCGAC 229
 ||:|||||:|||||
 1 GGUCUCGACGUCGAC 17

RESULT 1879
 ABZ60566
 ID ABZ60566 standard; RNA; 17 BP.

XX AC ABZ60566;

XX DT 21-MAR-2003 (first entry)

XX DE Human K-Ras DNAzyme substrate #678.

XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PA WO200297114-A2.

XX PI Mcswigen J;

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswigen J;

XX PD WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 98; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 640 TCACCCAGGCTGAGTG 656
 :|||||:|||||:
 DB 1 UCACCCAGGCTGAGT 17

RESULT 1880
 ABZ60604
 ID ABZ60604 standard; RNA; 17 BP.
 XX AC ABZ60604;
 XX

DT 21-MAR-2003 (first entry)
 XX DE Human K-Ras DNAzyme substrate #716.
 XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PA WO200297114-A2.

XX PI Mcswigen J;

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswigen J;

XX PD WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 98; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
 CC ribozymes of the invention

XX SQ Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.6e+03;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 202 TTGTCAGGCTGCTC 218
 :||:|||||:|||||:
 DB 1 UUGGCGAGGCTGCTC 17

RESULT 1881
 ABZ60597
 ID ABZ60597 standard; RNA; 17 BP.

XX AC ABZ60597;

XX DT 21-MAR-2003 (first entry)

XX DE Human K-Ras DNAzyme substrate #709.

XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PA WO200297114-A2.

XX 05-DEC-2002.
XX
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswigen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 98; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
XX CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 4 A; 0 C; 1 G; 0 T; 12 U; 0 Other;
XX
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 29.4%; Pred. No. 1.6e+03;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1067 TAAATTTTGTATTTTCA 1083
XX :||:||||:||||:|
XX 1 UAAUUUUUGUAAUUUUA 17
XX
XX
XX RESULT 1882
XX ABZ61843/C
XX ID ABZ61843 standard; RNA; 17 BP.
XX
XX AC ABZ61843;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human H-Ras DNAzyme target #634.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX

PI Mcswigen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 123; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytosatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
XX CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 6 A; 3 C; 6 G; 0 T; 2 U; 0 Other;
XX
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 831 CCTGTGATCTGCTGTC 847
XX :||:||||:||||:|
XX 17 CCTATGATCTGCTGTC 1
XX
XX
XX RESULT 1883
XX ABZ60567
XX ID ABZ60567 standard; RNA; 17 BP.
XX
XX AC ABZ60567;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human K-Ras DNAzyme substrate #679.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswigen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 98; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX

CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in AB259889 - AB262216, AB264544 - AB265531, AB265520 - AB265524,
CC AB265530 - AB265585 represent substrate/target sequences for the human
CC ribozymes of the invention

SQ Sequence 17 BP; 4 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 646 AGGCTGAGTGCACTGG 662
DB 1 AGGCTGGAUGCAGUGG 17

RESULT 1884
ID ACC64751 standard; DNA; 17 BP.
XX
AC ACC64751;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1998.
XX
KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002MO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Tejerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 264; 738pp; French.
XX
SQ The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 881 GAGCCACACGCCCCGC 897
DB 1 GATCCACACGCCCCGC 17

RESULT 1885
ID ACC6479 standard; DNA; 17 BP.
XX
AC ACC6479;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5726.
XX
KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002MO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Tejerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 700; 738pp; French.
XX
SQ The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia

SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCGCTGCTCGGC 853
DB 1 GATCGCTGCTCGTC 17

RESULT 1886
ID ADB44008 standard; DNA; 17 BP.
XX
AC ADB44008;

XX 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #4311.
 XX
 XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN MO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002MO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PR (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PA Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-441574/41.
 DR
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS
 XX Disclosure; Page 538; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 CC
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 492 GATCAGCTCTACTGCA 508
 1 GATCAGCTCTACTGCA 17
 XX
 RESULT 1887
 ID ADB41143 standard; DNA; 17 BP.
 XX
 AC ADB41143;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX

XX
 DE Tumour suppression/reversion associated nucleotide #1466.
 XX
 XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN MO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002MO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PR (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PA Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-441574/41.
 DR
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS
 XX Disclosure; Page 203; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 CC
 XX
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 Db 479 AGTGCAGTGTGTGATC 495
 17 AGTGCAGTGTGTGATC 1
 XX
 RESULT 1888
 ID ADB43650 standard; DNA; 17 BP.
 XX
 AC ADB43650;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #3973.
 XX

KM cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.

OS Homo sapiens.
 XX MO2003040369-A2.
 XX
 XX 15-MAY-2003.
 PD
 XX 17-SEP-2002; 2002MO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-441574/41.
 DR
 XX
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS
 XX Disclosure; Page 496; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and/or treatment
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 CC
 SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 837 GATCTGCTGCTGCTGCGC 853
 |||||
 Db 1 GATCTGCTGCTGCTGCGC 17

RESULT 1889
 ADB44570
 ID ADB44570 standard; DNA; 17 BP.
 XX
 AC ADB44570;
 DE
 XX 18-DEC-2003 (first entry)
 DT
 XX Tumour suppression/reversion associated nucleotide #4893.
 DE
 XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.

XX
 OS Homo sapiens.
 XX MO2003040369-A2.
 XX
 XX 15-MAY-2003.
 PD
 XX 17-SEP-2002; 2002MO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-441574/41.
 DR
 XX
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS
 XX Disclosure; Page 604; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and/or treatment
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 CC
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 492 GATCAGAGCTCAGTCA 508
 |||||
 Db 1 GATCAGAGCTCAGTCA 17

RESULT 1890
 ADB44878
 ID ADB44878 standard; DNA; 17 BP.
 XX
 AC ADB44878;
 DE
 XX 18-DEC-2003 (first entry)
 DT
 XX Tumour suppression/reversion associated nucleotide #5201.
 DE
 XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.

```
XX 15-MAY-2003.
PD 17-SEP-2002; 2002WO-IB004219.
XX PF 17-SEP-2001; 2001FR-00011981.
XX PR 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-441574/41.
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS Disclosure; Page 640; 771pp; French.
XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 837 GATCTGCTGCTGCTGCGC 853
XX DB 1 GATCTGCTGCTGCTGCGC 17
XX
XX RESULT 1891
XX ID ADB44306 standard; DNA; 17 BP.
XX AC ADB44306;
XX XX
XX DT 18-DEC-2003 (first entry)
XX DE Tumour suppression/reversion associated nucleotide #4629.
XX XX
XX KW cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS Homo sapiens.
XX XX
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
```

```
XX 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-441574/41.
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS Disclosure; Page 573; 771pp; French.
XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 837 GATCTGCTGCTGCTGCGC 853
XX DB 1 GATCTGCTGCTGCTGCGC 17
XX
XX RESULT 1892
XX ID ADB44574/C
XX AC ADB44574 standard; DNA; 17 BP.
XX XX
XX DT 18-DEC-2003 (first entry)
XX DE Tumour suppression/reversion associated nucleotide #4897.
XX XX
XX KW cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS Homo sapiens.
XX XX
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
```

XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX
XX Disclosure; Page 604; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 224 CCCGACCTCAGATGATC 240
Db 17 CCCGACCTCAGATGATC 1

RESULT 1893
ADB44518/c
ID ADB44518 standard; DNA; 17 BP.
XX
XX ADB44518;
XX
XX 18-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #4841.
XX
XX cytotactic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
XX virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX
XX Homo sapiens.
XX
XX MO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002MO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
DR

XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX
XX Disclosure; Page 597; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 5 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 479 AGTGCAGTGGTGGATC 495
Db 17 AGTGCAGTGGTGGATC 1

RESULT 1894
ADE14015
ID ADE14015 standard; DNA; 17 BP.
XX
XX ADE14015;
XX
XX 29-JAN-2004 (first entry)
XX
XX Optineurin promoter motif, repeat element or regulatory region #124.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;
XX glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
XX
XX US2003190617-A1.
XX
XX 09-OCT-2003.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX (MORI/) MORISSETTE J.
XX
XX Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
PT

PT optineurin promoter to diagnose, prognosis and treat glaucoma and related disorders.

PS Claim 11; SEQ ID NO 126; 159pp; English.

XX

CC The invention relates to an isolated nucleic acid (N1) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter appearing as ADE13890. Also included are the optineurin promoter operably linked to a heterologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample obtained from a cell or bodily fluid (comprising detecting a polymorphism in a promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence of an optineurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive disorder resulting in loss of visual field in a patient (or the severity of progression of glaucoma in a patient, comprising providing amplification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optineurin promoter and amplifying the DNA) and detecting a polymorphism (comprising obtaining a sample containing human genomic DNA, providing a nucleic acid capable of detecting a SNP located within an optineurin promoter, and detecting the polymorphism). The invention is used to diagnose and prognose glaucoma and also to treat glaucoma related disorders. The present sequence is an optineurin promoter motif, repeat element or putative regulatory region.

CC

XX

SO Sequence 17 BP; 4 A; 1 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 589 GGCTAATTTTATTTT 605
1 GGCTAATTTTATTTT 17

Db

RESULT 1895
ADE14019/c
ID ADE14019 standard; DNA; 17 BP.
XX
AC ADE14019;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #128.
XX
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder;
KM glaucoma related disorder; motif; repeat element; regulatory region.
OS Homo sapiens.
XX
PN US2003190617-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00091281.
XX
PR 06-MAR-2002; 2002US-00091281.
XX
PA (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
PI Raymond V, Morissette J, Si E;
XX
DR WPI; 2003-864168/80.
XX

PT New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognosis and treat glaucoma and related disorders.

PS Claim 11; SEQ ID NO 130; 159pp; English.

XX

XX

CC The invention relates to an isolated nucleic acid (N1) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter appearing as ADE1890. Also included are the optineurin promoter operably linked to a heterologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample obtained from a cell or bodily fluid (comprising detecting a polymorphism in a promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence of an optineurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive disorder resulting in loss of visual field in a patient (or the severity of progression of glaucoma in a patient, comprising providing amplification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optineurin promoter and amplifying the DNA) and detecting a polymorphism (comprising obtaining a sample containing human genomic DNA, providing a nucleic acid capable of detecting a SNP located within an optineurin promoter, and detecting the polymorphism). The invention is used to diagnose and prognose glaucoma and also to treat glaucoma related disorders. The present sequence is an optineurin promoter motif, repeat element or putative regulatory region.

CC

XX

SO Sequence 17 BP; 11 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 770 TTTTGATTTTAGTAG 786
17 TTTTATTTTATTTAGTAG 1

Db

RESULT 1896
ADE43565/c
ID ADE43565 standard; DNA; 17 BP.
XX
AC ADE43565;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human IDB sequencing primer, SEQ ID 170.
XX
KW Neurodegenerative disease; uPA; SNGG; IDE; KNSL1; LIPA; TNFRSF6;
KM Alzheimer's disease; neuroprotective; neurotrophic; gene therapy;
XX
OS Homo sapiens.
XX
PN WO2003054143-A2.
XX
PD 03-JUL-2003.
XX
PF 25-OCT-2002; 2002WO-US034679.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 08-NOV-2001; 2001US-0336929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (NEUR-) NEUROGENETICS INC.

PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Becker KD, Veljicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
 PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DJ;
 XX WPI; 2003-559131/52.
 DR
 XX
 PT Determining a predisposition for or the occurrence of neurodegenerative
 PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
 PT the presence or absence of an allelic variant of one or more polymorphic
 PT regions.
 XX
 XX Example 3; Page 276; 848pp; English.
 PS
 XX The present invention relates to a method (M1) for determining a
 CC predisposition for or the occurrence of neurodegenerative disease in a
 CC subject. The method comprises detecting in a target nucleic acid obtained
 CC from the subject the presence or absence of an allelic variant of one or
 CC more polymorphic regions of one or more genes selected from uPA
 CC (urokinase plasminogen activator), SNCG (gamma-gynuclein), IDE (insulin-
 CC degrading enzyme), KNS1L (Kinesin-like protein 1), LIPA (lysosomal acid
 CC lyase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
 CC presence of at least one of the allelic variant of one or more
 CC polymorphic regions is indicative of a predisposition for or the
 CC occurrence of neurodegenerative disease. The genes are all located on
 CC chromosome 10. M1 is useful for determining a predisposition for or the
 CC occurrence of, and for treating neurodegenerative disease, particularly
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used
 CC in the method of the invention.
 CC
 XX Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 646 AGGCTGAGTGCAGTGC 662
 DB 17 ACGCTGGAGTGCAGTGC 1
 RESULT 1897
 ADI50915/C
 ID ADI50915 standard; DNA; 17 BP.
 XX
 AC ADI50915;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID3418.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cyostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 PD 27-MAR-2003.
 PP 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 DR
 XX New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 3418; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cyostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpc_sequences
 CC
 XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 479 AGTCAAGTGGTGCATC 495
 DB 17 AGTCAAGTGGTGCATC 1
 RESULT 1898
 ADI50723/C
 ID ADI50723 standard; DNA; 17 BP.
 XX
 AC ADI50723;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID3226.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cyostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 PD 27-MAR-2003.
 PP 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 DR
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 3226; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytosstatic, vinticide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

SO Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
Db 17 AGTGCAGTGTGTGATC 1

RESULT 1899
ADIS2180/C
ID ADIS2180 standard; DNA; 17 BP.
XX ADIS2180;
AC ADIS2180;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID4683.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX cytosstatic; vinticide; neuroprotective; nootropic; neuroleptic; probe;
XX primer; PCR; gene chip; antisense; viral disease; tumour;
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX OS
XX MO2003025177-A2.
XX PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002MO-IB004523.
PF
XX 17-SEP-2001; 2001FR-00011980.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313354/30.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; SEQ ID NO 4683; 30pp; French.

CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytosstatic, vinticide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,

CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

SO Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
Db 17 AATGCAGTGTGTGATC 1

RESULT 1900
ADIS0051/C
ID ADIS0051 standard; DNA; 17 BP.
XX ADIS0051;
AC ADIS0051;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2554.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX cytosstatic; vinticide; neuroprotective; nootropic; neuroleptic; probe;
XX primer; PCR; gene chip; antisense; viral disease; tumour;
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX OS
XX MO2003025177-A2.
XX PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002MO-IB004523.
PF
XX 17-SEP-2001; 2001FR-00011980.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313354/30.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; SEQ ID NO 2554; 30pp; French.

CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytosstatic, vinticide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

SO Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
|||||
DB 17 AGTGCAGTGTGTGATC 1

RESULT 1901
AD151643/c
ID AD151643 standard; DNA; 17 BP.
XX AC AD151643;
XX DT 15-APR-2004 (first entry)
XX DE Human tumour suppression/reversion-related DNA sequence SeqID4146.
XX KM tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KM cytoskeletal; virocidic; neuroprotective; neurotropic; neuroleptic; probe;
XX KM primer; PCR; gene chip; antisense; viral disease; tumour;
XX KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX OS Homo sapiens.
XX PN WO2003025177-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002MO-IB004523.
XX PR 17-SEP-2001; 2001FR-00011980.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313354/30.
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumours and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; SEQ ID NO 4146; 30pp; French.
XX XX
XX CC This invention relates to novel isolated nucleic acid sequences involved
XX CC in the phenomena of tumour suppression, tumour reversion, apoptosis
XX CC and/or resistance to viruses. The invention may be useful for the
XX CC development of compounds with a cytostatic, virocidic, neuroprotective,
XX CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
XX CC probes and primers for detecting, identifying, quantifying and/or
XX CC amplifying nucleic acid, for example as one component of a gene chip, in
XX CC vitro as antisense reagents and for production of recombinant
XX CC polypeptides. The invention may therefore be useful for preparation of
XX CC pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterized by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia. The
XX CC present sequence is that of a nucleic acid sequence of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/publishedpct_sequences
XX XX
XX SQ Sequence 17 BP; 6 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
|||||
DB 17 AGTGCAGTGTGTGATC 1

RESULT 1902
ACC52610/c
ID ACC52610 standard; DNA; 17 BP.
XX AC ACC52610;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #1377.
XX KM se; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KM tumour regression; apoptosis; virus resistance; diagnosis;
XX KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX XX
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 358; 798pp; French.
XX XX
XX CC This sequence represents an isolated nucleic acid sequence associated
XX CC with tumour suppression or regression, apoptosis or virus resistance. The
XX CC invention relates to these sequences or sequences having at least 80%
XX CC identity to them, and polypeptides encoded by the sequences or
XX CC polypeptides having 80% identity to the polypeptide sequences. The
XX CC invention is used to diagnose or treat viral disease or disease
XX CC characterized by development of tumour cells or cellular degeneration
XX CC
XX SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
|||||
DB 17 AGTGCAGTGTGTGATC 1

RESULT 1903
ACC51497/c
ID ACC51497 standard; DNA; 17 BP.
XX AC ACC51497;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #264.
XX KM se; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KM tumour regression; apoptosis; virus resistance; diagnosis;
XX KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.

```
XX 27-DEC-2002.
PD 20-JUN-2001; 2001FR-00008139.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 101; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
   |||||
   17 AATGCAGTGTGTGATC 1
DB

RESULT 1904
ID ACC54006 standard; DNA; 17 BP.
XX AC ACC54006;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2773.
XX SS; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 680; 798pp; French.
```

```
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 1 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATTCGCTGCTCGGC 853
   |||||
   1 GATTCGCCGCTCGGC 17
DB

RESULT 1905
ID ACC53324/c
XX AC ACC53324;
XX DT 27-JUN-2003 (first entry)
XX DE Human tumour suppressor sequence #2091.
XX SS; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX OS Homo sapiens.
XX PN FR2826373-A1.
XX PD 27-DEC-2002.
XX PF 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX DR WPI; 2003-250498/25.
XX PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 523; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match      1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
   |||||
   17 AGTGCAGTGTGTGATC 1
DB
```

```
RESULT 1906
ACCS4016
ID ACC54016 standard; DNA; 17 BP.
XX
AC
XX
XX
ACCS4016;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #2783.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
OS Homo sapiens.
XX
XX FR2826373-A1.
XX
XX PD 27-DEC-2002.
XX
XX PF 20-JUN-2001; 2001FR-00008139.
XX
XX PR 20-JUN-2001; 2001FR-00008139.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX PI Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 683; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 837 GATCTGCTGCTCGGC 853
DB 1 GATCTGCTGCTCGGC 17
RESULT 1907
ACCS1566/c
ID ACC51566 standard; DNA; 17 BP.
XX
AC
XX
XX ACC51566;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #333.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
OS Homo sapiens.
XX
```

```
PN FR2826373-A1.
XX
XX PD 27-DEC-2002.
XX
XX PF 20-JUN-2001; 2001FR-00008139.
XX
XX PR 20-JUN-2001; 2001FR-00008139.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX PI Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 117; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 224 CCCGACCTCAGATGATC 240
DB 17 CCCGACCTCAGATGATC 1
RESULT 1908
ACCS2881
ID ACC52881 standard; DNA; 17 BP.
XX
AC
XX
XX ACC52881;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #1648.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
OS Homo sapiens.
XX
XX FR2826373-A1.
XX
XX PD 27-DEC-2002.
XX
XX PF 20-JUN-2001; 2001FR-00008139.
XX
XX PR 20-JUN-2001; 2001FR-00008139.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX PI Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
```

PS Claim 1; Page 421; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 1 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGGC 853
DB 1 GATCCGCTGCTCGGC 17

RESULT 1909
ACC53359/c
ID ACC53359 standard; DNA; 17 BP.

XX ACC53359;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #2126.

XX ss: tumour suppressor; antitumour; cytostatic; tumour suppression;

KW tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.

XX Homo sapiens.

OS
XX
PN FR2826373-A1.

PD 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

PR 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

PA Tuijinder M, Telerman A, Amson R;

PI WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.

XX
PS Claim 1; Page 531; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 653 AGTGCACTGGCGCATC 669
|||||

DB 17 AGTGCACTGGCGCATC 1

RESULT 1910

ACC54020
ID ACC54020 standard; DNA; 17 BP.

XX ACC54020;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #2787.

XX ss: tumour suppressor; antitumour; cytostatic; tumour suppression;

KW tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.

XX Homo sapiens.

OS
XX
PN FR2826373-A1.

PD 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

PR 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

PA Tuijinder M, Telerman A, Amson R;

PI WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.

XX
PS Claim 1; Page 683; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGGC 853
DB 1 GATCTGCTGCTCGGC 17

RESULT 1911

ADL49918
ID ADL49918 standard; RNA; 17 BP.

XX ADL49918;

DT 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #1032.

XX antiense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

KW central nervous system injury; CNS injury; spinal cord injury; cancer;

KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
XX MO200281628-A2.
XX
PD 17-OCT-2002.
XX
XX 03-APR-2002; 2002MO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
DR
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3499; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 10 C; 3 G; 0 T; 3 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 371 CACCTGCTCAGCCTCC 387
DB 1 CACCTGCTCAGCCTCC 17
RESULT 1914
ADLS0193
ID ADLS0193 standard; RNA; 17 BP.
XX
XX ADLS0193;
AC
XX
DT 20-MAY-2004 (first entry)
XX
XX Human PKR substrate sequence #1307.
DE
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
XX MO200281628-A2.
XX
PD 17-OCT-2002.
XX
XX 03-APR-2002; 2002MO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
DR
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3726; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 940 TTACCCAGGCTGAGTG 956
DB 1 TTACCCAGGCTGAGTG 17
RESULT 1915
ADLS0202
ID ADLS0202 standard; RNA; 17 BP.
XX
XX ADLS0202;
AC
XX
DT 20-MAY-2004 (first entry)
XX
XX Human PKR substrate sequence #1316.
DE
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW autoimmune disease; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; de.
XX
XX Unidentified.
XX
XX WO200281628-A2.
PN PD 17-OCT-2002.
XX
PE 03-APR-2002; 2002WO-US010512.
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-031531SP.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI Blatt L, Chowrira B, Haeblerl P, Mswigen J, Fonaugh K,
XX WPI, 2003-058513/05.
DR Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D₂ receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.

Pt PT Claim 59; SEQ ID NO 3735; 317pp; English.

PS The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, Nogo, prostaglandin D₂ receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.

CC CC Sequence 17 BP; 2 A; 8 C; 2 G; 0 T; 5 U; 0 Other;

XX XX

SQ Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0,

Oy 532 ATCTTCTGCCCTACGC 548
| : | : | : | : |||||
Db 1 ATTUCCUCGGCCTCACGC 17

RESULT 1916
ADL50201
ID ADL50201 standard; RNA; 17 BP.
XX
XX AC ADL50201;
XX DT 20-MAY-2004 (first entry)
DE Human PKR substrate sequence #3315.
XX
XX antisenase oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D₂ receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KM	*retenosis; asthma; Crohn's disease; diabetes; obesity;
KM	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KV	substrate; de.
XX	
OS	Unidentified.
PN	
PD	MO200281628-A2.
PB	17-OCT-2002.
PP	03-APR-2002; 2002WO-US010512.
PR	05-APR-2001; 2001US-00827395.
PR	29-MAY-2001; 2001US-0294412P.
PR	28-AUG-2001; 2001US-0315315P.
PA	(RIBO-) RIBOZYME PHARM INC.
PI	Blaett L, Chowrira B, Haeblerl F, Mcswiggen J, Fosnaugh K;
DR	WPI, 2003-058513/05.
PT	Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor. Ikappab kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
PS	Claim 59; SEQ ID NO 3734; 317pp; English.
MX	The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NODG, prostaglandin D2 receptor (PTGDR), Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.
SQ	Sequence 17 BP; 3 A; 3 C; 5 G; 0 T; 6 U; 0 Other;
Query Match	1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity	58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0.	
DY	636 GGCTTCAGGTATTTCTC 712 ::: 1 GGGUCCAAGAUGCUC 17
ID	ADL49951 standard; RNA, 17 BP.
AC	ADL49951;
DT	20-MAY-2004 (first entry)
DE	Human PKR substrate sequence #1065.
KM	antisense oligonucleotide; neurite growth inhibitor, NODG;
KM	prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW	protein kinase PKR; cerebrovascular accident;
KW	central nervous system injury; CNS injury; spinal cord injury; cancer; melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 OS Unidentified.
 XX MO200281628-A2.
 XX 17-OCT-2002.
 PD 03-APR-2002; 2002MO-US010512.
 PF 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
 PI WPI; 2003-058513/05.
 DR Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX Claim 59; SEQ ID NO 3464; 317bp; English.
 PS
 XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 SQ Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;
 XX
 SQ
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 716 CCCGAGCCTCTGAGTA 732.
 Db 1 CCUCAGCCUCCUGAGUA 17
 RESULT 1920
 ADL50198
 ID ADL50198 standard; RNA; 17 BP.
 XX
 AC ADL50198;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1312.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 OS Unidentified.
 XX MO200281628-A2.
 XX 17-OCT-2002.
 PD 03-APR-2002; 2002MO-US010512.
 PF 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
 PI WPI; 2003-058513/05.
 DR Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX Claim 59; SEQ ID NO 3731; 317bp; English.
 PS
 XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
 XX
 SQ
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 1.6e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 672 GGCTCACTGCACCTCT 688
 Db 1 GGCTCAGCCGACUCCU 17
 RESULT 1921
 ADL50418
 ID ADL50418 standard; RNA; 17 BP.
 XX
 AC ADL50418;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1532.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3951, 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 1.6e+03;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 699 TTCAGTATTCCTCG 715
Db 1 UUCAAGUAGUUCUCUG 17
RESULT 1922
ADL49930
ID ADL49930 standard; RNA; 17 BP.
XX
AC ADL49930;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1044.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3463; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 715 GCCCAGCCCTCTGACT 731
Db 1 GCCUCAGCCUCCUGAGU 17
RESULT 1923
ADL50731
ID ADL50731 standard; RNA; 17 BP.
XX
AC ADL50731;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1845.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX	restenosis; asthma; Crohn's disease; diabetes; obesity;
XX	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX	great rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX	substrate; ds.
XX	Unidentified.
XX	
XX	WO200281628-A2.
XX	
XX	17-OCT-2002.
XX	
XX	03-APR-2002; 2002WO-US010512.
XX	
XX	05-APR-2001; 2001US-00827395.
XX	29-MAY-2001; 2001US-0294412P.
XX	28-AUG-2001; 2001US-0315315P.
XX	
XX	(RIBO-) RIBOZYME PHARM INC.
XX	
XX	Blatt L, Chowwira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX	
XX	WPI; 2003-058513/05.
XX	
XX	Claim 59; SEQ ID NO 3736; 317pp; English.
XX	
XX	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX	that down regulate the expression or inhibit the function of a receptor
XX	for a neurite growth inhibitor; NOGO, prostaglandin D2 receptor (PTGDR),
XX	Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX	invention are useful for treating: cerebrovascular accident, central
XX	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX	disease, lupus, multiple sclerosis, transplant/graft rejection,
XX	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX	nucleic acids of the invention are also useful for down-regulating the
XX	expression of a target gene and as a diagnostic tool to examine genetic
XX	defects and mutations within diseased cells or to detect the presence of a
XX	target RNA in a cell. The present RNA sequence represents a human PKR
XX	substrate sequence.
XX	
XX	Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;
XX	
XX	Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX	Best Local Similarity 76.5%; Pred. No. 1.6e+03;
XX	Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX	
XX	713 CTGCCCCAGCCCTCCGGA 729
XX	
XX	1 CUGCCUCAGCCUCCUGA 17
XX	
XX	RESULT 1926
XX	ADL50749
XX	ID ADL50749 standard, RNA, 17 BP.
XX	
XX	ADL50749;
XX	
XX	20-MAY-2004 (first entry)
XX	
XX	Human PKR substrate sequence #1863.
XX	
XX	antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX	prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX	protein kinase PKR; cerebrovascular accident;
XX	central nervous system injury; CNS injury; spinal cord injury; cancer;
XX	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW	retemousis; asthma; Crohn's disease; diabetes; obesity;
KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW	graft rejection; ischaemia; reperfusioin; glomerulonephritis; sepsis;
KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX	substrate; da.
XX	Unidentified.
XX	
PN	WO200281628-A2.
XX	
PD	17-OCT-2002.
XX	
PE	03-APR-2002; 2002WO-US010512.
XX	
PR	05-APR-2001; 2001US-00827395.
XX	
PR	29-MAY-2001; 2001US-0294412P.
XX	
PR	28-AUG-2001; 2001US-0315315P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
XX	
P1	Blaett L, Chowrira B, Haeblerl P, Mcwiggan J, Fossnaugh K;
XX	
DR	WP1; 2003-058513/05.
XX	
PT	Novel enzymatic nucleic acid that down-regulates expression of neurite
PT	growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX	protein kinase PKR genes, for treating cancer and inflammatory disease.
XX	
PS	Claim 59; SEQ ID NO 4282; 317bp; English.
XX	
CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC	that down regulate the expression or inhibit the function of a receptor
CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC	Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC	invention are useful for treating: cerebrovascular accident, central
CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC	disease, lupus, multiple sclerosis, transplant/graft rejection, allergic
CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC	nucleic acids of the invention are also useful for down-regulating the
CC	expression of a target gene and as a diagnostic tool to examine genetic
CC	drifts and mutations within diseased cells or to detect the presence of a
CC	target RNA in a cell. The present RNA sequence represents a human PKR
CC	substrate sequence.
XX	
CC	
SQ	Sequence 17 BP; 6 A; 6 C; 2 G; 0 T; 3 U; 0 Other;
XX	
QY	Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX	Best Local Similarity 76.5%; Pred. No. 1.6e+03;
ID	Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
DB	1123 AACCTCGACCTCAGG 1139
XX	: :
XX	1 AAACUCCUGACCUCAG 17
XX	
RESULT 1927	
ADL49908	
ID	ADL49908 standard; RNA; 17 BP.
XX	
AC	ADL49908;
XX	
DT	20-MAY-2004 (first entry)
XX	
DS	Human PKR substrate sequence #1022.
XX	
KM	antisense oligonucleotide; neurite growth inhibitor; NOGO;
KM	prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KM	protein kinase PKR; cerebrovascular accident;
KM	central nervous system injury; CNS injury; spinal cord injury; cancer;
KM	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX OS Unidentified.
XX PN WO200281628-A2.
XX PD 17-OCT-2002.
XX PF 03-APR-2002; 2002WO-US010512.
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
XX DR WPI; 2003-058513/05.
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX PS Claim 59; SEQ ID NO 3441; 317bp; English.
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX CC that down regulate the expression or inhibit the function of a receptor
XX CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX CC invention are useful for treating: cerebrovascular accident, central
XX CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX CC reestenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX CC disease, lupus, multiple sclerosis, transplant/graft rejection,
XX CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX CC nucleic acids of the invention are also useful for down-regulating the
XX CC expression of a target gene and as a diagnostic tool to examine genetic
XX CC drifts and mutations within diseased cells or to detect the presence of a
XX CC target RNA in a cell. The present RNA sequence represents a human PKR
XX CC substrate sequence.
XX CC
XX SQ Sequence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 70.6%; Pred. No. 1.6e+03;
XX Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 938 TGTATCCAGGCTGAG 954
Db 1 UGUGCCAGGCTGAG 17
RESULT 1928
ADL50213
ID ADL50213 standard; RNA; 17 BP.
XX
XX AC ADL50213;
XX DT 20-MAY-2004 (first entry)
XX DE Human PKR substrate sequence #1327.
XX
XX XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX OS Unidentified.
XX PN WO200281628-A2.
XX PD 17-OCT-2002.
XX PF 03-APR-2002; 2002WO-US010512.
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
XX DR WPI; 2003-058513/05.
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX PS Claim 59; SEQ ID NO 3746; 317bp; English.
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX CC that down regulate the expression or inhibit the function of a receptor
XX CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX CC invention are useful for treating: cerebrovascular accident, central
XX CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX CC reestenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX CC disease, lupus, multiple sclerosis, transplant/graft rejection,
XX CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX CC nucleic acids of the invention are also useful for down-regulating the
XX CC expression of a target gene and as a diagnostic tool to examine genetic
XX CC drifts and mutations within diseased cells or to detect the presence of a
XX CC target RNA in a cell. The present RNA sequence represents a human PKR
XX CC substrate sequence.
XX CC
XX SQ Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 70.6%; Pred. No. 1.6e+03;
XX Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 197 CCATGTGTCAGGCTG 213
Db 1 CCAUGUGGCCAGGCTG 17
RESULT 1929
ADL50738
ID ADL50738 standard; RNA; 17 BP.
XX
XX AC ADL50738;
XX DT 20-MAY-2004 (first entry)
XX DE Human PKR substrate sequence #1852.
XX
XX XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 XX WPI; 2003-058513/05.
 DR
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 4271; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 52.9%; Pred. No. 1.6e+03;
 Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 698 GTTCAAGTATTCTCCT 714
 Db 1 GTUACAUGAUGUCCU 17
 ADL50212
 ID ADL50212 standard; RNA; 17 BP.
 XX
 AC ADL50212;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1326.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 XX WPI; 2003-058513/05.
 DR
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3745; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.6e+03;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 795 TTCACCAAGTTCGCCAG 811
 Db 1 UUCACCAUGUGGCCAG 17
 ADL49917
 ID ADL49917 standard; RNA; 17 BP.
 XX
 AC ADL49917;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1031.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN MO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002MO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3450; 317bp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Db Best Local Similarity 70.6%; Pred. No. 1.6e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 674 CTCACGCAACCTCTGC 690
 ||:|||||:||||
 1 CTCACGCAACCTCTGC 17
 RESULT 1932
 ADL49926
 ID ADL49926 standard; RNA; 17 BP.
 XX
 AC ADL49926;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1040.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN MO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002MO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3459; 317bp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Db Best Local Similarity 64.7%; Pred. No. 1.6e+03;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 1006 GATTCTCTGCTCTGAC 1022
 ||:|||||:||||
 1 GATTCTCTGCTCTGAC 17
 RESULT 1933
 ADL49965
 ID ADL49965 standard; RNA; 17 BP.
 XX
 AC ADL49965;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1079.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 XX WO200281628-A2.
 PN
 XX
 PD 17-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010512.
 PF
 XX
 XX 05-APR-2001; 2001US-00827395.
 PR
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3498; 317pp; English.
 XX
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 1 A; 10 C; 3 G; 0 T; 3 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 370 CCACCTGCTGCTGCTC 386
 Db 1 CCACCTGCTGCTGCTC 17
 RESULT 1934
 ADL50214
 ID ADL50214 standard; RNA; 17 BP.
 XX
 AC ADL50214;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1328.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 XX WO200281628-A2.
 PN
 XX
 PD 17-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010512.
 PF
 XX
 XX 05-APR-2001; 2001US-00827395.
 PR
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3747; 317pp; English.
 XX
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 CC
 XX
 SQ Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.6e+03;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 202 TTGTCAGGCTGCTC 218
 Db 1 TTGTCAGGCTGCTC 17
 RESULT 1935
 ADL50747
 ID ADL50747 standard; RNA; 17 BP.
 XX
 AC ADL50747;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1861.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX reestenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
OS Unidentified.
XN WO200281628-A2.
PN 17-OCT-2002.
PP
PR 03-APR-2002; 2002WO-US010512.
PF
PX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX (RIBO-) RIBOZYME PHARM INC.
PA Blact L, Chowrira B, Haeblerl P, Mcswigen J, Poonaugh K,
PI WPI; 2003-058513/05.
DR
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR gene, for treating cancer and inflammatory disease.
PS Claim 59; SEQ ID NO 4280; 317pp; English.
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC reestenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX Sequence 17 BP; 1 A; 4 C; 7 G; 0 T; 5 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
DY 201 GTTGTCAGCGTGTCT 217
|::||| |||||::|:
Db 1 GUUGGCACGCGUCGUU 17
RESULT 1936
ADL49434
ID ADL49434 standard; RNA; 17 BP.
XX
AC ADL49434;
XX
DT 20-MAY-2004 (first entry)
XX Human PKR substrate sequence #548.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; Rheumatoid arthritis;

Query	717	CCGAGCCTCCGTGAGTAG	733
DB	1	CCGAGCCTCCGTGAGTAG	17
Sequence	17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;		
Query Match	1.6%;	Score 15.4;	DB 1;
Best Local Similarity	76.5%;	Pred. No. 1.6e+03;	
Matches	13; Conservative	3; Mismatches	1; Indels 0; Gaps 0;
ADL50197	ADL50197	standard; RNA; 17 BP.	
ADL50197;			
20-MAY-2004	(first entry)		
Human PKR substrate sequence #1311.			
antisense oligonucleotide; neurite growth inhibitor; NOGO;			
proteoglycan D2 receptor; PTGDR; Ikappab kinase; IKK;			
protein kinase PKR; cerebrovascular accident;			
central nervous system injury; CNS injury; spinal cord injury; cancer;			
melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;			

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3730; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 XX
 SQ Sequence 17 BP; 2 A, 6 C, 4 G, 0 T, 5 U, 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.6e+03;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 665 CAATCTGGCTCACTGC 681
 Db 1 CAGUCUGGUCACUCC 17
 |||:||||:|||||
 |||:||||:|||||
 RESULT 1938
 ADL50748
 ID ADL50748 standard; RNA; 17 BP.
 XX
 AC ADL50748;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1862.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 4281; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.
 XX
 SQ Sequence 17 BP; 4 A, 5 C, 5 G, 0 T, 3 U, 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.6e+03;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1109 GTCAGGCTGCTCAAA 1125
 Db 1 GCCAGGCTGCTCAAA 17
 |||:||||:|||||
 |||:||||:|||||
 RESULT 1939
 ADL49906
 ID ADL49906 standard; RNA; 17 BP.
 XX
 AC ADL49906;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #1020.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX rectorinosis; asthma; Crohn's disease; diabetes; obesity;
XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX allergic; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX substrate; ds.
XX Unidentified.
XX
XX WO200281628-A2.
XX
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
XX 29-MAY-2001; 2001US-0294412P.
XX 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
XX WPI, 2003-058513/05.
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX Claim 59; SEQ ID NO 3439; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection,
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX
XX Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 64.7%; Pred. No. 1.6e+03;
XX Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX 936 TCTGTTACCCAGGCTGG 952
XX :||::|||||:|:
XX 1 UCUUGUCCCGACGUG 17
XX
XX RESULT 1940
XX ADL49929
XX ID ADL49929 standard; RNA; 17 BP.
XX
XX AC ADL49929;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human PKR substrate sequence #1043.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW		xesterosis; ashma; Crohn's disease; diabetes; obesity;
KV		autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM		graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW		allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KX		substrate; de.
XO		
XX		Unidentified.
XS		
YN		WO200281628-A2.
YP		17-OCT-2002.
ZP		
PE		03-APR-2002; 2002WO-US010512.
XX		
PR		05-APR-2001; 2001US-00827395. PR 29-MAY-2001; 2001US-0294412P. PR 28-AUG-2001; 2001US-0315315P.
XA	(RIBO-)	RIBOZYME PHARM INC.
PB		
PI	Blaiz L,	Chowrira B, Haeblerl P, Mcswiggen J, Fossnaugh K; DR MPI; 2003-058513/05.
PT		
PP		Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D ₂ receptor (IKAPPAB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
PS	Claim 59;	SEQ ID NO 3462; 317pp; English.
XX		The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D ₂ receptor (PTGDR), IKAPPAB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, reostenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopie dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.
SQ	Sequence 17 BP;	1 A; 9 C; 3 G; 0 T; 4 U; 0 Other;
	Query Match	1.6%; Score 15.4; DB 1; Length 17;
	Best Local Similarity	76.5%; Pred.No.1.6e+03;
MATCHES	13; Conservative	3; Mismatches 1; Indels 0; Gaps 0.
DY	712 CCTGCCCAAGCGTCTGTG 728	
ID	: : :	
DB	:	1 CCUGCUCACGCUCUCCUG 17
RESULT 1941		
ADL49950		
ID	ADL49950 standard; RNA;	17 BP.
XX		
AC	ADL49950;	
DT	20-MAY-2004	(first entry)
DS		Human PKR substrate sequence #1064.
KW		antisense oligonucleotide; neurite growth inhibitor; NOGO;
KV		prostaglandin D ₂ receptor; PTGDR; ikappab kinase; IKK;
KM		protein kinase PKR; cerebrovascular accident;
KW		central nervous system injury; CNS injury; spinal cord injury; cancer;
KX		melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3483; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 2 A; 3 C; 7 G; 0 T; 5 U; 0 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 199 ATGTTGTCAGGCTGGT 215
Db 1 AUGUGGCCAGGCGUGU 17
|||:|||||:|||||:
|:|:|:|:|:|:|:|:|:
RESULT 1942
ADL49430
ID ADL49430 standard; RNA; 17 BP.
XX
AC ADL49430;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #544.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2963; 317pp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.6e+03;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 701 CAACTTATTCCTGCGC 717
Db 1 CAAGGAAUUCUCUCGUC 17
|||:|||||:|||||:
|:|:|:|:|:|:|:|:|:
RESULT 1943
ADH54043/C
ID ADH54043 standard; DNA; 17 BP.
XX
AC ADH54043;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human neurodegenerative disease-related sequencing primer SegID170.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW gamma-synuclein; SNCA; insulin degrading enzyme; IDE;
KW kinein-like protein 1; KNSL1; lysosomal acid lipase; LIPA;
KW tumor necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; PCR;
KW primer; ss; sequencing.

```
XX OS Homo sapiens.
XX PN US2003224380-A1.
XX PD 04-DEC-2003.
XX PF 25-OCT-2002; 2002US-00282174.
XX PR 25-OCT-2001; 2001US-0339525P.
XX PR 25-OCT-2001; 2001US-0348065P.
XX PR 02-NOV-2001; 2001US-0336983P.
XX PR 08-NOV-2001; 2001US-0336929P.
XX PR 08-NOV-2001; 2001US-0338010P.
XX PR 09-NOV-2001; 2001US-0338363P.
XX PR 04-DEC-2001; 2001US-0337052P.
XX PR 28-MAR-2002; 2002US-0368919P.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Becker KD, Veljceleb J, Elliott KJ, Wang X, Tanzi RE;
XX PI Bertram L, Saunders AJ, Mullin KM, Sampson AJ;
XX DR MPI; 2004-060538/06.
XX PT Determining a predisposition for or the occurrence of neurodegenerative
XX PT disease, particularly Alzheimer's disease, comprises determining the
XX PT presence of a polymorphism in the UPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
XX PT gene.
XX PS Example 3; SEQ ID NO 170; 205bp; English.
XX CC This invention relates to a novel method of determining a predisposition
XX CC for or the occurrence of neurodegenerative disease comprising detecting
XX CC in a target nucleic acid obtained from the subject the presence of an
XX CC allelic variant of polymorphic regions of human genes selected from
XX CC uridine kinase plasmogen activator (UPA), gamma-synuclein (SNCG), insulin
XX CC degrading enzyme (IDE), kinasin-like protein 1 (KNSL1), lysosomal acid
XX CC lipase (LIPA) and tumor necrosis factor receptor SF6 (TNFRSF6). The
XX CC method is useful in determining the presence or predisposition to a
XX CC neurodegenerative disease, particularly Alzheimer's disease. The present
XX CC sequence is that of a sequencing primer which was used for sequencing of
XX CC a region of the human IDE gene in the exemplification of the invention.
XX SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 646 AGCGTGGAGTGCAGTGG 662
DB 17 AGCGTGGAGTGCAGTGG 1
ID ADK13186 standard; DNA; 17 BP.
XX ADK13186;
XX AC
XX ADK13186;
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Human glioma endothelial marker (GEM) long tag SEQ ID NO:364.
XX KW glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;
XX KW anticancer; anti-glioma; immune response; cytostatic;
XX KW multi-drug sensitive glioma; human; long tag; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS WO2004016758-A2.
XX PN
```

```
XX ED 26-FEB-2004.
XX PF 15-AUG-2003; 2003WO-US025614.
XX PR 15-AUG-2002; 2002US-0403390P.
XX PR 01-APR-2003; 2003US-0458978P.
XX PA (GEN2 ) GENZYME CORP.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Madden SL, Wang CJ, Cook BP, Latteza J, Walter K;
XX PI MPI; 2004-247973/23.
XX DR
XX PT Diagnosing glioma by detecting expression product of any one of 255
XX PT genes, glioma endothelial markers, in brain tissue sample suspected of
XX PT being neoplastic, and comparing the expression with expression in normal
XX PT brain tissue sample.
XX PS Example 2; SEQ ID NO 364; 114pp; English.
XX CC The present invention describes a method (M1) for aiding in the diagnosis
XX CC of glioma. (M1) involves detecting an expression product of at least one
XX CC gene (I) in a first brain tissue sample (T) suspected of being
XX CC neoplastic, where (I) is chosen from any one of 255 genes (glioma
XX CC endothelial markers (GEMs)) as given in specification, and comparing the
XX CC expression of (I) in (T) with expression of (I) in a second normal brain
XX CC tissue sample (R), where increased expression of (I) in (T) relative to
XX CC (R), identifies (T) as likely to be neoplastic. Also described: (1)
XX CC treating (M2) glioma involves contacting cells of the glioma with an
XX CC antibody that specifically binds to a extracellular epitope; (2)
XX CC identifying (M3) a test compound as potential anticancer or anti-glioma
XX CC drug involves contacting a test compound with the cell which expresses
XX CC (1), monitoring an expression product of the at least one gene and
XX CC identifying test compound as a potential anticancer drug if it decreases
XX CC the expression of at least one gene; (3) identifying (M4) a test compound
XX CC as potential anticancer or anti-glioma drug involves contacting a test
XX CC compound with the cell which expresses mRNA of at least one gene
XX CC identified by a tag as described above, monitoring mRNA of the gene, and
XX CC identifying the test compound as a potential anticancer drug if it
XX CC decreases the expression of at least one gene; and (4) inducing (M5) an
XX CC immune response to glioma involves administering to a mammal, a protein
XX CC or (1). (1) have cytostatic activities, and can be used to trigger immune
XX CC destruction of glioma cells, and as immune response inducers. (M1) is
XX CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi
XX CC drug sensitive glioma in a human. (M5) is useful for inducing an immune
XX CC response to a glioma in a mammal having glioma or in a mammal who has had
XX CC a glioma surgically removed. The present sequence represents a human GEM
XX CC long tag oligonucleotide, which is used in the exemplification of the
XX CC present invention.
XX SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 646 AGCGTGGAGTGCAGTGG 662
DB 17 AGCGTGGAGTGCAGTGG 1
ID ADL82347 standard; DNA; 17 BP.
XX ADL82347;
XX AC
XX ADL82347;
XX AC
XX DT 20-MAY-2004 (first entry)
XX DE Human ER+ breast cancer differentially expressed sequence #317.
XX KW
```

KW gene therapy; ds; breast cancer; human; ER+ breast cancer.
XX
OS Homo sapiens.
XX
PN US2003166026-A1.
XX
PD 04-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00339782.
XX
PR 09-JAN-2002; 2002US-0348053P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
PI Goodman LJ, Bowen BA;
XX
DR WPI; 2004-069003/07.
XX
PT Vector containing nucleic acid associated with breast cancer, useful for
PT treating, diagnosing and characterizing breast cancer, also related
PT polypeptides and antibodies.
XX
PS Claim 1; SEQ ID NO 318; 61pp; English.
XX
CC The invention relates to a composition which contains at least one vector
CC (B) containing a nucleic acid (I) associated with breast cancer. The
CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
CC -specific antibodies (Ab) are used to predict characteristics (e.g.
CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
CC used to modulate characteristics of such cells; to identify breast cancer
CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
CC or its products). The present sequence represents a human ER+ breast
CC cancer differentially expressed sequence.
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 224 CCCGACCTCATGATC 240
DB 17 CCCGACCTCATGATC 1
XX
RESULT 1946
ADL82349/C
ID ADL82349 standard; DNA; 17 BP.
XX
AC ADL82349;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ER+ breast cancer differentially expressed sequence #319.
XX
KM Gene therapy; ds; breast cancer; human; ER+ breast cancer.
XX
OS Homo sapiens.
XX
PN US2003166026-A1.
XX
PD 04-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00339782.
XX
PR 09-JAN-2002; 2002US-0348053P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
PI Goodman LJ, Bowen BA;
XX
DR WPI; 2004-069003/07.
XX

XX
PT Vector containing nucleic acid associated with breast cancer, useful for
PT treating, diagnosing and characterizing breast cancer, also related
PT polypeptides and antibodies.
XX
PS Claim 1; SEQ ID NO 320; 61pp; English.
XX
CC The invention relates to a composition which contains at least one vector
CC (B) containing a nucleic acid (I) associated with breast cancer. The
CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
CC -specific antibodies (Ab) are used to predict characteristics (e.g.
CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
CC used to modulate characteristics of such cells; to identify breast cancer
CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
CC or its products). The present sequence represents a human ER+ breast
CC cancer differentially expressed sequence.
SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 479 AGTGCAGTGTGTGATC 495
DB 17 AGTGCAGTGTGTGATC 1
XX
RESULT 1947
ADL82453/C
ID ADL82453 standard; DNA; 17 BP.
XX
AC ADL82453;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ER+ breast cancer differentially expressed sequence #423.
XX
KM gene therapy; ds; breast cancer; human; ER+ breast cancer.
XX
OS Homo sapiens.
XX
PN US2003166026-A1.
XX
PD 04-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00339782.
XX
PR 09-JAN-2002; 2002US-0348053P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
PI Goodman LJ, Bowen BA;
XX
DR WPI; 2004-069003/07.
XX
PT Vector containing nucleic acid associated with breast cancer, useful for
PT treating, diagnosing and characterizing breast cancer, also related
PT polypeptides and antibodies.
XX
PS Claim 1; SEQ ID NO 424; 61pp; English.
XX
CC The invention relates to a composition which contains at least one vector
CC (B) containing a nucleic acid (I) associated with breast cancer. The
CC vector (B), also polypeptides (II) encoded by (I), are used for treatment
CC of breast cancer. Arrays based on (I), (II), or their fragments, and (II)
CC -specific antibodies (Ab) are used to predict characteristics (e.g.
CC invasiveness or stage) of breast cancer, and (I), or its fragments, are
CC used to modulate characteristics of such cells; to identify breast cancer
CC genes and to detect breast cancer (by detecting polymorphic nucleic acid
CC or its products). The present sequence represents a human ER+ breast
CC cancer differentially expressed sequence.
SQ


```
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 653 AGTGCAGTGGCGCATC 669
17 AGTGCAGTGGCGCATC 1
Db
RESULT 1948
ADP08740/c
ID ADP08740 standard; DNA; 17 BP.
AC ADP08740;
DT 26-AUG-2004 (first entry)
XX
XX Extend primer 77 used to genotype human glycoprotein VI polymorphism.
DE
XX breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;
KW GP6; GPIV; GPVI; chromosome 19q13.4; ss; PCR; primer; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
XX WO2004047767-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI
XX WPI; 2004-441082/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 3; Page 83; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer which comprises detecting the presence or absence of one
XX or more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a risk of breast cancer,
XX as well as therapeutic and prophylactic treatments that specifically
XX target breast cancer, such as gene therapy. The current sequence is that
XX of an extend primer of the invention which was used to genotype single
XX nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
XX GPIV; GPVI) DNA which is located at chromosomal position 19q13.4.
XX
XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 391 AGTGCCTGGATTACAG 407
17 AGTGCCTGGATTACAG 1
Db
RESULT 1949
ADP09251/c
ADP09251/c
```

```
ID ADP09251 standard; DNA; 17 BP.
XX
XX ADP09251;
AC
XX 26-AUG-2004 (first entry)
DT
XX Extend primer 46 used to genotype human chromogranin B polymorphism.
DE
XX breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;
KW secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
XX WO2004047767-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI
XX WPI; 2004-441082/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 5; Page 102; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer which comprises detecting the presence or absence of one
XX or more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a risk of breast cancer,
XX as well as therapeutic and prophylactic treatments that specifically
XX target breast cancer, such as gene therapy. The current sequence is that
XX of an extend primer of the invention which was used to genotype single
XX nucleotide polymorphisms within human chromogranin B (CHGB; secretogranin
XX 1; SCG1) DNA which is located at chromosomal position 20pter-p12.
XX
XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 871 TTACAGCGGTGAGCCAC 887
17 TTATAGCGGTGAGCCAC 1
Db
RESULT 1950
ADP09278/c
ID ADP09278 standard; DNA; 17 BP.
AC ADP09278;
DT 26-AUG-2004 (first entry)
XX
XX Extend primer 73 used to genotype human chromogranin B polymorphism.
DE
XX breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;
KW secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
```

```
PN WO2004047767-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX MPI; 2004-441082/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 5; Page 103; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer which comprises detecting the presence or absence of one
XX or more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a risk of breast cancer,
XX as well as therapeutic and prophylactic treatments that specifically
XX target breast cancer, such as gene therapy. The current sequence is that
XX of an Extend primer of the invention which was used to genotype single
XX nucleotide polymorphisms within human chromosome B (CHGB;secretogranin
XX 1;SCG1) DNA which is located at chromosomal position 20pter-p12.
XX
XX Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 866 TGGGATTACAGCGCTGA 882
XX |||||
XX 17 TGGGATTACAGCGCTTA 1
XX
XX RESULT 1951
XX ADP08765
XX ID ADP08765 standard; DNA; 17 BP.
XX
XX ADP08765;
XX
XX 26-AUG-2004 (first entry)
XX
XX Extend primer 102 used to genotype human glycoprotein VI polymorphism.
XX breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;
XX GP6; GPVI; GPVI; chromosome 19q13.4; ss; PCR; primer; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO2004047767-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX MPI; 2004-441082/41.
XX
```

```
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 3; Page 84; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer which comprises detecting the presence or absence of one
XX or more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a risk of breast cancer,
XX as well as therapeutic and prophylactic treatments that specifically
XX target breast cancer, such as gene therapy. The current sequence is that
XX of an Extend primer of the invention which was used to genotype single
XX nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
XX GPVI;GPVI) DNA which is located at chromosomal position 19q13.4.
XX
XX Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 1.6e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1032 ACCTGGGATTACGGGCA 1048
XX |||||
XX 1 ACCTGGGATTACGGGCA 17
XX
XX RESULT 1952
XX AD080011
XX ID AD080011 standard; DNA; 17 BP.
XX
XX AD080011;
XX
XX 26-AUG-2004 (first entry)
XX
XX CENPC1 extend primer #62.
XX
XX Cytostatic; Gene therapy; breast cancer; human; DLG1; KIA0783; DPF3;
XX CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;
XX Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2004047514-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037943.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX MPI; 2004-441037/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the DLG1, KIA0783, DPF3 or CENPC1 regions
XX which are associated with breast cancer in a nucleic acid sample from a
XX subject.
XX
XX Example 6; Page 91; 227pp; English.
XX
XX The present invention relates to a method for identifying a subject at
XX risk of breast cancer. The method comprising detecting the presence or
XX absence of one or more polymorphic variations associated with breast
XX cancer in a nucleic acid sample from a subject. The nucleic acid sample
XX comprises the DLG1 region (AD079402), KIA0783 region (AD079403), DPF3
XX region (AD079404) or CENPC1 region (AD079405). The gene DLG1 (discs,
```

CC large homolog 1 (Drosophila) is also known as synapse-associated protein
CC 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
CC gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
CC has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
CC novel gene with unknown function, however, being a zinc finger protein,
CC it likely to be a transcription factor. The gene DPF3 (D4, zinc and
CC double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
CC and 2810403B03Rik. DPF3 is a Rho family guanine-nucleotide exchange
CC factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The
CC gene CENPCL (centromere protein C1) is also known as Centromere
CC autoantigen C1. CENPCL has been mapped to chromosomal position 4q12-
CC q13.3. CENPCL is a centromere autoantigen and a component of the inner
CC kinetochore plate. The CENPCL protein is required for maintaining proper
CC kinetochore size and a timely transition to anaphase. The method is
CC useful for identifying a subject at risk of breast cancer, for early
CC diagnosis, prevention and treatment of breast cancer, to analyze and
CC predict a response to a breast cancer treatment, and in clinical drug
CC trials. The present sequence was used in an example from the invention.
CC
SQ Sequence 17 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 389 AAGTGTGGGATTACA 405
Db 1 AGAGTGTGGGATTACA 17

RESULT 1953

ADO79480
ID ADO79480 standard; DNA; 17 BP.

AC ADO79480;

DT 26-AUG-2004 (first entry)

XX DLG1 extend primer #12.

XX Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;
XX CENPCL; SNP; single nucleotide polymorphism;
XX synapse-associated protein 97, hdlg; SAP97; chromosome 3q29; extend;
XX primer; ss.

OS Homo sapiens.

PN WO2004047514-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037943.

PR 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441037/41.

XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPCL regions
XX which are associated with breast cancer in a nucleic acid sample from a
XX subject.

XX Example 3; Page 73; 227pp; English.

XX The present invention relates to a method for identifying a subject at
XX risk of breast cancer. The method comprising detecting the presence or
XX absence of one or more polymorphic variations associated with breast
XX cancer in a nucleic acid sample from a subject. The nucleic acid sample

CC comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPF3
CC region (ADO79404) or CENPCL region (ADO79405). The gene DLG1 (discs-
CC large homolog 1 (Drosophila)) is also known as synapse-associated protein
CC 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
CC gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
CC has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
CC novel gene with unknown function, however, being a zinc finger protein,
CC it likely to be a transcription factor. The gene DPF3 (D4, zinc and
CC double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
CC and 2810403B03Rik. DPF3 is a Rho family guanine-nucleotide exchange
CC factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The
CC gene CENPCL (centromere protein C1) is also known as Centromere
CC autoantigen C1. CENPCL has been mapped to chromosomal position 4q12-
CC q13.3. CENPCL is a centromere autoantigen and a component of the inner
CC kinetochore plate. The CENPCL protein is required for maintaining proper
CC kinetochore size and a timely transition to anaphase. The method is
CC useful for identifying a subject at risk of breast cancer, for early
CC diagnosis, prevention and treatment of breast cancer, to analyze and
CC predict a response to a breast cancer treatment, and in clinical drug
CC trials. The present sequence was used in an example from the invention.
CC
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 877 GCGTGAGCCACACGCC 893
Db 1 GCCTGAGCCACACACC 17

RESULT 1954

ADO80017
ID ADO80017 standard; DNA; 17 BP.

AC ADO80017;

DT 26-AUG-2004 (first entry)

XX CENPCL extend primer #68.

XX Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;
XX CENPCL; SNP; single nucleotide polymorphism; centromere protein C1;
XX Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.

OS Homo sapiens.

PN WO2004047514-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037943.

PR 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441037/41.

XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPCL regions
XX which are associated with breast cancer in a nucleic acid sample from a
XX subject.

XX Example 6; Page 91; 227pp; English.

XX The present invention relates to a method for identifying a subject at
XX risk of breast cancer. The method comprising detecting the presence or
XX absence of one or more polymorphic variations associated with breast

CC cancer in a nucleic acid sample from a subject. The nucleic acid sample
CC comprises the DLG1 region (AD079402), KIAA0783 region (AD079403), DPF3
CC region (AD079404) or CENPCI region (AD079405). The gene DLG1 (discs,
CC large homolog 1 (Drosophila)) is also known as synapse-associated protein
CC 97, hdig or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
CC gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
CC has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
CC novel gene with unknown function, however, being a zinc finger protein,
CC it likely to be a transcription factor. The gene DPF3 (D4, zinc and
CC double PHD finger, family 3) is also known as CERP4, cer-d4, FJL14079
CC and 2810403B03R1K. DPF3 is a Rho family guanine-nucleotide exchange
CC factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The
CC gene CENPCI (centromere protein C1) is also known as Centromere
CC autotigen C1. CENPCI has been mapped to chromosomal position 4q12-
CC q13.3. CENPCI is a centromere autotigen and a component of the inner
CC kinetochore plate. The CENPCI protein is required for maintaining proper
CC kinetochore size and a timely transition to anaphase. The method is
CC useful for identifying a subject at risk of breast cancer, for early
CC diagnosis, prevention and treatment of breast cancer, to analyze and
CC predict a response to a breast cancer treatment, and in clinical drug
CC trials. The present sequence was used in an example from the invention.

XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 871 TTACAGGCGTACGCCAC 887

DB 1 TTACAGGTGTGAGCCAC 17

RESULT 1955

AAQ20109 standard; DNA; 18 BP.

XX AAQ20109;

XX 01-APR-1992 (first entry)

XX Cross-linking oligomer 943 to target human TNF Receptor mRNA.

XX deoxyribonucleic acid; major groove; ethanoino group;

XX tumor necrosis factor; receptor; messenger RNA; aziridinylcytosine;

XX cross-linking group; ss.

XX Synthetic.

XX OS

XX Key

XX modified_base

XX 5

XX Location/Qualifiers

XX /tag= a

XX /mod_base= OTHER

XX /note= "N-methyl-8-oxo-2'-deoxyadenine"

XX modified_base

XX 18

XX /tag= b

XX /mod_base= OTHER

XX /note= "N4N4-ethanocytosine"

XX WO9118997-A.

XX 12-DEC-1991.

XX 25-MAY-1990; 90US-00529346.

XX 25-MAY-1990; 90US-00529346.

XX 14-JAN-1991; 91US-00640654.

XX (GILE-) GILEAD SCI INC.

XX Matteucci MD, Krawczyk S,

XX WPI; 1992-007480/01.

XX New sequence-specific non-photo-activated crosslinking agents - bind to
XX the major groove of duplex DNA and are esp. useful for treating latent
XX infections e.g. HIV.

XX Example 4; Page 27; 42pp; English.

XX The oligomer was designed to target human TNF receptor mRNA beginning at
XX nucleotide 2354 and to covalently cross-link to the target via the N4N4-
XX ethanocytosine group. See also AAQ20108

XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 444

DB 1 TTTTATTTTATTTT 17

RESULT 1956

AAQ30448 standard; DNA; 18 BP.

XX AAQ30448;

XX 25-MAR-2003 (revised)

XX 07-DEC-1992 (first entry)

XX Oligomer TNFR943 for forming triplex with HUMNFR target duplex.

XX Human tumor necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;

XX HPV; malignancy; hepatitis; inflammation; ss.

XX Synthetic.

XX OS

XX Key

XX modified_base

XX 5

XX Location/Qualifiers

XX /tag= a

XX /mod_base= OTHER

XX /note= "N6 methyl-8-oxo-2'-deoxyadenine"

XX modified_base

XX 18

XX /tag= b

XX /mod_base= OTHER

XX /note= "OTHER= N4 N4 ethanocytosine"

XX WO9209705-A1.

XX 11-JUN-1992.

XX 25-NOV-1991; 91WO-US008811.

XX 23-NOV-1990; 90US-00617907.

XX 18-JAN-1991; 91US-00643382.

XX 08-APR-1991; 91US-00683420.

XX 17-APR-1991; 91US-00686544.

XX 17-APR-1991; 91US-00686546.

XX 17-APR-1991; 91US-00686547.

XX 27-SEP-1991; 91US-00766733.

XX (GILE-) GILEAD SCI INC.

XX Froehler B, Krawczyk S, Matteucci MD, Milligan J,

XX WPI; 1992-217083/26.

XX New oligomers contg. modified bases - which form a triplex with G-C

XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,

XX herpes malignancy and inflammation.

XX Claim 12; Page 72; 77pp; English.

XX The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
 CC a putine rich sequence contd. on one strand of the duplex. The oligomer,
 CC and others like it are useful in diagnosis and therapy of diseases
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
 CC hepatitis B, herpes, malignant tumours and inflammation. The tripe
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. (See also AA025452-25501
 CC and AA030226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PD field.)
 CC
 SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 428 TTTTATTTTATTTT 444
 1 TTTTATTTT 17
 Db
 RESULT 1957
 AA221792/c
 ID AA221792 standard; DNA; 18 BP.
 AC AA221792;
 XX
 XX 01-DEC-1999 (first entry)
 DT
 XX Exemplary oligonucleotide primer D9S737 (Rev).
 DE
 XX neoplasia; mutant; target nucleotide; hybridization; lung cancer; ss;
 KM neck cancer; head cancer; saliva test; chemotherapy; early detection;
 KM primer; PCR; amplification.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9946408-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US005220.
 XX
 PR 10-MAR-1998; 98US-00038637.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Sidransky D;
 XX
 DR WPI; 1999-551428/46.
 XX
 PT Detection of cancers comprises assaying for a genetic mutation associated
 PT with cancer.
 XX
 PS Disclosure, Page 28; 99pp, English.
 XX
 CC This is an exemplary oligonucleotide primer, for use in the detection of
 CC neoplastic related gene mutations. There are over 40 known proto-
 CC oncogenes and suppressor genes to date, which control growth,
 CC development, and cell differentiation. Regulation of these genes can,
 CC under certain circumstances, be altered and normal cells can assume
 CC neoplastic growth characteristics. The invention provides a method for
 CC detecting a neoplastic disorder of the head and neck or lung in a
 CC subject. The detection of a target mutant nucleotide sequence in the
 CC saliva is indicative of a neoplastic disorder of the head, neck or lung.
 CC This allows early detection and therefore treatment of the preneoplasia
 CC or cancer, and can also be used to monitor high risk patients undergoing
 CC chemoprevention or chemotherapy

XX Sequence 18 BP; 5 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1120 CTCAAACTCTGACCTC 1136
 18 CTCAAACTCTGACCTC 2
 Db
 RESULT 1958
 AAF76529/c
 ID AAF76529 standard; DNA; 18 BP.
 AC AAF76529;
 XX
 XX 11-MAY-2001 (first entry)
 DT
 XX Human EFEMP1 coding sequence PCR primer #32.
 DE
 XX Human; EGF-containing fibrillin-like extracellular matrix protein 1;
 KM EFEMP1; macular degeneration; chromosome 2; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200112823-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 30-MAY-2000; 2000WO-US014965.
 XX
 PR 28-MAY-1999; 99US-00322357.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Stone EM, Sheffield VC;
 XX
 DR WPI; 2001-218354/22.
 XX
 PT Screening assays to identify compounds that modulate EGF-containing
 PT fibrillin like extracellular matrix protein 1 bioactivity, which are
 PT useful for treating or preventing macular degeneration.
 XX
 PS Example 1; Page 67; 92pp; English.
 XX
 CC The present invention describes a method for identifying compounds which
 CC modulate the activity of epidermal growth factor-containing fibrillin
 CC like extracellular matrix protein 1 (EFEMP1). The human EFEMP1 coding and
 CC protein sequences are also provided. Compounds of the invention can be
 CC used in the treatment of macular degeneration and other diseases related
 CC to EFEMP1. The present sequence is a PCR primer for a fragment of the
 CC EFEMP1 gene
 CC
 SQ Sequence 18 BP; 3 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
 Oy 971 CGGCTCACTGCACTC 987
 18 CAGCTCACTGCACTC 2
 Db
 RESULT 1959
 AAH40898
 ID AAH40898 standard; DNA; 18 BP.
 AC AAH40898;
 XX
 XX 14-AUG-2001 (first entry)
 DT

XX SNP specific lower PCR primer SEQ ID 3694.
 XX
 DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX
 XX SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 XX
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 XX
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX
 XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT
 PT acid sample.
 XX
 PS Claim 1; Page 68; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC
 CC primer extension (SNP) primers, and the sequences of regions flanking
 CC
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC
 CC includes kits for determining the presence or absence of a SNP, using the
 CC
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC
 CC performing a single-nucleotide primer extension reaction. The
 CC
 CC oligonucleotides are useful for determining the presence, absence or
 CC
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC
 CC assess by association analysis the genotype of an individual or group of
 CC
 CC individuals, having a pathological phenotypic trait suspected of being
 CC
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC
 CC traits also include symptoms of or susceptibility to multifactorial
 CC
 CC disease of which a component is or may be genetic such as autoimmune
 CC
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC
 CC microorganism. The method is also useful in forensic investigations and
 CC
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC
 CC for a human SNP containing DNA sequence
 CC
 XX
 SO Sequence 18 BP; 4 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 966 AATCTGGGCTCACTGCA 982
 DB 2 AATCTGGGCTCACTGCA 18
 XX
 RESULT 1960
 AAH38514/C
 ID AAH38514 standard; DNA; 18 BP.
 XX
 AC AAH38514;
 XX

DT 14-AUG-2001 (first entry)
 XX
 XX SNP specific lower PCR primer SEQ ID 1310.
 XX
 DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 XX
 XX SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 XX
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 XX
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 XX
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 XX
 XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT
 PT acid sample.
 XX
 PS Claim 1; Page 56; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC
 CC primer extension (SNP) primers, and the sequences of regions flanking
 CC
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC
 CC includes kits for determining the presence or absence of a SNP, using the
 CC
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC
 CC performing a single-nucleotide primer extension reaction. The
 CC
 CC oligonucleotides are useful for determining the presence, absence or
 CC
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC
 CC assess by association analysis the genotype of an individual or group of
 CC
 CC individuals, having a pathological phenotypic trait suspected of being
 CC
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC
 CC traits also include symptoms of or susceptibility to multifactorial
 CC
 CC disease of which a component is or may be genetic such as autoimmune
 CC
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC
 CC microorganism. The method is also useful in forensic investigations and
 CC
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC
 CC for a human SNP containing DNA sequence
 CC
 XX
 SO Sequence 18 BP; 3 A; 10 C; 2 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 947 GGCTGAGTGCATGAC 963
 DB 18 GGCTGAGTGCATGAC 2
 XX
 RESULT 1961
 AAH40802
 ID AAH40802 standard; DNA; 18 BP.
 XX
 AC AAH40802;
 XX

XX 14-AUG-2001 (first entry)
 XX SNP specific lower PCR primer SEQ ID 3598.
 DE
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 68; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH4994 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g., to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX
 SQ Sequence 18 BP; 3 A; 10 C; 3 G; 2 T; 0 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 DB 376 GCCTCAGGCTCCCAAG 392
 2 GCCTCGGCTCCCAAG 18
 RESULT 1962
 ABK27429/C
 ID ABK27429 standard; DNA; 18 BP.
 XX

AC ABK27429;
 XX 09-APR-2002 (first entry)
 XX
 DE Colon cancer associated CDNA CATX-2, 3' PCR primer.
 XX
 KW Human; colon cancer; tumour; abnormal cell growth; melanoma;
 KW cervical cancer; colorectal adenocarcinoma; Wilms' tumour; leukaemia;
 KW lymphoma; antitense therapy; CATX; probe; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200111047-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 08-AUG-2000; 2000WO-US021606.
 XX
 PR 09-AUG-1999; 99US-0147933P.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Bowman BM, Wang K;
 XX
 DR WPI; 2002-121548/16.
 XX
 PT New isolated nucleic acid involved in growth regulation in human colonic
 PT epithelial cells, termed CATX, for diagnosing and treating abnormal cell
 PT growth, and for use as a probe/primer for detecting tumors.
 XX
 PS Example; Page 87; 130pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (I) involved in growth
 CC regulation in human colonic epithelial cells, termed CATX. (I) is useful
 CC as a probe/primer for detecting tumours, preferably colon cancer. The
 CC nucleic acid, encoded polypeptide and antibody are useful in diagnosis
 CC and treatment of abnormal cell growth (such as cervical cancer,
 CC melanoma, colorectal adenocarcinoma, Wilms' tumour, leukaemia and
 CC lymphoma), in screening assays for the treatment of abnormal cell
 CC growth, for raising antibodies, and to screen for peptide analogues and
 CC antagonists. (I) is useful as a biomarker for human tumour cells, e.g.,
 CC colon cancer cells, for generating probes and primers designed for
 CC identifying and/or cloning homologues in other cell types, in antisense
 CC therapy, and in tissue profiling. (I) identifies cancer cells at an early
 CC stage of development, so that premalignant cells can be identified prior
 CC to their spreading throughout the human body. (I) allows early detection
 CC of potentially cancerous conditions, and treatment of the cancerous
 CC conditions prior to spread of the cancer cells throughout the body, or
 CC prior to development of an irreversible cancerous condition. ABK27426-
 CC ABK27469 represent human colon cancer associated coding sequences and
 CC primers of the invention
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 DB 644 CCAGGCTGAGTGCAGT 660
 18 CCAGGCTGAGTGCAGT 2
 RESULT 1963
 ABS97649
 ID ABS97649 standard; DNA; 18 BP.
 XX
 AC ABS97649;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human glutathione-S-transferase 12 (GST12) PCR primer #3.
 XX

Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
cytochrome P450 A2; CYP450A2; cytochrome P450 02B; CYP45002B1; LTF;
adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase;
NADPH quinone oxidoreductase 2; NQO2; sulfoxonoyl transferase; STM;
UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
multidrug resistance associated protein 3; cancer; prostate;
acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
altered drug metabolism; cardiovascular function; colorectal tumour;
central nervous system; pulmonary; immunological.

OS Homo sapiens.
XX
XX MO200257410-A2.
XX
XX 25-UTL-2002.
XX
XX 28-NOV-2001; 2001WO-US044838.
XX
XX 28-NOV-2000; 2000US-00724389.
XX
XX (DNAS-) DNA SCI LAB INC.
XX
XX Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.

XX Example 12; Page 122; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid
XX molecule comprising at least one base variation from that of a known
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1),
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
XX sulfoxonoyl transferase (STM), UDP-glucuronosyl transferase 2B4
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX The polymorphisms in the human genes cited in the invention are useful as
XX genetic linkage markers for locating and characterizing the genes that
XX are responsible for specific traits within the genome and eventually
XX identifying the genes responsible for a variety of disorder-related
XX traits as a result of their e.g., overexpression, constitutive
XX expression, mutation or underexpression, which may be used in diagnosing
XX and/or treating the disorder. The nucleic acid molecules comprising the
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1,
XX AKMT, EPHX2, GST12, HNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX used to screen for altered cardiovascular function, in COX2 for altered
XX susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
XX nervous system function, in FLAP and HNMT for altered pulmonary,
XX immunological or haematological function, in KLK2 for altered serine

CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention

XX SEQ Sequence 18 BP; 4 A, 5 C, 4 G, 5 T, 0 U, 0 Other;

Qy Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. NO. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 935 CTCTGTTACCGAGCTG 951
1 CTATGTTACCGAGCTG 17

RESULT 1964
ADG14613
ID ADG14613 standard; DNA; 18 BP.
XX
XX ADG14613;
AC
XX 26-FEB-2004 (first entry)
XX
XX Human IL-10 regulatory region PCR primer IL10-2763AR, SEQ ID NO:4.
XX
XX Therapeutic response; therapeutic outcome; interferon-alpha-2b;
XX ribavirin; hepatitis C virus; HCV infection; interleukin-10;
XX IL-10 regulatory region; single nucleotide polymorphism; SNP; haplotype;
XX genotype; cytotoxic T-lymphocyte antigen-4; CTLA-4 promoter;
XX CTLA-4 exon 1; bacterial infection; meningococcal infection;
XX rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
XX inflammatory bowel disease; multiple sclerosis; human; PCR; primer; ss.

OS Homo sapiens.
XX
XX WO200268699-A1.
XX
XX 06-SEP-2002.
XX
XX 27-FEB-2002; 2002WO-US006207.
XX
XX 27-FEB-2001; 2001US-0271811P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Yee L, Tang J, Kaslow RA, Van Leeuwen DJ;
XX
XX WPI; 2002-707021/76.
XX
XX Predicting a therapeutic response comprises comparing a first nucleic
XX acid allele in an interleukin-10 (IL-10) regulatory region with a second
XX nucleic acid allele in the IL-10 regulatory region associated with a
XX known outcome.

XX Claim 12; SEQ ID NO 4; 34pp; English.

XX The invention relates to a method for predicting an individual's
XX therapeutic response to the administration of interferon-alpha-2b and
XX ribavirin for the treatment of a pathological condition, especially
XX hepatitis C virus (HCV) infection. The method involves determining which
XX allelic form is present at positions -3575, -2763, -1082, -819 and -592
XX of the interleukin-10 (IL-10) regulatory region, and comparing these with
XX the allelic forms at these positions which are associated with a known
XX outcome of interferon-alpha-2b and ribavirin administration. Presence of
XX the single nucleotide polymorphisms -592A and -819T, the -592A/A or -
XX 819T/T genotypes, the combination of -592A/-819T as a haplotype,
XX homozygosity for -592A/-819T, -592A/-819T as a genotype, or possession of
XX the (108)TATA haplotype (encompassing positions -3575, -2763, -1082, -
XX 819 and -592) is associated with a sustained response to interferon-alpha
XX -2b and ribavirin therapy. In contrast, the presence of -592C and -819C,
XX or the (108)TACC haplotype indicates that the patient will be non-
XX responsive to this therapy. The method optionally further comprises

CC detection of the allele at position -318 of the cytotoxic T-lymphocyte
CC antigen-4 (CTLA-4) promoter and the allele at position 49 of exon 1 of
CC the CTLA-4 gene. The invention also encompasses kits and oligonucleotide
CC primers for use in the methods of the invention. The method and primers
CC are useful for identifying and analysing genetic polymorphisms in the IL-
CC 10 regulatory region and/or cytotoxic T-lymphocyte antigen-4 which can be
CC used in predicting an individual's response to therapeutic intervention
CC with interferon-alpha-2b and ribavirin for HCV infection, and for
CC predicting the responsiveness of an individual to therapy for a
CC pathological condition, or for predicting the outcome of therapeutic
CC intervention in pathological conditions such as bacterial infection (e.g.
CC meningococcal infection), rheumatoid arthritis, systemic lupus
CC erythematosus, Sjogren's syndrome, inflammatory bowel disease or multiple
CC sclerosis. The present sequence is related to the invention.

SQ Sequence 18 BP; 4 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 885 CACCACGCCGGCTTAT 901
Db 2 CACCACGCCGGCTTAT 18

RESULT 1965
ABZ10660/C
ID ABZ10660 standard; DNA; 18 BP.
AC ABZ10660;
XX
XX
DT 16-JUN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #800.
XX
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KM cytosine methylation state; probe; primer; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Gueclig D, Howe A, Mueller J;
PI Olek A, Pienbrock C, Adorjan P, Grabs G, Leese R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwabe I, Ziebarth H;
XX
XX WPI; 2003-018942/01.
XX
DR
XX
PT Detecting and differentiating between haematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 55; 117pp; English.

CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118

CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used; for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients

SQ Sequence 18 BP; 6 A; 0 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 928 AATCTCACTCTTACC 944
Db 17 AATCTCACTCTTACC 1

RESULT 1966
ADM47300/C
ID ADM47300 standard; DNA; 18 BP.
AC ADM47300;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX NOVX oligonucleotide forward primer. SEQ ID No 133.
DE
XX
XX NOVX; cytostatic; gene therapy; vaccine; cancer; chromosome mapping;
KM primer; ss.
KM
XX
XX Unidentified.
OS
XX
PN WO2003083039-A2.
XX
PN
XX
PD 09-OCT-2003.
XX
PF 03-JUL-2002; 2002WO-US021485.
XX
PF
XX 05-JUL-2001; 2001US-0303046P.
PR 09-JUL-2001; 2001US-0303828P.
PR 11-JUL-2001; 2001US-0304502P.
PR 12-JUL-2001; 2001US-0305011P.
PR 13-JUL-2001; 2001US-0305262P.
PR 16-JUL-2001; 2001US-0305673P.
PR 17-JUL-2001; 2001US-0306085P.
PR 24-JUL-2001; 2001US-0307536P.
PR 27-JUL-2001; 2001US-0308228P.
PR 30-JUL-2001; 2001US-0308877P.
PR 14-AUG-2001; 2001US-0312203P.
PR 17-SEP-2001; 2001US-0322640P.
PR 19-SEP-2001; 2001US-0323484P.
PR 21-SEP-2001; 2001US-0323821P.
PR 25-SEP-2001; 2001US-0323948P.
PR 25-SEP-2001; 2001US-0324711P.
PR 09-OCT-2001; 2001US-0327893P.
PR 21-NOV-2001; 2001US-0331768P.
PR 21-FEB-2002; 2002US-0359191P.
PR 22-FEB-2002; 2002US-035939P.
PR 28-FEB-2002; 2002US-0360923P.
PR 01-MAR-2002; 2002US-0360830P.
PR 01-MAR-2002; 2002US-0361178P.
PR 05-MAR-2002; 2002US-0361748P.
PR 12-MAR-2002; 2002US-0363429P.

KW obesity; inflammatory marker; low density lipoprotein; cholesterol;
KW high density lipoprotein; angina; atherosclerosis; microsatellite marker;
XX ss.
OS Homo sapiens.
XX Synthetic.
PN WO2004035741-A2.
XX
XX 29-APR-2004.
XX
XX 16-OCT-2003; 2003WO-US032556.
XX
XX 17-OCT-2002; 2002US-041943P.
XX 21-FEB-2003; 2003US-0449331P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Helgadottir A, Gurney ME, Gulcher JR;
XX WPI; 2004-357211/33.
XX
XX Use of leukotriene synthesis inhibitor for manufacture of a medicament
PT for treatment for myocardial infarction or susceptibility to myocardial
PT infarction in individual.
XX
XX Disclosure; SEQ ID NO 22; 306bp; English.
XX
XX The present invention describes using a leukotriene synthesis inhibitor
CC (1) for the manufacture of a medicament for the treatment of myocardial
CC infarction or susceptibility to myocardial infarction in an individual.
CC Also described is a method (M1) for the treatment of acute coronary
CC syndrome (ACS) in an individual comprising administering (1). (1) has
CC antiatherosclerotic, cardiac and antianginal activities, and can be used
CC as a leukotriene biosynthesis inhibitor, and a leukotriene receptor
CC antagonist. (1) can be used for the manufacture of a medicament for the
CC treatment of myocardial infarction or susceptibility to myocardial
CC infarction in an individual who has at least one risk factor chosen from
CC an at-risk haplotype for myocardial infarction, an at-risk haplotype in
CC the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a
CC FLAP nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-
CC LO) gene promoter; in an individual who has at least one risk factor
CC chosen from diabetes, hypertension, hypercholesterolaemia, elevated
CC lip(a), obesity, past or current smoker; in an individual having elevated
CC inflammatory marker chosen from C-reactive protein (CRP), serum amyloid
CC A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue
CC necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
CC soluble intervascular adhesion molecule (sICAM), E-selectin, matrix
CC metalloproteinase type-1, matrix metalloproteinase type-2, matrix
CC metalloproteinase type-3 and matrix metalloproteinase type-9; in an
CC individual having increased low density lipoprotein (LDL) cholesterol
CC and/or decreased high density lipoprotein (HDL) cholesterol; in an
CC individual having increased leukotriene synthesis; in an individual
CC having previous myocardial infarction or acute coronary syndrome (ACS)
CC event; stable angina; or in an individual who has atherosclerosis or who
CC requires treatment to restore blood flow in arteries. (M1) is useful for
CC treating an individual suffering from acute coronary syndrome chosen from
CC unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-
CC elevation myocardial infarction (STEMI). The human FLAP gene is located
CC on chromosome 13, more specifically to 13q12. The present sequence
CC represents a microsatellite marker used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 1 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 943 CCCAGGCTGGAGTCA 959
DB 17 CCCAGGCTGGAGTCA 1

RESULT 1969
AD043261/C
ID AD043261 standard; DNA; 18 BP.
XX
XX AD043261;
XX
XX 29-UTR-2004 (first entry)
XX
XX Bipolar and unipolar affective disorder marker D12SDK1 primer D12SDK1F.
XX
XX Bipolar affective disorder; Unipolar affective disorder; diagnosis;
KW marker; neuroleptic; gene therapy; PCR; primer; human; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004040016-A2.
XX
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-GB004684.
XX
XX 31-OCT-2002; 2002GB-00025360.
XX
XX (UCLB-) UCL BIOMEDICA.
XX (EWAL/) EWALD M V.
XX
XX Ewald H, Kalsi G, Mcguillan A, Gurling HMD, Degen B, Mors O;
PI Kruse T, Lundorf MD;
XX
XX WPI; 2004-376206/35.
XX
XX Diagnosing, prognosing, or determining the susceptibility to, a
PT neuropsychiatric disorder using a C12 candidate gene region marker by
PT determining the structure, level of expression or activity of a
PT polypeptide encoded by the gene.
XX
XX Claim 19; Page 79; 96pp; English.
XX
XX The present sequence is that of primer D12SDK1F which, with primer
CC D12SDK1R AD043262, can be used to amplify D12SDK1, a novel microsatellite
CC marker associated with bipolar affective disorder and genetically related
CC unipolar affective disorder. D12SDK1 comprises a dinucleotide repeat. 8
CC Alleles (134-152 bp) have been detected. A locus for bipolar disorder and
CC related unipolar affective disorders has been fine mapped on chromosome
CC 12 (C12) for the first time and several genes that are carrying mutations
CC increasing susceptibility to bipolar disorder have been identified. The
CC region is approximately 2 million base pairs of DNA in the chromosome 1
CC region 15q24.3 on the short arm of chromosome 12 between markers D12S2705
CC and D12S340. The inventors genotyped 21 newly described and previously
CC published microsatellite markers in a sample of 381 Danish and British
CC bipolar patients and compared the frequency of marker alleles to a
CC matched control group. Differences in allele frequencies, which were
CC highly statistically significant, were found for 10 of these markers.
CC Based on the results, the invention provides markers and methods of using
CC them in diagnosing, or determining the susceptibility of an individual
CC to, bipolar and genetically related unipolar affective disorders and
CC related neuropsychiatric disorders, and methods for identifying markers
CC and compounds for use as part of therapeutic and/or diagnostic methods. A
CC method of treatment comprises administering a substance that modulates
CC expression of a candidate gene or which modulates the level of activity
CC of a candidate gene product.
XX
XX Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 482 GCAAGTGTGTGATCACA 498
DB 18 GCAAGTGTGTGATCACA 2

```

RESULT 1970
ADO48762
ID ADO48762 standard; DNA; 18 BP.
XX
XX
AC ADO48762;
XX
XX
DT 12-AUG-2004 (first entry)
XX
XX
DE Human neuropilin 1 (NRP1) extension PCR primer #64.
XX
XX
KW human; melanoma; single nucleotide polymorphism; SNP; neuropilin 1; NRP1;
KW mannose receptor C type 2; MRC2; extension PCR; primer; ss; genotyping.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200404163-A2.
XX
XX
PD 27-MAY-2004.
XX
XX
PF 06-NOV-2003; 2003WO-US035876.
XX
XX
PR 06-NOV-2002; 2002US-0424475P.
XX
XX
PR 23-JUL-2003; 2003US-0489703P.
XX
XX
PA (SEQU-) SEQUENOM INC.
XX
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
XX
DR WPI; 2004-411720/38.
XX
XX
PT Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
XX
PS Example 3; Page 79; 176pp; English.
XX
XX
CC The invention comprises a method for identifying a subject at risk of
CC melanoma. The invention involves detecting the presence or absence of one
CC or more polymorphic variations associated with melanoma in the neuropilin
CC 1 (NRP1) or mannose receptor C type 2 (MRC2) genes. The method of the
CC invention is useful for identifying subjects at risk and treating
CC melanoma. The present DNA sequence represents an extension PCR primer
CC that was used to detect single nucleotide polymorphisms within human
CC NRP1.
XX
XX
SQ Sequence 18 BP; 4 A; 3 C; 6 G; 4 T; 0 U; 1 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 392 GTGCTGGATTACAGGC 408
DB 1 GTACTGGATTACAGGC 17
XX
XX
RESULT 1971
ADO48745
ID ADO48745 standard; DNA; 18 BP.
XX
XX
AC ADO48745;
XX
XX
DT 12-AUG-2004 (first entry)
XX
XX
DE Human neuropilin 1 (NRP1) extension PCR primer #47.
XX
XX
KW human; melanoma; single nucleotide polymorphism; SNP; neuropilin 1; NRP1;
KW mannose receptor C type 2; MRC2; extension PCR; primer; ss; genotyping.
XX
XX
OS Homo sapiens.
XX

```

```

PN WO200404163-A2.
XX
XX
PD 27-MAY-2004.
XX
XX
PF 06-NOV-2003; 2003WO-US035876.
XX
XX
PR 06-NOV-2002; 2002US-0424475P.
XX
XX
PR 23-JUL-2003; 2003US-0489703P.
XX
XX
PA (SEQU-) SEQUENOM INC.
XX
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
XX
DR WPI; 2004-411720/38.
XX
XX
PT Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
XX
PS Example 3; Page 78; 176pp; English.
XX
XX
CC The invention comprises a method for identifying a subject at risk of
CC melanoma. The invention involves detecting the presence or absence of one
CC or more polymorphic variations associated with melanoma in the neuropilin
CC 1 (NRP1) or mannose receptor C type 2 (MRC2) genes. The method of the
CC invention is useful for identifying subjects at risk and treating
CC melanoma. The present DNA sequence represents an extension PCR primer
CC that was used to detect single nucleotide polymorphisms within human
CC NRP1.
XX
XX
SQ Sequence 18 BP; 4 A; 3 C; 6 G; 4 T; 0 U; 1 Other;
XX
XX
Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
QY 392 GTGCTGGATTACAGGC 408
DB 1 GTGCTGGATTACAGGC 17
XX
XX
RESULT 1972
ADO56946/C
ID ADO56946 standard; DNA; 18 BP.
XX
XX
AC ADO56946;
XX
XX
DT 12-AUG-2004 (first entry)
XX
XX
DE Human CARK/FPCT proximal SNP probe #12.
XX
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;
KW single nucleotide polymorphism; CARK; FPCT;
KW cardiac ankyrin repeat kinase; fucose-1-phosphate guanylyltransferase;
KW probe.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200404164-A2.
XX
XX
PD 27-MAY-2004.
XX
XX
PF 06-NOV-2003; 2003WO-US035879.
XX
XX
PR 06-NOV-2002; 2002US-0424475P.
XX
XX
PR 23-JUL-2003; 2003US-0489703P.
XX
XX
PA (SEQU-) SEQUENOM INC.
XX
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM;
XX

```

DR WPI; 2004-411721/38.
 XX Identifying a subject at risk of melanoma, useful for treating melanoma,
 PT comprises detecting the presence or absence of one or more polymorphic
 PT variations associated with melanoma in a nucleic acid sample from a
 PT subject.
 XX
 XX Example 7; Page 120; 295pp; English.
 XX
 CC The invention relates to a method of identifying a subject at risk of
 CC melanoma comprising detecting the presence or absence of one or more
 CC polymorphic variations associated with melanoma in a nucleic acid sample
 CC from a subject. Preventing melanoma in a subject comprises detecting the
 CC presence or absence of one or more polymorphic variations associated with
 CC melanoma in a nucleic acid sample from a subject; and administering a
 CC melanoma preventative to a subject in need thereof based upon the
 CC presence or absence of the one or more polymorphic variations in the
 CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
 CC exposure to the subject. The methods, nucleic acids, proteins, and
 CC compositions are useful for treating melanoma. The present sequence
 CC represents a human cardiac ankyrin repeat kinase/fucose-1-phosphate
 CC guanylyltransferase, CARK/FPGT, proximal probe.
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 1 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 832 CTGTGATCTGCTGCC 848
 DB 17 CTGCTGATCTGCTGCC 1
 XX
 RESULT 1973
 ADOS6480
 ID ADO56480 standard; DNA; 18 BP.
 XX
 AC ADO56480;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #5.
 XX
 DE gene therapy; human; ss; melanoma;
 KW melanoma associated polymorphic variation; SNP;
 KW single nucleotide polymorphism; cyclin-dependent kinase 10, CDK10, probe.
 XX
 OS Homo sapiens.
 XX
 PN WO2004044164-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035879.
 XX
 PR 06-NOV-2002; 2002US-0424475P.
 PR 23-JUL-2003; 2003US-0489703P.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Roch RB, Nelson MR, Braun A, Kammerer SM;
 XX
 WPI; 2004-411721/38.
 XX
 CC Identifying a subject at risk of melanoma, useful for treating melanoma,
 CC comprises detecting the presence or absence of one or more polymorphic
 CC variations associated with melanoma in a nucleic acid sample from a
 CC subject.
 XX
 XX Example 5; Page 83; 295pp; English.
 XX
 CC The invention relates to a method of identifying a subject at risk of

CC melanoma comprising detecting the presence or absence of one or more
 CC polymorphic variations associated with melanoma in a nucleic acid sample
 CC from a subject. Preventing melanoma in a subject comprises detecting the
 CC presence or absence of one or more polymorphic variations associated with
 CC melanoma in a nucleic acid sample from a subject; and administering a
 CC melanoma preventative to a subject in need thereof based upon the
 CC presence or absence of the one or more polymorphic variations in the
 CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
 CC exposure to the subject. The methods, nucleic acids, proteins, and
 CC compositions are useful for treating melanoma. The present sequence
 CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
 XX
 SQ Sequence 18 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 1 Other;
 XX
 Query Match 1.6%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 249 TCGGCTCCCAAGTGC 265
 DB 1 TCGGCTCCCAAGAGC 17
 XX
 RESULT 1974
 ADOS7017/C
 ID ADO57017 standard; DNA; 18 BP.
 XX
 AC ADO57017;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human CARK/FPGT proximal SNP probe #83.
 XX
 DE gene therapy; human; ss; melanoma;
 KW melanoma associated polymorphic variation; SNP;
 KW single nucleotide polymorphism; CARK; FPGT;
 KW cardiac ankyrin repeat kinase; fucose-1-phosphate guanylyltransferase;
 KW probe.
 XX
 OS Homo sapiens.
 XX
 PN WO2004044164-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035879.
 XX
 PR 06-NOV-2002; 2002US-0424475P.
 PR 23-JUL-2003; 2003US-0489703P.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Roch RB, Nelson MR, Braun A, Kammerer SM;
 XX
 WPI; 2004-411721/38.
 XX
 CC Identifying a subject at risk of melanoma, useful for treating melanoma,
 CC comprises detecting the presence or absence of one or more polymorphic
 CC variations associated with melanoma in a nucleic acid sample from a
 CC subject.
 XX
 XX Example 7; Page 121; 295pp; English.
 XX
 CC The invention relates to a method of identifying a subject at risk of
 CC melanoma comprising detecting the presence or absence of one or more
 CC polymorphic variations associated with melanoma in a nucleic acid sample
 CC from a subject. Preventing melanoma in a subject comprises detecting the
 CC presence or absence of one or more polymorphic variations associated with
 CC melanoma in a nucleic acid sample from a subject; and administering a
 CC melanoma preventative to a subject in need thereof based upon the
 CC presence or absence of the one or more polymorphic variations in the
 CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
 CC exposure to the subject. The methods, nucleic acids, proteins, and

CC compositions are useful for treating melanoma. The present sequence
CC represents a human cardiac ankyrin repeat kinase/fucose-1-phosphate
CC guanylyltransferase, CARK/FPKT, proximal probe.

XX
SQ Sequence 18 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 1 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 832 CTGTGATCTGCTGCC 848
DB 17 CTGTGATCTGCTGCC 1

RESULT 1975

ADP08750
ID ADP08750 standard; DNA; 18 BP.

AC ADP08750;

XX 26-AUG-2004 (first entry)

DE Extend primer 87 used to genotype human glycoprotein VI polymorphism.

XX breast cancer; cytosolic; gene therapy; human; platelet glycoprotein VI;
KM GP6; GPVI; GPIV; chromosome 19q13.4; ss; PCR; primer; SNP;
XX single nucleotide polymorphism.

OS Homo sapiens.

XX WO2004047767-A2.

XX 10-JUN-2004.

XX 25-NOV-2003; 2003WO-US037966.

XX 25-NOV-2002; 2002US-0429136P.

XX 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENC INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441082/41.

PT Identifying a subject at risk of breast cancer by detecting the presence
PT or absence of one or more nucleotide polymorphic variations, useful for
PT diagnosing, preventing and/or treating breast cancer.

XX Example 3; Page 83; 286pp; English.

CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of an extend primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
CC GPIV;GPVI) DNA which is located at chromosomal position 19q13.4.

XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 207 CAGGCTGCTGCTGACT 223

DB 2 CAGGCTGCTGCTGACT 18

RESULT 1976
ADQ78196
ID ADQ78196 standard; DNA; 18 BP.

XX ADQ78196;

XX 09-SEP-2004 (first entry)

DE PCR primer used to amplify cancer related genes for biochip Segid 878.

XX mini-sequencing; Cpg island; methylation specific PCR; MSP;
KM multiplex MSP PCR; cancer; PCR; primer; ss; microarray chip.

XX Unidentified.

OS KR2003069752-A.

XX 27-AUG-2003.

XX 07-MAY-2002; 2002KR-00025108.

XX 20-FEB-2002; 2002KR-00009132.

XX (GOOD-) GOODGENE INC.

XX Choi HI, Eom TH, Jun BI, Kim OH, Mun UC, Oh MY, Song MG;

XX WPI; 2004-095256/10.

PT Mini-sequencing type oligonucleotide chip for detecting methylation of
PT promoter Cpg islands of multiple genes, useful for detecting cancer.

XX Claim 13; SEQ ID NO 878; 248pp; Korean.

CC This invention relates to a novel mini-sequencing type DNA
CC oligonucleotide chip. Specifically, it refers to a chip that is useful
CC for detecting methylation of promoter Cpg islands occurring in multiple
CC genes. The present invention describes using oligonucleotide primers to
CC determine the position of a target gene and promoter Cpg islands, this
CC constitutes treating DNA of the target gene with sodium bisulfite in
CC order to carry out methylation specific (MSP) PCR or multiplex MSP PCR to
CC amplify the sodium bisulfite treated DNA and sequencing the PCR product
CC to confirm the hypomethylation site of the promoter Cpg islands of
CC multiple genes. Accordingly, the chip comprises primer sequences designed
CC from these PCR products that have amine linkers of 12 carbons attached to
CC the 5'-terminal, which are spotted onto the glass slide coated with 3-
CC aminopropyltrimethoxysilane and 1,4-diisocyanate using an array robot.
CC The resulting mini-sequencing chip is useful for detecting cancer, thereby
CC accurately and rapidly detecting methylation of Cpg islands of multiple
CC genes. This oligonucleotide sequence is a PCR primer given in an
CC exemplification of the invention.

XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 443

DB 2 TTTTATTTTATTTT 18

RESULT 1977

AAH39033/C
ID AAH39033 standard; DNA; 19 BP.

XX AAH39033;

XX 14-AUG-2001 (first entry)

DE SNP specific upper PCR primer SEQ ID 1829.

XX Brinkmann U, Hoffmeyer S, Eichelbaum M, Roots I;
XX
XX
XX WPI; 2001-159855/16.
XX
XX
XX New polynucleotide encoding a molecular variant Multi Drug Resistance
PT (MDR)-1 polypeptide is useful for diagnosing and treating diseases
PT associated with abnormal MDR-1 expression or function, e.g. cancer.
XX
XX
XX Disclosure; Page 121; 154pp; English.
XX
XX The present invention provides nucleotides encoding molecular variants of
CC the human multi drug resistance-1 (MDR-1) protein. These can be used to
CC identify compounds capable of treating multidrug resistance and
CC sensitivity interfering resulting from polymorphisms in MDR-1, which can
CC lead to difficulties in treating cancer, cardiovascular, neuronal,
CC inflammatory and CNS diseases
XX
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 832 CTTGTGATCGCTGCTC 850
DB 1 CTTGTGATCGCTGCTC 19

RESULT 1980
ACF62694/c
ID ACF62694 standard; DNA; 19 BP.
XX
XX ACF62694;
AC
XX 08-OCT-2003 (first entry)
DT
XX
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:523.
DE
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KM cytochrome p450; subfamily I1A; nifedipine oxidase; polypeptide 5;
KM cytostatic; PCR primer; ss.
XX
XX Synthetic.
OS
XX MO2003013534-A2.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002MO-EP008219.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PT
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX
XX Heinrich G, Kerb R;
PI
XX
XX WPI; 2003-268144/26.
DR
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily I1A, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX
XX Disclosure; Page 46; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily I1A (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention

CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
XX
SQ Sequence 19 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 1 Other;

Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 832 CTTGTGATCGCTGCTC 850
DB 19 CTTGTGATCGCTGCTC 1

RESULT 1981
ACF62695
ID ACF62695 standard; DNA; 19 BP.
XX
XX ACF62695;
AC
XX
XX 08-OCT-2003 (first entry)
DT
XX
XX Cancer based on CYP3A5 related oligonucleotide SEQ ID NO:524.
DE
XX
XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KM cytochrome p450; subfamily I1A; nifedipine oxidase; polypeptide 5;
KM cytostatic; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO2003013534-A2.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002MO-EP008219.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
PT
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX
XX Heinrich G, Kerb R;
PI
XX
XX WPI; 2003-268144/26.
DR
XX
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily I1A, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX
XX Disclosure; Page 46; 86pp; English.
XX
XX The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily I1A (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention

SO Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCTGCCTC 850
DB 1 CTCGTGATCTGCTGCCTC 19
RESULT 1982
ADB21365/c
ID ADB21365 standard; DNA; 19 BP.
XX
AC ADB21365;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:523.
XX
KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
KM ds.
XX
OS Unidentified.
XX
PA WO2003013533-A2.
XX
PI Heinrich G, Kerb R;
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
PD WPI; 2003-354397/33.
XX
PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Disclosure; Page 55; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 1 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCTGCCTC 850
DB 1 CTCGTGATCTGCTGCCTC 1

RESULT 1983
ADB21366
ID ADB21366 standard; DNA; 19 BP.
XX
AC ADB21366;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:524.
XX
KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene;
KM ds.
XX
OS Unidentified.
XX
PA WO2003013533-A2.
XX
PI Heinrich G, Kerb R;
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
PD WPI; 2003-354397/33.
XX
PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Disclosure; Page 55; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCTGCTGCCTC 850
DB 1 CTCGTGATCTGCTGCCTC 19
RESULT 1984
ADB88454/c
ID ADB88454 standard; DNA; 19 BP.
XX
AC ADB88454;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human UGT1A1 variant allele sequence fragment SEQ ID NO:523.
XX
KM 89; irinotecan; cancer; UGT1A1; cytosolic; topoisomerase I inhibitor;

KW colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KM ovarian cancer; pancreatic cancer; malignant glioma;
XX uridine diphosphate glycosyltransferase1 member A1.
OS Homo sapiens.
XX
XX WO2003013536-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008217.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-289896/28.
XX
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
XX Disclosure; Page 60; 107pp; English.
XX
XX The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a patient,
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
XX Sequence 19 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 1 Other;
SQ
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 832 CTTGTGATCTGCTGCCTC 850
DB 19 CTCGTGATCTGCGCCGCTC 1
XX
XX RESULT 1985
ADB88455
ID ADB88455 standard; DNA; 19 BP.
XX
XX ADB88455;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Human UGT1A1 variant allele sequence fragment SEQ ID NO:524.
XX
XX
XX ss; irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
KM colorectal cancer; cervical cancer; gastric cancer; lung cancer;
KM ovarian cancer; pancreatic cancer; malignant glioma;
KM uridine diphosphate glycosyltransferase1 member A1.
XX
XX Homo sapiens.
XX
XX WO2003013536-A2.
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008217.
PF

XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-289896/28.
XX
XX
XX Use of irinotecan to treat cancer patient by determining if patient has
PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX
XX Disclosure; Page 60; 107pp; English.
XX
XX The invention relates to the novel use of irinotecan to treat a patient
CC suffering from cancer. This involves determining if the patient has one
CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
CC more of such variant alleles, irinotecan is administered in an increased
CC or decreased amount in comparison to the amount that is administered
CC without regard to the patient's alleles in the UGT1A1 gene. The invention
CC has cytostatic activity. A composition of the invention acts as a patient,
CC topoisomerase I inhibitor. The method is useful for treating a patient,
CC an animal e.g. mouse or a human, preferably African or Asian, suffering
CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
CC pancreatic cancer or malignant glioma. The present sequence is udes in
CC the exemplification of the invention.
XX
XX Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;
SQ
XX
XX Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 832 CTTGTGATCTGCTGCCTC 850
DB 1 CTCGTGATCTGCGCCGCTC 19
XX
XX RESULT 1986
ADB97438
ID ADB97438 standard; DNA; 19 BP.
XX
XX ADB97438;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Human MDRI variant allele sequence fragment SEQ ID NO:524.
XX
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDRI; cytostatic; human; de; CYP3A5; MRP1; MDRI;
KM TOP1.
XX
XX Homo sapiens.
XX
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002WO-EP008218.
PF
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;
XX
XX WPI; 2003-289145/26.
DR
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT

PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 84; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 832 CTTGTGATCTGCTGCTC 850
DB 1 CTCGTATCTGCGCGCTC 19
XX
RESULT 1987
ADB97437/c
ID ADB97437 standard; DNA; 19 BP.
XX
AC ADB97437;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 variant allele sequence fragment SEQ ID NO:523.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDR1; cytosstatic; human; ds; CYP3A5; MRP1; TOP1.
KM
XX
OS Homo sapiens.
XX
PN WO2003013537-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008218.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 84; 130pp; English.
XX
XX The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 1 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 832 CTTGTGATCTGCTGCTC 850
DB 19 CTCGTATCTGCGCGCTC 1
XX
RESULT 1988
ADB92629
ID ADB92629 standard; DNA; 19 BP.
XX
AC ADB92629;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 variant allele sequence fragment SEQ ID NO:524.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDR1; cytosstatic; ds; human; UGT1A1; MRP1; TOP1.
KM
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008220.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX WPI; 2003-342400/32.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; Page 55; 104pp; English.
XX
XX The invention relates to a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 1 Other;
XX
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 832 CTTGTGATCTGCTGCTC 850
DB 1 CTCGTATCTGCGCGCTC 19
XX
RESULT 1989

ADB92628/c
ID ADB92628 standard; DNA; 19 BP.
XX
AC ADB92628;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDRI variant allele sequence fragment SEQ ID NO:523.
XX
XX Irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM multidrug resistance 1; MDRI; cytosolic; ds; human; UGT1A1; MRP1; TOP1.
XX
XX Homo sapiens.
OS
XX
XX WO2003013535-A2.
PN
PD 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-BP008220.
PF
XX
XX 23-JUL-2001; 2001EP-00117608.
PR
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
XX Heinrich G, Kerb R;
PI
XX WPI; 2003-342400/32.
DR
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
XX
XX Disclosure; Page 55; 104pp; English.
PS
XX
XX The invention relates to a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDRI) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.
XX
XX
SQ Sequence 19 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 1 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 832 CTTGTGATCGCCTGCTC 850
DB 19 CTCGTGATCGCCGCTC 1

RESULT 1990
ADN02393
ID ADN02393 standard; DNA; 19 BP.
XX
XX ADN02393;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX PCR primer 2 used to amplify human thioredoxin reductase exon 11 gDNA.
DE
XX late-onset neurodegenerative disease; D-amino acid oxidase; DAO;
KM flavin dinucleotide; FAD-dependent oxidase;
KM D-amino acid oxidase; EC:1.4.3.3; neuroprotective;
KM antiparkinsonian; amyotrophic lateral sclerosis; ALS; Parkinson's;
KM Alzheimer's; gene therapy; human; ss; PCR; primer; thioredoxin reductase;
XX TXNRD1; exon 11.
XX
OS Homo sapiens.

XX
XX WO2004033723-A2.
PN
XX
XX 22-APR-2004.
PD
XX
XX 06-OCT-2003; 2003WO-GB004337.
PF
XX
XX 09-OCT-2002; 2002GB-00023424.
PR
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA
XX Mitchell J, De Belleruche J;
PI
XX WPI; 2004-348204/32.
DR
XX
XX Determining an increased risk of a late-onset neurodegenerative disease
PT to a patient comprises analyzing a sample from the patient to determine
PT whether the patient has a D-amino acid oxidase (DAO) abnormality.
XX
XX
XX Example 2; SEQ ID NO 121; 209pp; English.
PS
XX
XX The invention relates to a novel method for determining an increased risk
CC of a late-onset neurodegenerative disease to a patient which comprises
CC analysing a sample from the patient to determine whether the patient has
CC a D-amino acid oxidase (DAO) abnormality, where the presence of a DAO
CC abnormality is an indication that the patient has an increased risk of
CC the late-onset neurodegenerative disease. DAO is a flavin dinucleotide
CC (FAD)-dependent oxidase which catalyses the oxidative deamination of D-
CC amino acids (EC:1.4.3.3). The method of the invention has neuroprotective
CC and antiparkinsonian applications and may be useful in determining an
CC increased risk of a late-onset neurodegenerative disease to a patient, as
CC well as in preparing a medicament for treating a late-onset
CC neurodegenerative disease, such as amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease (PD) or Alzheimer's disease (AD), possibly via gene
CC therapy. The current sequence is that of a PCR primer 2 of the invention
CC which was used to amplify human thioredoxin reductase (TXNRD1) exon 11
CC gDNA.
XX
XX
SQ Sequence 19 BP; 2 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 829 GACCTTGATCTGCTC 845
DB 3 GACCTGATCTGCTC 19

RESULT 1991
AAI78387/c
ID AAI78387 standard; DNA; 51 BP.
XX
XX AAI78387;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ:5328.
DE
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR
XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.
PA Shimkete RA, Leach M;
XX WPI, 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
PT
PS Claim 1, Page 2140, 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA55314 to AA553329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 9 A; 16 C; 16 G; 10 T; 0 U; 0 Other;
Query Match 1.6%; Score 15.4; DB 1; Length 51;
Best Local Similarity 61.0%; Pred. No. 2e+03;
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 472 AGGATGAAGTCAGTGGTGTATCATCAGACTGACGACCT 512
DB 41 AGGTTGCGTGTGACCCAGAGATGTCACCTTCACTCCAGCCT 1
RESULT 1992
AD056498/c
ID AD056498 standard; DNA; 18 BP.
XX
AC AD056498;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #23.
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;
KW single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
XX
OS Homo sapiens.
XX
XX WO2004044164-A2.
XX
XX 27-MAY-2004.
XX
XX 06-NOV-2003; 2003WO-US035879.
XX
XX 06-NOV-2003; 2002US-0424475P.
XX 23-JUL-2003; 2003US-0489703P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM;
XX WPI, 2004-411721/38.
XX
DR

XX
PT Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.
XX
XX Example 5, Page 84, 295pp; English.
XX
XX The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
XX
SQ Sequence 18 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 1 Other;
Query Match 1.5%; Score 15.2; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 867 GGGATTACAGGCGCTGA 882
DB 18 BGGATTACAGGCGCTGA 3
RESULT 1993
AB257114/c
ID AB257114 standard; DNA; 41 BP.
XX
AC AB257114;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human KIAA0608 protein 10.12 probe, SEQ ID NO:9.
XX
KW Human; KIAA0608 protein 10.12; recombinant production; gene therapy;
KW peptic ulcer; diabetes; probe; ss.
XX
OS Homo sapiens.
XX
XX CN1355220-A.
XX
XX 26-JUN-2002.
XX
XX 24-NOV-2000; 2000CN-00127565.
XX
XX 24-NOV-2000; 2000CN-00127565.
XX
XX (UYFU-) UNITV FUDAN.
XX
XX Mao Y, Xie Y;
XX
XX WPI, 2003-000145/01.
XX
XX Polypeptide-human KIAA0608 protein 10.12 and polynucleotide encoding it.
XX
XX Example 6, Page 22 (Disclosure); 35pp; Chinese.
XX
XX The invention relates to human KIAA0608 protein 10.12 (ABP58674) and
CC nucleic acids encoding it (AB257108). The protein has a molecular weight
CC of 10 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. KIAA0608
CC protein 10.12 can be used in the treatment of a variety of diseases such
CC as peptic ulcers and diabetes. Sequences AB257113-AB257114 represent
CC human KIAA0608 protein 10.12 probes used in an exemplification of the

DE Human conservative amino acid changing SNP nucleic acid SEQ:6638.
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
OS Homo sapiens.
XX MO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000MO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX (CURA-) CURAGEN CORP.
XX Shinketsu RA, Leach M;
XX PI Shinketsu RA, Leach M;
XX DR MPI; 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX Claim 1; Page 2537; 2653pp; English.
XX
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM5314 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the activity of polypeptides
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX Sequence 51 BP; 10 A; 12 C; 18 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 15.2; DB 1; Length 51;
Best local Similarity 59.1%; Pred. No. 2e+03;
Matches 26; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1028 AAGCAGCTGGGATTACGGGACCTGCGACACACCCCGCTAATT 1071
DB 5 AATTAGCTGGGCGTGGTGGCGGCGCTGTAAATCCAGCTACTT 48
RESULT 1999
AAT52114
ID AAT52114 standard; RNA; 15 BP.
XX
AC AAT52114;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Human ICM hammerhead ribozyme target sequence (nt. position 2860).
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
88.
XX
XX Homo sapiens.
XX OS
XX MO9523225-A2.
XX PD 31-AUG-1995.
XX PF 23-FEB-1995; 95MO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX PR 29-MAR-1994; 94US-00218934.
XX PR 04-APR-1994; 94US-00222795.
XX PR 07-APR-1994; 94US-00224483.
XX PR 15-APR-1994; 94US-00227958.
XX PR 15-APR-1994; 94US-00228041.
XX PR 18-MAY-1994; 94US-00245736.
XX PR 06-JUL-1994; 94US-00271280.
XX PR 15-AUG-1994; 94US-00291932.
XX PR 16-AUG-1994; 94US-00291433.
XX PR 17-AUG-1994; 94US-00293620.
XX PR 19-AUG-1994; 94US-00293520.
XX PR 02-SEP-1994; 94US-00300000.
XX PR 08-SEP-1994; 94US-00303039.
XX PR 23-SEP-1994; 94US-00311486.
XX PR 28-SEP-1994; 94US-00311749.
XX PR 28-SEP-1994; 94US-00314397.
XX PR 03-OCT-1994; 94US-00316771.
XX PR 07-OCT-1994; 94US-00319492.
XX PR 11-OCT-1994; 94US-00321993.
XX PR 04-NOV-1994; 94US-00334847.
XX PR 10-NOV-1994; 94US-00337608.
XX PR 28-NOV-1994; 94US-00345516.
XX PR 16-DEC-1994; 94US-00357577.
XX PR 23-DEC-1994; 94US-00363233.
XX PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowitra B, Dizenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpelisky A, Kisch K, Matulic-Adamic U, Mcswiggen JA;
PI Modak A, Pavco P, Belgileman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX MPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICM-1 target sequences and thereby
CC inhibit ICM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
XX Sequence 15 BP; 3 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
SQ

Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 725 CCTGAGTACGCTGGA 739
|||:||||:|||||
Db 1 CCTGAGTACGCTGGA 15

RESULT 2000

AAK30969
ID AAK30969 standard; DNA; 15 BP.

AAK30969;

21-MAY-1999 (first entry)

Tag sequence of a transcript increased in colorectal cancer.

Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KM diagnosis; prognosis; treatment; ss.

OS Homo sapiens.

PN WO9853319-A2.

26-NOV-1998.

20-MAY-1998; 98MO-US010277.

21-MAY-1997; 97US-0047352P.

(UYJO) UNIV JOHNS HOPKINS.

Vogelstein B, Kinzler KM;

WPI; 1999-070161/06.

Use of isolated gene transcripts - useful for developing products for the
diagnosis, prognosis and treatment of cancers, particularly colon and
pancreatic cancer.

Claim 2; Page 23; 120pp; English.

AAK30947-31815 represent tag sequences of transcripts that are
differentially expressed in colorectal cancer, in pancreatic cancer, or
in both. The tag sequences can be used to identify genes by matching the
tag to a gen data base member, or by using the tag sequences as probes to
isolate unidentified genes from cDNA libraries. The tag sequences can
also be used in a method for diagnosing colon or pancreatic cancer in a
sample suspected of being neoplastic. The method comprises comparing the
level of at least one transcript in a first sample of a tissue to a
second sample, where the first sample is a colonic tissue suspected of
being neoplastic and the second sample is a normal human colonic tissue.
The transcript is identified by a tag selected from AAK30947-31815. The
methods of the invention can be used in the diagnosis, prognosis and
treatment of cancer

Sequence 15 BP; 2 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 CATGTTGCTCAGGCT 212
|||||:|||||
Db 1 CATGTTGCTCAGGCT 15

RESULT 2001

AAF98058
ID AAF98058 standard; DNA; 15 BP.

AAF98058;

19-JUN-2001 (first entry)

Human IGFBP3 allele specific oligonucleotide probe SEQ ID NO:97.

Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGFBP3;
single nucleotide polymorphism; SNP; allele specific oligonucleotide;
immunassay; detection; PCR primer; probe; ss.

OS Homo sapiens.

PN WO200111010-A2.

15-FEB-2001.

02-AUG-2000; 2000WO-US021097.

09-AUG-1999; 99US-0147860P.

(GENA-) GENA/ISSANCE PHARM INC.

Chew A, Denton RR, Duda A, Kiem SE, Lanz EM, Nandabalan K;

Stephens JC;

WPI; 2001-202766/20.

New polynucleotide for gene therapy, comprises nucleotide polymorphisms
in the immunoglobulin E receptor I alpha subunit gene.

Claim 15; Page 23; 99pp; English.

The present invention describes an isolated polynucleotide (I) comprising
a nucleotide sequence (S) which is a polymorphic variant of a reference
sequence for the human immunoglobulin E receptor I alpha subunit (IGFBP3)
gene or its fragment. The polymorphic variant comprises at least one
polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
(A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
a position corresponding to nucleotide 530. (I) can be used in gene
therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
encoded by (I) is useful in drug screening assays and in assays to
measure the binding affinity of one or more candidate drugs targeting
(II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
solution and also reacts with (II) on Western or immunoblots of
polyacrylamide gels on membrane supports or substrates. (III) is also
useful in immunoassays to detect (II) in biological samples. AAF97965 to
AAF98096 represent IGFBP3 allele specific oligonucleotide probes; AAF98097
to AAF98140 represent IGFBP3 gene polymorphism detection primers; and
AAF98141 to AAF98180 represent IGFBP3 gene PCR primers which are used in
the exemplification of the present invention

Sequence 15 BP; 2 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 CACCTGCTCAGGCT 385
|||||:|||||
Db 1 CACCTGCTCAGGCT 15

RESULT 2002

AAF97988/c
ID AAF97989 standard; DNA; 15 BP.

AAF97989;

19-JUN-2001 (first entry)

DE Human IGERA allele specific oligonucleotide probe SEQ ID NO:28.
 XX
 XX Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 KM immunosassay; detection; PCR primer; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20011010-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 02-AUG-2000; 2000WO-US021097.
 XX
 PR 09-AUG-1999; 99US-0147860P.
 XX
 PA (GENA-) GENA/ISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Klem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 XX
 DR WPI; 2001-202766/20.
 PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 PT in the immunoglobulin E receptor I alpha subunit gene.
 XX
 PS Claim 15; Page 21; 99pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) comprising
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 CC gene or its fragment. The polymorphic variant comprises at least one
 CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGERA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 CC the exemplification of the present invention
 CC
 CC
 SQ Sequence 15 BP; 2 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
 XX
 XX
 Query Match 1.5%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 377 CCTCAGCTCCCAA 391
 DB 15 CCTCAGCTCCCAA 1
 XX
 RESULT 2003
 AAF98057/c
 ID AAF98057 standard; DNA; 15 BP.
 AC AAF98057;
 XX
 DT 19-JUN-2001 (first entry)
 XX
 DE Human IGERA allele specific oligonucleotide probe SEQ ID NO:96.
 XX
 KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;

KW immunosassay; detection; PCR primer; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20011010-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 02-AUG-2000; 2000WO-US021097.
 XX
 PR 09-AUG-1999; 99US-0147860P.
 XX
 PA (GENA-) GENA/ISSANCE PHARM INC.
 XX
 PI Chew A, Denton RR, Duda A, Klem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 XX
 DR WPI; 2001-202766/20.
 PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 PT in the immunoglobulin E receptor I alpha subunit gene.
 XX
 PS Claim 15; Page 23; 99pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) comprising
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 CC gene or its fragment. The polymorphic variant comprises at least one
 CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGERA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 CC the exemplification of the present invention
 CC
 CC
 SQ Sequence 15 BP; 3 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 XX
 XX
 Query Match 1.5%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 383 CCTCCCAAGTCTG 397
 DB 15 CCTCCCAAGTCTG 1
 XX
 RESULT 2004
 AAF69438
 ID AAF69438 standard; DNA; 15 BP.
 AC AAF69438;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Human IL4Ralpha gene probe #78.
 XX
 KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
 KW allergic disease; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104270-A1.

XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000MO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Claim 15; Page 43; 188pp; English.
XX
XX The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
XX
SQ Sequence 15 BP; 2 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 647 GGCTGAGTGCAGTG 661
Db 1 GGCTGAGTGCAGTG 15
XX
RESULT 2005
ABK31922
ID ABK31922 standard; DNA; 15 BP.
XX
AC ABK31922;
XX
DT 23-APR-2002 (first entry)
XX
DE Human colon cancer SAGE tag #23.
XX
KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
OS Homo sapiens.
XX
PN US6333152-B1.
XX
PD 25-DEC-2001.
XX
PF 20-MAY-1998; 98US-00081646.
XX
PR 20-MAY-1998; 98US-00081646.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KM, Zhang L, Zhou W;
XX
DR WPI; 2002-153821/20.
XX

PT New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX⁶⁷⁴
PS Disclosure; Col 13; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (1)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
SQ Sequence 15 BP; 2 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 CATGTTGCTCAGGCT 212
Db 1 CATGTTGCTCAGGCT 15
XX
RESULT 2006
ADE14250/c
ID ADE14250 standard; DNA; 15 BP.
XX
AC ADE14250;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #359.
XX
DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
OS Homo sapiens.
XX
PN US2003190617-A1.
XX
PD 09-OCT-2003.
XX
PF 06-MAR-2002; 2002US-00091281.
XX
PR 06-MAR-2002; 2002US-00091281.
XX
PA (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
PI Raymond V, Morissette J, Si E;
XX
DR WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.
XX
XX Claim 11; SEQ ID NO 361; 15pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing

CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.

SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 CAGGCGTGAGCCACC 888
DB 15 CAGGCGTGAGCCACC 1

RESULT 2007
ADE14031/c
ID ADE14031 standard; DNA; 15 BP.
AC ADE14031;
XX
XX
DT 29-JAN-2004 (first entry)
DE Optineurin promoter motif, repeat element or regulatory region #140.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KM SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
OS
XX
XX US2003190617-A1.
PN
XX
XX 09-OCT-2003.
PD
XX
XX 06-MAR-2002; 2002US-00091281.
PF
XX
XX 06-MAR-2002; 2002US-00091281.
PR
XX
XX (SIEB/) SI E.
PA (RAYM/) RAYMOND V.
XX (MORT/) MORISSETTE J.
XX
XX Raymond V, Morissette J, SI E;
PI
XX
XX MPI; 2003-864168/80.
DR
XX
XX
PT New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.
XX
XX
PS Claim 11; SEQ ID NO 142; 159pp; English.

CC The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism

CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing
CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.

SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 CAGGCGTGAGCCACC 888
DB 15 CAGGCGTGAGCCACC 1

RESULT 2008
ACC84465
ID ACC84465 standard; DNA; 15 BP.
AC ACC84465;
XX
XX
DT 28-AUG-2003 (first entry)
DE NTP peptide encoding sequence #12.
XX
XX NTP peptide encoding sequence #12.
DE
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX
XX Unidentified.
OS
XX
XX WO2003008443-A2.
PN
XX
XX 30-JAN-2003.
PD
XX
XX 19-JUL-2002; 2002WO-CA001105.
PF
XX
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306151P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
PA
XX
XX Averbach PA;
PI
XX
XX MPI; 2003-247999/24.
DR P-PSDB; ABR63260.
XX
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX
PS Disclosure, Page 18; 77pp; English.

CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for

CC a pancreatic thread protein. The peptide is conjugated, linked or bound
 CC to a molecule chosen from antibody or its fragment, antibody-like binding
 CC molecule, where the molecule has a higher affinity for binding to a tumor
 CC or other target than binding to other cells. Treatment using NTP peptides
 CC can remove benign tumors with less risk and fewer of the undesirable side
 CC effects of surgery. The present sequence is an NTP encoding sequence
 XX
 XX Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.5%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1029 AGCAGCTGGATTAC 1043
 Db 1 AGCAGCTGGATTAC 15
 RESULT 2009
 AAD63090/c
 ID AAD63090 standard; DNA; 16 BP.
 XX
 XX AAD63090;
 XX
 XX 12-FEB-2004 (first entry)
 XX
 XX Human tandem tag DNA #24.
 DE
 XX
 XX Tandem tag; concatenated tag; human; ds.
 KW
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003190618-A1.
 PN
 XX
 XX 09-OCT-2003.
 PD
 XX
 XX 06-MAR-2002; 2002US-00092885.
 PF
 XX
 XX 06-MAR-2002; 2002US-00092885.
 PR
 XX
 XX (SAMA/) SAMAL B.
 PA
 PA (LITY/) LI Y.
 PA (HERM/) HERMIDA L C.
 PA (HOPP/) HOPPA N L.
 PA (JOHE/) JOHE K K.
 XX
 XX Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;
 PI
 XX
 XX WPI; 2003-831617/77.
 DR
 XX
 XX Generating five prime biased tandem tag libraries of cDNAs by isolating a
 PT sample of mRNAs, amplifying the released tags, concatenating the
 PT amplified tags to form concatenated tags, amplifying and isolating the
 PT concatenated tags.
 PT
 XX
 XX Disclosure; Page 6; 0pp; English.
 PS
 XX
 XX The present invention discloses a method for generating five prime biased
 CC tandem tag libraries of cDNAs. The step involves isolating a sample of
 CC mRNAs, amplifying the released tags, concatenating the amplified tags to
 CC form concatenated tags, amplifying and isolating the concatenated tags.
 CC The present sequence is human tandem tag DNA
 XX
 XX Sequence 16 BP; 3 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.5%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 673 GCTACTGCAACCTC 687
 Db 16 GCTACTGCAACCTC 2

RESULT 2010
 ADH59602/c
 ID ADH59602 standard; DNA; 16 BP.
 XX
 XX ADH59602;
 AC
 XX
 XX 25-MAR-2004 (first entry)
 DT
 XX
 XX Non-nucleotide probe of the invention #6.
 DE
 XX
 XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
 KW probe.
 KW
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003027328-A2.
 PN
 XX
 XX 03-APR-2003.
 PD
 XX
 XX 24-SEP-2002; 2002WO-US030573.
 PF
 XX
 XX 24-SEP-2001; 2001US-0324499P.
 PR
 XX
 XX (BOST-) BOSTON PROBES INC.
 PA (DAKO-) DAKOCYTOMATION DENMARK AS.
 PA
 PI
 XX
 XX Kirtsen NV, Hyldig-Nielsen JJ, Williams BF;
 DR WPI; 2003-421160/39.
 XX
 XX Non-nucleotide probe for suppressing binding of detectable nucleic acid
 PT probes to undesired sequences, has aggregate nucleobase sequence
 PT homologous to randomly distributed repeat sequence of genomic nucleic
 PT acid.
 PT
 XX
 XX Claim 10; SEQ ID NO 8; 103pp; English.
 PS
 XX
 XX The present sequence represents a non-nucleotide probe. The probe is
 CC useful for suppressing the binding of one or more detectable nucleic acid
 CC probes, that are greater than 100 base pairs and that have been derived
 CC from genomic nucleic acid, to one or more undesired sequences in an assay
 CC for determining target genomic nucleic acid of a sample. The method
 CC comprises contacting the sample with the mixture of probes (preferably
 CC comprising 5-50 probes), contacting the sample with the one or more
 CC detectable nucleic acid probes, and determining the target genomic
 CC nucleic acid of the sample by determining the hybridization of the one or
 CC more detectable nucleic acid probes to the target genomic nucleic acid of
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic
 CC found in paraffin embedded tissue material or frozen tissue sections. The
 CC probe is also useful in comparing a sample of genomic nucleic acid with
 CC that of a control sample using a genomic nucleic acid reference array.
 CC The method comprises treating a sample of genomic nucleic acid and
 CC control genomic nucleic acid, which are differentially labelled, the
 CC array or both the sample and control genomic nucleic acid and the array
 CC with the mixture of the probe under suitable hybridization conditions,
 CC contacting the array with treated mixture of sample and control genomic
 CC nucleic acid under suitable hybridization conditions, and comparing the
 CC intensities of the signals from the differential labels of the array to
 CC that caused by hybridization of the probes to genomic nucleic acid, thus
 CC determining one or more variations in copy numbers of sequences in the
 CC sample as compared with the control. The hybridization of the genomic
 CC identical sequences in the control. The hybridization of the genomic
 CC array is determined using an intercalating dye or a detectable acid hybrid
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
 CC The sample of genomic nucleic acid to be tested and the reference of
 CC nucleic acid are labelled with detectable moiety such that hybridization
 CC of the genomic array is determined by determining the presence, absence,
 CC amount or location of the detectable label on the one or more genomic
 CC arrays. The genomic array comprises nucleic acid that is prepared from
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
 CC represents a non-nucleotide probe of the invention.

XX Sequence 16 BP; 0 A; 4 C; 10 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 883 GCCACCAAGCCCGGC 897
15 GCCACCAAGCCCGGC 1
RESULT 2011
ADH59614
ID ADH59614 standard; DNA; 16 BP.
AC ADH59614;
XX
XX
XX 25-MAR-2004 (first entry)
XX
XX
XX Non-nucleotide probe of the invention #18.
XX
XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
XX probe.
XX
XX Synthetic.
XX
XX MO2003027328-A2.
XX
XX 03-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030573.
XX
XX 24-SEP-2001; 2001US-0324499P.
XX
XX (BOST-) BOSTON PROBES INC.
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX Kirszen NV, Hyldeg-Nielsen JU, Williams BF;
XX WPI; 2003-421160/39.
XX
XX Non-nucleotide probe for suppressing binding of detectable nucleic acid
XX probes to undesired sequences, has aggregate nucleobase sequence
XX homologous to randomly distributed repeat sequence of genomic nucleic
XX acid.
XX
XX Claim 10; SEQ ID NO 20; 103bp; English.
XX
XX The present sequence represents a non-nucleotide probe. The probe is
XX useful for suppressing the binding of one or more detectable nucleic acid
XX probes, that are greater than 100 base pairs and that have been derived
XX from genomic nucleic acid, to one or more undesired sequences in an assay
XX for determining target genomic nucleic acid of a sample. The method
XX comprising 5-50 probes), contacting the mixture of probes (preferably
XX detectable nucleic acid probes, and determining the target genomic
XX nucleic acid of the sample by determining the hybridization of the one or
XX more detectable nucleic acid probes to the target genomic nucleic acid of
XX the sample. The genomic nucleic acid is contained in a fixed tissue or a
XX cell, and the sample is metaphase spreads, interphase nucleic or nucleic
XX found in paraffin embedded tissue material or frozen tissue sections. The
XX probe is also useful in comparing a sample of genomic nucleic acid with
XX that of a control sample using a genomic nucleic acid reference array.
XX The method comprises treating a sample of genomic nucleic acid and
XX control genomic nucleic acid, which are differentially labelled, the
XX array or both the sample and control genomic nucleic acid and the array
XX with the mixture of the probe under suitable hybridization conditions,
XX contacting the array with treated mixture of sample and control genomic
XX nucleic acid under suitable hybridization conditions, and comparing the
XX intensities of the signals from the differential labels of the array to
XX that caused by hybridization of the probes to genomic nucleic acid, thus
XX determining one or more variations in copy numbers of sequences in the

CC sample as compared with the relative copy numbers of substantially
CC identical sequences in the control. The hybridization of the genomic
CC array is determined using an intercalating dye or a detectable antibody,
CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
CC The sample of genomic nucleic acid to be tested and the reference of
CC nucleic acid are labelled with detectable moiety such that hybridization
CC of the genomic array is determined by determining the presence, absence,
CC amount or location of the detectable label on the one or more genomic
CC arrays. The genomic array comprises nucleic acid that is prepared from
CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
CC represents a non-nucleotide probe of the invention.
XX
XX Sequence 16 BP; 2 A; 10 C; 4 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 883 GCCACCAAGCCCGGC 897
2 GCCACCAAGCCCGGC 16
RESULT 2012
ADQ3038/c
ID ADQ30388 standard; DNA; 16 BP.
XX
XX
XX ADQ30388;
XX
XX 09-SEP-2004 (first entry)
XX
XX
XX Human VR1 exon 1d transcription factor binding fragment #107.
XX
XX ds; VR1 receptor; vanilloid receptor type 1; modulator;
XX pain transmission; primary sensory neuron; transcription factor;
XX detection; MZFI; NFKappaB; NFAT; GATA1; sensitivity disorder; analgesia;
XX hypalgesia; hyperalgesia; neuralgia; myalgia; human.
XX
XX Homo sapiens.
XX
XX MO2004053120-A2.
XX
XX 24-JUN-2004.
XX
XX 01-DEC-2003; 2003WO-EP013522.
XX
XX 09-DEC-2002; 2002DE-01057421.
XX
XX (CHEF) GRUENTHAL GMBH.
XX
XX Weihe E, Bieller A, Schaefer MKH;
XX WPI; 2004-468868/44.
XX
XX New nucleic acid that modulates expression of the vanilloid receptor-1,
XX useful for control of pain or sensitivity disorders, comprises sequences
XX from control regions of the receptor gene.
XX
XX disclosure, Page 53; 68pp; German.
XX
XX This invention describes a novel nucleic acid containing a specific
XX segment having at least one region that modulates expression of the VR1
XX (vanilloid receptor type 1) receptor, or a functional derivative, allele
XX or fragment of this region, or a sequence that hybridizes to it under
XX standard conditions. The VR1 modulator is derived from one or more of
XX positions 221931-223944 of Genbank AF670399, 31673-36359 of AF63116, or
XX 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
XX pain, particularly in primary sensory neurons. The invention also
XX describes a vector that contains the VR1 modulator, host cells containing
XX this vector (other than human germ or embryonal stem cells) and a method
XX for modulating expression of the VR1 receptor by introducing the
XX modulator or the vector into a cell that contains the VR1 gene. The
XX products of the invention are used for detecting a transcription factor

CC From its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbent assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VRI receptor expression includes a
CC binding site for a transcription factor, e.g. MZ1, NFkBpB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC neuropalgia and myalgia, that are associated with activity of the VRI
CC receptor. This sequence represents a fragment of human VRI exon 1d DNA
CC which is capable of binding to a transcription factor.

XX Sequence 16 BP; 9 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 TGGCTAATTTTGTG 315
Db 16 TGGCTAATTTTGTG 2

RESULT 2013
AAA22972/c
ID AAA22972 standard; RNA; 17 BP.

AC AAA22972;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6198.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cyclostatic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KM dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO9950403-A2.

XX 07-OCT-1999.

PF 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcawiggen JA;

XX WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 254; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086

CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma (myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberculous scleritis, pot-wine stain, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 8 A; 3 C; 0 G; 0 T; 6 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 ATTTTAGTAGAGAT 790
Db 17 ATTTTAGTAGAGAT 3

RESULT 2014
AAA87041/c
ID AAA87041 standard; DNA; 17 BP.

AC AAA87041;

DT 15-JAN-2001 (first entry)

DE Probe to Alu2 human gene.

XX Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;
KM single nucleotide polymorphism; identification; viral load; probe;
KM genotyping; medical marker diagnosis; primer; target; mutation;
KM genetic disease; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO200049180-A1.

XX 24-AUG-2000.

PF 18-FEB-2000; 2000WO-US004242.

PR 18-FEB-1999; 99US-00252436.

PR 21-JUL-1999; 99US-00358972.

PR 25-AUG-1999; 99US-00383316.

XX (PROM-) PROMEGA CORP.

XX Shultz JW, Lewis MK, Leipe D, Mandrekar M, Kephart D, Rhodes RB;

XX Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;

XX WPI; 2000-565377/52.

PT Determining presence or absence of a predetermined endogenous nucleic
PT acid sequence by using an enzyme that depolymerizes the 3' end of an
PT oligonucleotide probe hybridized to a target sequence to release
PT identifier nucleotides.

XX Example; Page 373; 389pp; English.
XX The present invention describes a method (M1) for determining the
CC presence or absence of a predetermined endogenous nucleic acid target
CC sequence (ENMT). The method comprises hybridizing a probe having an

```
CC identifier nucleotide (IN) with ENAT which is treated with an enzyme that
CC depolymerises the 3' end of hybridised NA to release the INs. M1 is used
CC for determining the number of known sequence repeats present in a nucleic
CC acid target sequence in a nucleic acid sample. The method is also useful
CC for determining whether a nucleic acid target sequence in a sample is an
CC allele from a homozygous or heterozygous locus. The method is also useful
CC for detection of mutations, translocations and SNPs in nucleic acids
CC (including those associated with genetic disease), determination of viral
CC load, species identification, sample contamination, and analysis of
CC forensic samples. AAAB6791 to AAAB7079 and AAB12817 represent sequence
CC which are used in the exemplification of the present invention. N.B.
CC There is a discrepancy between the SEQ ID NO: and sequences given in the
CC examples, and the SEQ ID NO: and sequences given in the sequence listing
CC from the present invention
CC
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      635 CTCTGTACCCAGGC 649
        |||||
DB      15 CTCTGTACCCAGGC 1

RESULT 2015
ADB04312
ID ADB04312 strand; DNA; 17 BP.
AC ADB04312;
XX
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5298.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AECOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
PT
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5298; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
```

```
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      647 GGCTGAGTGCAGTG 661
        |||||
DB      3 GGCTGAGTGCAGTG 17

RESULT 2016
ADB04280
ID ADB04280 strand; DNA; 17 BP.
AC ADB04280;
XX
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5266.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AECOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
PT
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5266; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 4 A; 1 C; 4 G; 8 T; 0 U; 0 Other;
```


Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 614 TTTTGTGACACAG 628
DB 3 TTTTGTGACACAG 17

RESULT 2017

ADB04285
ID ADB04285 standard; DNA; 17 BP.

XX ADB04285;

XX 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5271.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-ANG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5271; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC alterations can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 4 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 617 TTTGACACAGCTCT 631
DB 1 TTTGACACAGCTCT 15

RESULT 2018
ABZ60369/c
ID ABZ60369 standard; RNA; 17 BP.

XX ABZ60369;

XX 21-MAR-2003 (first entry)

XX Human K-Ras DNAzyme substrate #481.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

XX WO200297114-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002MO-US016840.

XX 29-MAY-2001; 2001US-0294140P.

XX 06-JUN-2001; 2001US-0296249P.

XX 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;

XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 94; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

XX Sequence 17 BP; 14 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 595 TTTTATTTTATTTT 609
DB 15 TTTTATTTTATTTT 1

RESULT 2019

ABZ60598
ID ABZ60598 standard; RNA; 17 BP.

XX ABZ60598;

XX 21-MAR-2003 (first entry)

XX Human K-Ras DNAzyme substrate #710.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswigen J;
XX
PI MPI; 2003-140484/13.
XX
DR Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 98; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in AB259889 - AB262216, AB264544 - AB265531, AB265520 - AB265524,
CC AB266530 - AB266585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 0 C; 3 G; 0 T; 11 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
XX
QY 769 TTTTGTATTATTAG 783
DB 2 UUUUGUUAUUUUAG 16
XX
RESULT 2020
ACC65847
ID ACC65847 standard; DNA; 17 BP.
XX
AC ACC65847;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 3094.
XX
KW Cytostatic; vituicide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrentia; ss.
XX
XX Mus musculus.
OS
XX
PN WO2003025176-A2.
XX
XX 27-MAR-2003.

XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001PR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
PI MPI; 2003-333167/31.
XX
DR New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 392; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip, in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrentia
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 532 ATCTCTCTGCTCTCAG 546
DB 2 ATCTCTCTGCTCTCAG 16
XX
RESULT 2021
ACA62876/c
ID ACA62876 standard; DNA; 17 BP.
XX
AC ACA62876;
XX
DT 21-AUG-2003 (first entry)
XX
DE Repeated nucleic acid detection method, human probe Alu2.
XX
KW Repeated nucleic acid detection; human; alu; probe; ss.
XX
OS Homo sapiens.
XX
PN US2003022163-A1.
XX
PD 30-JAN-2003.
XX
PF 15-DEC-2000; 2000US-00733909.
XX
PR 21-JUL-1999; 99US-00358972.
PR 25-AUG-1999; 99US-00383316.
XX
PA (MAND/) MANDREKAR M N.
PA (TERR/) TEREBA A.
PA (SHUL/) SHULTZ J W.
XX
XX Mandrekar MN, Tereba A, Shultz JW;
XX
DR MPI; 2003-479484/45.
XX
PT Determining presence or absence of desired nucleic acids that contain
PT multiple repeats of predetermined nucleic acid target sequences in a
PT sample, by using nucleic acid hybridization methods.

XX Claim 1; Page 27; 31pp; English.
PS
XX The invention describes a method of determining presence or absence of a
CC desired nucleic acid (NA) that contains multiple repeats of a
CC predetermined NA target sequence in a NA sample. The method involves
CC providing a treated sample that may contain the desired NA in which
CC several predetermined repeating NA target sequences are hybridised with a
CC NA probe, analysing for presence or absence of the desired NA. The method
CC probe, and thereby the presence or absence of the desired NA. The method
CC is useful for determining the presence or absence of desired nucleic
CC acids that contain multiple repeats of a predetermined NA target
CC sequence. In a NA sample obtained from a biological sample, where the
CC repeated sequence includes several predetermined repeated sequence that
CC differ in length and/or sequence. The methods can be efficiently used for
CC distinguishing human and bacterial NA. The method is highly sensitive,
CC and enables detection and quantification of the presence of a NA without
CC the need to undergo a NA target sequence enrichment step prior to a NA
CC hybrid detection step. The method enables rapid and accurate detection of
CC a desired NA that contains multiple repeats of a NA target sequence. This
CC sequence represents a probe used to detect the human A1u repeat sequences
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 635 CTCTGTCACCCGAGC 649
DB 15 CTCTGTCACCCGAGC 1
RESULT 2022
ID ADB43123 standard; DNA; 17 BP.
XX
AC ADB43123;
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #3446.
XX
KM cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 434; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences, a
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides; a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 837 GATCTGCTCTCCCTCG 851
DB 1 GATCTGCTCTCCCTCG 15
RESULT 2023
ID AD148985 standard; DNA; 17 BP.
XX
AC AD148985;
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID1488.
XX
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytosstatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 1488; 30pp; French.
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytosstatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or

CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration. The
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 ATCTCTGCTGCTCAG 546
DB 2 ATCTCTGCTGCTCAG 16

RESULT 2024
AD148613/C
ID AD148613 standard; DNA; 17 BP.

XX AD148613;

DT 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID1116.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;

KM cytosolic; virocid; neuroprotective; neurotropic; neuroleptic; probe;

KM primer; PCR; gene chip; antisense; viral disease; tumour;

XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

OS Homo sapiens.

XX MO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001PR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX MPI; 2003-31354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; SEQ ID NO 1116; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

XX in the phenomena of tumour suppression, tumour reversion, apoptosis

XX and/or resistance to viruses. The invention may be useful for the

XX development of compounds with a cytosolic, virocid, neuroprotective,

XX neurotropic or neuroleptic activity. The DNA sequences may be useful as

XX probes and primers for detecting, identifying, quantifying and/or

XX amplifying nucleic acid, for example as one component of a gene chip, in

XX vitro as antisense reagents and for production of recombinant

XX polypeptides. The invention may therefore be useful for preparation of

XX pharmaceuticals for prevention and/or treatment of viral diseases that

XX are characterised by development of tumours or cell degeneration.

XX Specifically cancer but also Alzheimer's disease and schizophrenia. The

XX present sequence is that of a nucleic acid sequence of the invention.

XX Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TGCACTGGTGTGATC 495
DB 15 TGCACTGGTGTGATC 1

RESULT 2025
ADP45893/C
ID ADP45893 standard; DNA; 17 BP.

XX ADP45893;

DT 26-AUG-2004 (first entry)

XX Extend primer 85 used to genotype human ICAM-1/ICAM-4/ICAM-5 SNP.

XX breast cancer; cytosolic; gene therapy; human;

KM intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;

KM CD54; cell surface glycoprotein p3.58; ICAM-4;

KM Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;

XX 85; primer; PCR; SNP; single nucleotide polymorphism; probe.

XX Homo sapiens.

XX MO2004047623-A2.

XX 10-JUN-2004.

XX 25-NOV-2003; 2003WO-US037948.

XX 25-NOV-2002; 2002US-0429136P.

XX 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX MPI; 2004-441051/41.

XX Example 4; Page 84; 28pp; English.

XX The invention relates to a novel method for identifying a subject at risk

XX of breast cancer comprising detecting the presence or absence of one or

XX more polymorphic variations associated with breast cancer in a nucleic

XX acid sample from a subject. The method of the invention has cytostatic

XX applications and may be useful for identifying a subject at risk of

XX breast cancer, for early diagnosis, prevention and treatment of breast

XX cancer, possibly via gene therapy, as well as to analyse and predict a

XX response to a breast cancer treatment and in clinical drug trials. The

XX current sequence is that of an Extend primer (also described as probe) of

XX the invention which was used to genotype human intercellular adhesion

XX molecule ICAM-1/ICAM-4/ICAM-5 gDNA. ICAM-1 (human rhinovirus receptor, BB2

XX ; CD54; cell surface glycoprotein p3.58) has been mapped to chromosomal

XX position 19p13.3-p13.2, ICAM-4 (Landsteiner-Wiener blood group; LW) has

XX been mapped to chromosomal position 19p13.2-cen and ICAM-5

XX (telencephalin) has been mapped to chromosomal position 19p13.2.

XX Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

OY 650 TGGAGTGCAGTGGCG 664
17 TGGAGTGCAGTGGCG 3

RESULT 2026

AAV62683
ID AAV62683 standard; DNA; 18 BP.

XX AAV62683;

DT 15-FEB-1999 (first entry)

XX Tango-63 primer t63-r2.

XX Tango-63d; tumour necrosis factor receptor related protein; human;

KM apoptosis; cancer; autoimmune disease; neurodegenerative disease; primer;

XX Synthetic.

OS Homo sapiens.

XX WO9846643-A1.

XX 22-OCT-1998.

XX 16-APR-1998; 98WO-US007694.

XX 16-APR-1997; 97US-00843652.

XX (MILL-) MILENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D;

XX WPI; 1998-594562/50.

XX Isolated tumour necrosis factor related proteins - used to develop

PT products for the diagnosis and treatment of apoptosis-related disorders,

XX e.g. cancers, autoimmune disorders or neurodegenerative disorders.

XX Example 3; Page 67; 88pp; English.

XX Primer t63-r2 and t63-f2 (see AAV62682) are based on the 3' untranslated

CC region of the human Tango-63 gene. They were used in mapping studies of

CC the Tango-63 gene. The gene has been mapped on the Stanford Human Genome

CC Center G3 radiation hybrid panel close to marker D8S1734 with a LOD score

CC of 6. This map position is located in the most frequently lost region of

CC chromosome 8 between markers D8S133 and NBEFL. Tango-63 is alternatively

CC spliced (see AAV62672-73) to produce the Tango-63d and Tango-63e

CC polypeptides (see AAW79260-61) of the invention. Tango-63 nucleic acids

CC and polypeptides are used in methods for the diagnosis and treatment of

CC apoptosis-related disorders such as cancer, autoimmune and

XX neurodegenerative disease

XX Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 15; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 30-NOV-2001 (first entry)

XX Human Her-3 mRNA inhibiting antisense oligo ISIS # 19629.

XX Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;

XX antiinflammatory; cytostatic; antibacterial; antisense; ss.

XX Synthetic.

OS Homo sapiens.

XX US6277640-B1.

XX 21-AUG-2001.

XX 31-JUL-2000; 2000US-00630706.

XX 31-JUL-2000; 2000US-00630706.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM;

XX WPI; 2001-535134/59.

XX Antisense compounds capable of modulating expression of human Her-3,

XX member of epidermal growth factor family of receptor/tyrosine kinases,

XX useful for preventing or delaying infection, inflammation or tumor

XX formation.

XX Claim 1; Col 43-44; 49pp; English.

XX The invention provides antisense compounds capable of inhibiting the

XX expression of human Her-3, a member of epidermal growth factor (EGF)

XX family of receptor/tyrosine kinases. The antisense oligonucleotides are

XX useful for inhibiting the expression of Her-3 in cells or tissues. They

XX are commonly used as research reagents and in diagnostics for example, to

XX elucidate the function of particular genes. The antisense compounds are

XX also useful for distinguishing between functions of various members of a

XX biological pathway and for research use. They are also utilized for

XX diagnostics, therapeutics, prophylaxis and in kits. They are useful

XX for prophylactically, e.g. to prevent or delay infection, inflammation or

XX tumor formation. Sequences AAH47532-47615 represent chimeric antisense

XX phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap.

XX used for the inhibition of Her-3 mRNA expression

XX Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 15; DB 1; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1116 TGGTCTCAAACTCCT 1130

XX 1 TGGTCTCAAACTCCT 15

XX RESULT 2028

XX AAS13563

XX ID AAS13563 standard; DNA; 18 BP.

XX AAS13563;

XX 17-DEC-2001 (first entry)

XX PCR primer 1 used to amplify PAC 10406 (70 SP6) clone STS sequence.

XX Human; VMGLOW; glomulin; venous malformation glomangioma; PCR primer;

XX STS; sequence tagged site; PAC 10406; ss.

XX Homo sapiens.

XX WO200160856-A2.

XX 23-AUG-2001.
PD 16-FEB-2001; 2001WO-EP001760.
XX
PF 16-FEB-2000; 2000EP-00870022.
XX
PR 10-APR-2000; 2000US-0195777P.
XX
PR 22-DEC-2000; 2000EP-00870320.
XX
PA (UWLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Vikkula M;
XX
DR MPI; 2001-557643/52.
XX
PT New VMGLOM genes and polypeptides, useful in gene therapy or for
PT preventing, treating or alleviating disorders with vascular component,
PT e.g. varicosities, cardiopathies, cerebral disorders or cancer.
XX
PS Disclosure; Page 70; 157pp; English.
XX
CC The present invention relates to the isolation of novel human and mouse
CC VMGLOM polypeptides (long form and short form), and the nucleic acid
CC molecules encoding them. VMGLOMs (also referred to as gliomulins) are a
CC subtype of venous malformations (VMS) called gliomangiomas. In humans,
CC VMGLOM has been mapped to chromosome 1p21-22. VMGLOMs and the nucleic
CC acids encoding for them are useful as a medicament or for incorporation
CC into a diagnostic kit. Such medicaments are useful for preventing,
CC treating or alleviating disorders with a vascular component, particularly
CC where alteration of vascular smooth muscle cell phenotype is needed, e.g.
CC varicosities, cardiopathies or cardiomyopathies, cerebral disorders and
CC cancer. The nucleic acids are also useful in gene therapy. The present
CC sequence for PCR primer 1 is used to amplify PAC 10406 (70 SpE) clone SRS
CC sequence in the methods of the present invention
XX
SQ Sequence 18 BP; 5 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 880 TGAGCCACCAACGCC 894
Db 1 TGAGCCACCAACGCC 15
XX
RESULT 2029
ADE43701/c
ID ADE43701 standard; DNA; 18 BP.
XX
AC ADE43701;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human KNSL1 PCR primer, SEQ ID 306.
XX
KM Neurodegenerative disease; uPA; SNGG; IDE: KNSL1, LIPA; TNFRSF6;
KM Alzheimer's disease; neuroprotective; neurotrophic; gene therapy;
KM Chromosome 10; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003054143-A2.
XX
PD 03-JUL-2003.
XX
PF 25-OCT-2002; 2002WO-US034679.
XX
PR 25-OCT-2001; 2001US-0339525P.
XX
PR 08-NOV-2001; 2001US-0336929P.
XX
PR 08-NOV-2001; 2001US-0338010P.
XX
PR 09-NOV-2001; 2001US-0338363P.
XX
PR 04-DEC-2001; 2001US-0337052P.

PR 28-MAR-2002; 2002US-0368919P.
XX
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelabi G, Elliott KJ, Wang X, Tanzi RE, Bertram L,
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR MPI; 2003-559131/52.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT the presence or absence of an allelic variant of one or more polymorphic
PT regions.
XX
PS Example 3; Page 291; 848pp; English.
XX
CC The present invention relates to a method (M1) for determining a
CC predisposition for or the occurrence of neurodegenerative disease in a
CC subject. The method comprises detecting in a target nucleic acid obtained
CC from the subject the presence or absence of an allelic variant of one or
CC more polymorphic regions of one or more genes selected from uPA
CC (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulin-
CC degrading enzyme), KNSL1 (Kinein-1-like protein 1), LIPA (lysosomal acid
CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-Sf6), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the
CC occurrence of, and for treating neurodegenerative disease, particularly
CC Alzheimer's disease. The present sequence is a PCR primer, which was used
CC in the method of the invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 730 GTAGCTGGGACTACA 744
Db 15 GTAGCTGGGACTACA 1
XX
RESULT 2030
ABX11281
ID ABX11281 standard; DNA; 18 BP.
XX
AC ABX11281;
XX
DT 29-APR-2003 (first entry)
XX
DE Human Tango-63 mapping primer t63-r2.
XX
XX
KM Human; ss; PCR; inflammation; viral encephalitis; meningitis;
KM multiple sclerosis; stroke; Alzheimer's disease; polycythaemia vera;
KM hyperproliferative myeloid disease; chronic myelogenous leukaemia;
KM HIV infection; autoimmune disease; systemic lupus erythematosus;
KM Rheumatoid arthritis; type 1 diabetes; septic shock; graft rejection;
KM cerebral malaria; cachexia; cardiovascular disorder; angina pectoris;
KM myocardial infarction; hypertension; atherosclerosis; primer;
KM haematologic disease; aplastic anaemia; chronic neutropenia;
KM myelodysplastic syndrome; Tango-63; chromosome 8.
XX
OS Homo sapiens.
XX
PN US2002160446-A1.
XX
PD 31-OCT-2002.
XX
PR 16-MAR-2001; 2001US-00811088.
XX
PR 14-NOV-2000; 2000US-00712726.

XX (HOLT/) HOLTZMAN D A.
PA (GEAR/) GEARING D P.
PA (PAN/) PAN Y.
XX Holtzman DA, Gearing DP, Pan Y;
PI WPI; 2003-265759/26.
XX
XX New isolated nucleic acid molecule encoding thymotaxin (Tango-45), Tango-
PT 63d, Tango-67e, Tango-67, or huchordin polypeptide, useful for diagnosing
PT and treating disorders, e.g. cancer, inflammation, stroke or diabetes.
XX
XX Disclosure; Page 19; 79pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding
CC thymotaxin (also known as Tango-45), Tango-63d, Tango-637e, Tango-67, or
CC huchordin polypeptide, including sequences 90% identical to them,
CC fragments of at least 15 nucleotides and allelic variants. Also included
CC are a host cell or a non-mammalian host cell containing the novel nucleic
CC acid, the encoded polypeptides (or allelic variants, sequences 90%
CC identical or fragments), an antibody or antibody substance that
CC selectively binds with one of the proteins, and identifying a compound
CC that binds with the proteins and/or modulates the proteins' activity.
CC Thymotaxin is a member of the C-C family of chemokines, Tango-63e and -d
CC are members of the tumour necrosis factor superfamily, Tango-67 is a
CC growth factor family member. The thymotaxin gene is located on human
CC chromosome 16 and Tango-63 on chromosome 8. The nucleic acid molecules
CC and polypeptides are useful for diagnosing and treating disorders
CC associated with aberrant expression or activity, of the nucleic acid or
CC polypeptide, such as inflammation (e.g. viral encephalitis, viral or
CC bacterial meningitis, multiple sclerosis, stroke or Alzheimer's disease),
CC hyperproliferative myeloid disease (e.g. chronic myelogenous leukaemia or
CC polycythemia vera), HIV infection, autoimmune diseases (e.g. systemic
CC lupus erythematosus, rheumatoid arthritis, type 1 diabetes, septic shock,
CC graft rejection, cerebral malaria or cachexia), cardiovascular disorders
CC (e.g. angina pectoris, myocardial infarction, hypertension or
CC atherosclerosis), or haematologic diseases (e.g. aplastic anaemia,
CC chronic neutropenia or myelodysplastic syndromes). The polypeptides are
CC useful for generating antibodies, which are therapeutically useful. The
CC nucleic acid molecules are useful as primers or probes to detect
CC mutations or polymorphisms in the gene. The methods are useful for
CC identifying compounds that modulate the expression or activity of the
CC polypeptide. The present sequence is a PCR primer used to map the Tango-
CC 63 gene
XX
SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 GCTCAGGATTC 1012
DB 1 GCTCAGGATTC 15
RESULT 2031
ADE77489
ID ADE77489 standard; DNA; 18 BP.
XX
XX ADE77489;
AC
XX 29-JAN-2004 (first entry)
DT
XX
DE Tango-63 chromosome mapping primer #2.
XX
KW ss; human; thymotaxin; Tango-45; Tango 63d; Tango-63e; Tango-67;
KW huchordin; Tango-66; brain disorder; inflammation;
KW cerebrovascular disease; tumour; skeletal muscle disorder;
KW motor neuron disorder; myopathy; muscle metabolic disease;
KW proliferative disorder; heart disorder; ischaemic heart disease;
KW atherosclerosis; hypertension; angina pectoris;
KW

KW hypertrophic cardiomyopathy; congenital heart disease;
KW cardiovascular disorder; pancreatic disorder; diabetes mellitus;
KW testicular disorder; leukocytic disorder; leukopenia; leukocytosis;
KW malignant lymphoma; immune disorder; TNF-related disorder;
KW T cell disorder; chromosome mapping; primer.
XX
XX Homo sapiens.
OS
XX
XX US2003125540-A1.
PN
XX
XX 03-JUL-2003.
PD
XX
XX 06-DEC-2002; 2002US-00314410.
PF
XX
XX 16-APR-1997; 97US-00843651.
PR
XX 26-SEP-1997; 97US-00938365.
PR 16-JUL-1999; 99US-00354809.
PR 14-NOV-2000; 2000US-00712726.
PR 10-JAN-2001; 2001US-00757421.
PR 16-MAR-2001; 2001US-00811088.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Holtzman DA, Gearing DP, Pan Y;
PI WPI; 2004-009153/01.
XX
XX Nucleic acid encode a C-C family chemokine, thymotaxin, two polypeptides
PT similar to the TNF receptor superfamily, a soluble growth factor and
PT huchordin are useful to treat skeletal muscle, heart, cardiovascular and
PT other disorders.
XX
XX Disclosure; SEQ ID NO 21; 78pp; English.
XX
XX The invention relates to isolated nucleic acids encoding thymotaxin
CC (Tango-45), Tango 63d, Tango-63e, Tango-67 and huchordin (Tango-66).
CC Thymotaxin, Tango-63 and Tango-67 are useful to treat disorders of the
CC brain, inflammations, cerebrovascular diseases, tumours, skeletal muscle
CC disorders, motor neuron disorders, myopathies, metabolic diseases of the
CC muscle, diseases and disorders associated with the spleen, lung,
CC intestine, colon, liver, kidney, reproductive system, ovaries, placenta
CC and prostate, and proliferative disorders. Thymotaxin, Tango-63, Tango-67
CC and huchordin are useful to treat heart disorders such as ischaemic heart
CC disease, atherosclerosis, hypertension, angina pectoris, hypertrophic
CC cardiomyopathy and congenital heart disease, cardiovascular disorders,
CC pancreatic disorders including diabetes mellitus, and testicular
CC disorders. Thymotaxin and Tango-63 are useful to treat leukocytic
CC disorders such as leukopenia, leukocytosis and malignant lymphomas, and
CC immune disorders. Tango-63 is useful to treat TNF-related and T cell
CC disorders. The present sequence represents Tango-63 chromosome mapping
CC primer #2.
XX
SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 GCTCAGGATTC 1012
DB 1 GCTCAGGATTC 15
RESULT 2032
ADH54179/C
ID ADH54179 standard; DNA; 18 BP.
XX
XX ADH54179;
AC
XX 25-MAR-2004 (first entry)
DT
XX Human neurodegenerative disease-related PCR primer SeqID306.
DE
XX

human; neurodegenerative disease, urkinase plasminogen activator; uPA; gamma-synuclein; SNCG; insulin degrading enzyme; IDE; uPA; kinesin-like protein 1; KNSL1; lysosomal acid lipase; LIPA; tumour necrosis factor receptor SF6; TNFRSF6; Alzheimer's disease; PCR; primer; ss.

Homo sapiens.

US2003224380-A1.

04-DEC-2003.

25-OCT-2002; 2002US-00282174.

25-OCT-2001; 2001US-0339525P.

25-OCT-2001; 2001US-0348065P.

02-NOV-2001; 2001US-0336983P.

08-NOV-2001; 2001US-0336929P.

08-NOV-2001; 2001US-0338010P.

09-NOV-2001; 2001US-0338363P.

04-DEC-2001; 2001US-0337052P.

28-MAR-2002; 2002US-0368919P.

(GENO) GEN HOSPITAL CORP.

Becker KD, Valicelbi G, Elliott KJ, Wang X, Tanzi RE; Bertram L, Saunders AJ, Mullin KM, Sampson AJ;

WPI; 2004-060538/06.

Determining a predisposition for or the occurrence of neurodegenerative disease, particularly Alzheimer's disease, comprises determining the presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSP6 gene.

Example 3; SEQ ID NO 306; 205pp; English.

This invention relates to a novel method of determining a predisposition for or the occurrence of neurodegenerative disease comprising detecting in a target nucleic acid obtained from the subject the presence of an allelic variant of polymorphic regions of human genes selected from urkinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The method is useful in determining the presence or predisposition to a neurodegenerative disease, particularly Alzheimer's disease. The present sequence is that of a PCR primer which was used for amplification of a region of the human KNSL1 gene in the exemplification of the invention.

Sequence 18 BP; 3 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 18; Best Local Similarity 100.0%; Pred No. 1.8e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

730 GTAGCTGGGACTTACA 744
|||||
15 GTAGCTGGGACTTACA 1

RESULT 2033
ADO48722/c

ID ADO48722 standard; DNA; 18 BP.

ADO48722;

12-AUG-2004 (first entry)

Human neuropilin 1 (NRP1) extension PCR primer #24.

human; melanoma; single nucleotide polymorphism; SNP; neuropilin 1; NRP1; mannose receptor C type 2; MRC2; extension PCR; primer; ss; genotyping.

OS	Homo sapiens.
XX	
XX	WO200404163-A2.
XX	
PD	27-MAY-2004.
XX	
PF	06-NOV-2003; 2003WO-US035876.
XX	
XX	06-NOV-2002; 2002US-0424475P.
PR	23-JUL-2003; 2003US-0489703P.
PA	(SEQU-) SEQUENOM INC.
XX	
PI	Roth RB, Nelson MR, Braun A, Kammerer SM;
DR	WPI; 2004-411720/38.
XX	
PT	Identifying a subject at risk of melanoma, useful for treating melanoma,
PT	comprises detecting the presence or absence of one or more polymorphic
PT	variations associated with melanoma in a nucleic acid sample from a
PT	subject.
XX	
PS	Example 3; Page 78; 176pp; English.
XX	
CC	The invention comprises a method for identifying a subject at risk of
CC	melanoma. The invention involves detecting the presence or absence of one
CC	or more polymorphic variations associated with melanoma in the neupoplin
CC	1 (NRP1) or mannos receptor C type 2 (MRC2) genes. The method of the
CC	invention is useful for identifying subjects at risk and treating
CC	melanoma. The present DNA sequence represents an extension PCR primer
CC	that was used to detect single nucleotide polymorphisms within human
CC	NRP1.
XX	
SQ	Sequence 18 BP; 1 A; 3 C; 9 G; 4 T; 0 U; 1 Other;
XX	
Query Match	1.5%; Score 15; DB 1; Length 18;
Best Local Similarity	100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	884 CCACCACGCCCGGCT 898
DB	16 CCACCACGCCCGGCT 2
RESULT 2034	
AA173067	
ID	AA173067 standard; DNA; 51 BP.
XX	
AC	AA173067;
XX	
DT	09-NOV-2001 (first entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:8.
XX	
KW	Human, single nucleotide polymorphism; SNP; genome; gene therapy;
KW	protein therapy; vaccine; probe; diagnostic assay; detection;
KW	quantitation; restorative therapy; polymorphic; de.
XX	
OS	Homo sapiens.
XX	
FN	WO200140521-A2.
XX	
PD	07-JUN-2001.
XX	
PF	30-NOV-2000; 2000WO-US032758.
XX	
XX	30-NOV-1999; 99US-0168138P.
PR	29-NOV-2000; 2000US-00726173.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
XX	

CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SO Sequence 51 BP; 10 A; 15 C; 15 G; 11 T; 0 U; 0 Other;

Query Match: 1.5%; Score 15; DB 1; Length 51;
Best Local Similarity 61.5%; Pred. No. 2e+03;
Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 388 CAAGTGTGAGTATACAGCCGCGCTGCTGCGC 426
DB 47 CAGTGAGCTGAGTACAGCCACTGCTCAGCTG3GC 9

RESULT 2037
AA174502
ID AA174502 standard; DNA; 51 BP.
AC AA174502;
XX
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1443.
XX
KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000MO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimketa RA, Leach M;
PI
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 495; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples

SO Sequence 51 BP; 13 A; 16 C; 12 G; 10 T; 0 U; 0 Other;

Query Match: 1.5%; Score 15; DB 1; Length 51;
Best Local Similarity 67.7%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 260 AAGTGTGATATACAGACTGCGCCACCATGCC 290
DB 3 AGGAGTTGAGACCAAGCTTGCCACCATGCC 33

RESULT 2038
AA179093
ID AA179093 standard; DNA; 51 BP.
AC AA179093;
XX
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6034.
XX
KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KM protein therapy; vaccine; probe; diagnostic assay; detection;
KM quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000MO-US032758.
XX
PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimketa RA, Leach M;
PI
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 2356; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 12 A; 15 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 1.5%; Score 15; DB 1; Length 51;
Best Local Similarity 61.5%; Pred. No. 2e+03;
Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 388 CAAGTGTGGATTACAGGCGTGCAGCGTGCCTGACC 426
DB 13 CAGTGTGACCGAGATCACACATTGACTCCAGCCTGAGAC 51

RESULT 2039

AAQ22632/C
ID AAQ22632 standard; DNA; 18 BP.

XX AAQ22632;

AC 08-JUL-1992 (first entry)

XX Antisense oligonucleotide #4 targeted to ICAM-1 3'-UTR (2849-2866).

XX Intercellular adhesion molecule-1; inhibitor; phosphorothioate bond;
KM triple helix; ss.

XX Synthetic.

XX WO9203139-A.

PN 05-MAR-1992.

PD 23-JUL-1991; 91MO-US005209.

XX 14-AUG-1990; 90US-00567286.

PR (ISIS-) ISIS PHARM INC.

XX Bennett CF, Mirabelli CK, Mira;

PI WPI; 1992-096579/12.

XX New oligonucleotides hybridisable to cell adhesion modulators - for
PT treatment and diagnosis of e.g. allograft rejection, cancer, AIDS etc.

PT and diagnosis of intercellular adhesion dysfunction.

XX Example 5; Page 39; 75pp; English.

CC This antisense oligonucleotide was designed to hybridise to the 3'-UTR of
CC human ICAM-1 mRNA. The same sequence was synthesised in phosphodiester
CC and phosphorothioate forms. The oligonucleotides were tested for
CC inhibition of ICAM-1 expression on the surface of interleukin-1-beta-
CC stimulated cells in two different cell lines. The phosphodiester
CC oligonucleotide did not inhibit ICAM-1 expression, but the
CC phosphorothioate (P=S) form did. See AAQ22629-Q22631 and AAQ22633

XX Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 533 TCCTCCCTCCCTCAGCCTC 550
DB 18 TCCTCCCTCCCTCAGCCTC 1

RESULT 2040
AAQ20160/C
ID AAQ20160 standard; DNA; 18 BP.
XX
AC AAQ20160;

XX 01-APR-1992 (first entry)
DT Cross-linking oligomer 723 to target Herpes Simplex Virus 1.
XX deoxyribonucleic acid; major groove; HSV; inverted polarity region;
DE covalent cross-linking group; ss.
XX Synthetic.
KM
XX
OS
XX
FH Key
FT modified_base
FT 1 Location/Qualifiers
FT /*tag= a
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 2
FT /*tag= b
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 3
FT /*tag= c
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 4
FT /*tag= d
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 5
FT /*tag= e
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 7
FT /*tag= f
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 9
FT /*tag= g
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 10
FT /*tag= h
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 11
FT /*tag= i
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 12. 18
FT /*tag= j
FT /label= inverted_polarity_region
FT /note= "see comments"
FT 13
FT /*tag= k
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 14
FT /*tag= l
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 15
FT /*tag= m
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 17
FT /*tag= n
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT
XX WO9118997-A.
XX
XX 12-DEC-1991.
XX
XX 25-MAY-1990; 90US-00529346.

```
XX 25-MAY-1990; 90US-00529346.
PR 14-JAN-1991; 91US-00640654.
XX (GILE-) GILEAD SCIE INC.
XX
XX Matteucci MD, Krawczyk S;
PI WPI; 1992-007480/01.
XX
XX New sequence-specific non-photo-activated crosslinking agents - bind to
PT the major groove of duplex DNA and are esp. useful for treating latent
PT infections e.g. HIV.
XX
XX Example 4; Page 29; 42pp; English.
XX
XX This oligomer contains an inverted polarity region formed from an o-
CC xyloto dimer synthon. Residues 11 and 12 are linked via an o-xyloto group
CC (i.e. nucleotides that have xyloto sugar linked via the o-xylene ring).
CC The sequence is designed to target the Herpes Simplex virus 1 beginning
CC at nucleotide 10996 and to covalently cross-link to it. See also AAQ20151
CC -Q20161
XX
XX Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 594 ATTTTATTTTATTTT 611
DB 18 ATTTTATTTTATTTT 1
XX
XX RESULT 2041
XX AAQ34110/C
XX ID AAQ34110 standard; DNA; 18 BP.
XX
XX AAQ34110;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Sequence of a microsatellite from clone T61A60B.
DE
XX PCR: selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; se.
XX
XX Bos taurus.
OS
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
PD
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 375; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
```

```
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
DB 18 TTTTATTTTATTTT 1
XX
XX RESULT 2042
XX AAQ30310/C
XX ID AAQ30310 standard; DNA; 18 BP.
XX
XX AAQ30310;
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
XX Oligomer HSV723 for forming triplex with HSV target duplex.
DE
XX Herpes simplex virus 1; AIDS; modified; HIV; RSV; HPV; malignancy;
XX hepatitis; inflammation; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX modified_base 1 /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 2 /tag= b
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 3 /tag= c
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 4 /tag= d
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 5 /tag= e
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 7 /tag= f
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 9 /tag= g
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX modified_base 10 /tag= h
XX /mod_base= OTHER
XX /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
```

FT	misc_feature	11..12	
FT		/*tag=	0
FT		/note=	"O-xylosio dimer synthon linkage"
FT	modified_base	11	
FT		/*tag=	1
FT		/mod_base=	OTHER
FT		/note=	"OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	misc_feature	12..18	
FT		/*tag=	n
FT		/label=	inverted_polarity_region
FT		/note=	"see comments"
FT	modified_base	13	
FT		/*tag=	j
FT		/mod_base=	OTHER
FT		/note=	"OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	modified_base	14	
FT		/*tag=	k
FT		/mod_base=	OTHER
FT		/note=	"OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	modified_base	15	
FT		/*tag=	1
FT		/mod_base=	OTHER
FT		/note=	"OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT	modified_base	17	
FT		/*tag=	m
FT		/mod_base=	OTHER
FT		/note=	"OTHER= N6 methyl-8-oxo 2' deoxyadenine"
PN	MO9209705-A1.		
PD	11-JUN-1992.		
PD			
PF	25-NOV-1991;	91WO-US008811.	
PR			
PR	23-NOV-1990;	90US-00617907.	
PR	18-JAN-1991;	91US-00643382.	
PR	08-APR-1991;	91US-00683420.	
PR	17-APR-1991;	91US-00686544.	
PR	17-APR-1991;	91US-00686546.	
PR	17-APR-1991;	91US-00686547.	
PR	27-SEP-1991;	91US-00766733.	
PA	(GILE-) GILEAD SCI INC.		
PI	Frøehler B, Krawczyk S, Matteucci MD, Milligan J;		
PI			
XX	WPI, 1992-217083/26.		
XX			
XX	New oligomers contg. modified bases - which form a triplex with G-C		
XX	doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,		
XX	herpes malignancy and inflammation.		
PS	Claim 12; Page 67; 77pp; English.		
XX			
XX	The synthetic oligomer is capable of forming a triplex at physiological		
CC	pH with a purine rich target sequence by coupling into the major groove		
CC	of the duplex. The specific target sequence of this oligomer is a herpes		
CC	simplex virus I duplex beginning at nucleotide 10996 contg. a purine-rich		
CC	region concentrated on one chain of the duplex. The oligomer, and others		
CC	like it are useful in diagnosis and therapy of diseases characterised by		
CC	specific DNA duplex targets, e.g. respiratory syncytial virus, HIV,		
CC	hepatitis, herpes, malignant tumours and inflammation. The triple helices		
CC	form under mild conditions thus assays may be carried out without		
CC	subjecting the test specimen to harsh conditions. The oligomer contains		
CC	an inverted polarity region formed from an o-xylosio dimer synthon. The		
CC	linking gp. is o-xylosio (nucleosides have the 3' positions of xylosio		
CC	sugars linked via the o-xylosio ring). Two nucleosides are coupled through		
CC	cc a xylene residue to form the dimer synthon. This additional modifications		
CC	may render the oligomer stable to nuclease activity. The oligomer is able		
CC	to inhibit gene expression, as verified by in vitro systems. See also		
CC	AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN		
CC	field.)		
XX			

```

SQ Sequence 18 BP; 13 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 594 ATTTTATTTTATTTATTTT 611
   |||||||
DB 18 ATATTATTTATTTATTTT 1

RESULT 2043
AA062001/c
ID AA062001 standard; DNA; 18 BP.
XX
XX AA062001;
AC
XX
XX 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
DE Guanine quartet containing oligomer, #12.
XX
XX Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
XX human cytomegalovirus; influenza virus; inflammation; telomere length;
XX neurological disorders; phospholipase A2 activity; hyperproliferation;
XX malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
XX
XX Synthetic.
OS
XX
XX Key location/Qualifiers
FH misc_feature 1..18
FT /*tag= a
FT /note= "Phosphorothionate intersugar linkages"
XX
XX PN MO9408053-A1.
XX
XX PD 14-APR-1994.
XX
XX PF 29-SEP-1993; 93WO-US0009297.
XX
XX PR 29-SEP-1992; 92US-00954185.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Hanecek RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL,
XX PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL,
XX
XX WPI; 1994-135613/16.
XX
XX PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
XX PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
XX PT of chromosomes.
XX
XX PS Disclosure; Page 108; 144pp; English.
XX
XX The sequences given in AA061990-2001 are oligonucleotides which contain
XX G4 or G3 stretches and which may be used for inhibiting replication of
XX herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
XX influenza virus, or for treating inflammatory and neurological disorders
XX caused by phospholipase A2 activity in cases of hyper- proliferation,
XX malignancy, cardiovascular disease and snake bite. Oligonucleotides such
XX as these, may be used for inhibiting division of malignant cells by
XX CC modulating telomere length, which may also retard aging. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 533 TCCTCCTGCTCAGCCTC 550
   |||||

```

DE	PCR primer.
XX	Synthetic oligo; solid phase immunoassay; ss.
KM	Synthetic.
OS	Synthetic.
PN	MO9426932-A1.
XX	
PD	24-NOV-1994.
XX	
PF	13-MAY-1994; 94WO-US005407.
XX	
PR	13-MAY-1993; 93US-00061694.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	Fields HA, Khudyakov YE;
XX	
DR	WPI, 1995-006819/01.
XX	
PT	Solid phase immunoassay using oligo:nucleotide as label - also new
PT	conjugates of oligo:nucleotide coupled to antigenic peptide; partic. for
PT	diagnosing hepatitis C or E virus infection.
XX	
PS	Example; Page 12; 34pp; English.
XX	
CC	AA62941 and AA62942 are examples of synthetic immunoreactive peptides.
CC	They are used in a method for detecting an antigen in a subject. The
CC	method involves binding the antigen to a solid support and then reacting
CC	it with an immunoreactive ligand (L) bound to an oligo; removing any
CC	unreacted L, and then detecting the presence of the oligo. A similar
CC	method can be used to detect Abs, in which case the ligand is an oligo-
CC	labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC	to be detected at very low levels. An exemplary oligo is AA075024 which
CC	can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC	a synthetic peptide. In the example, peptide AA62941 was coupled to
CC	oligo AA075024 using dilaucinimidyl suberate. Serum samples suspected to
CC	contain HBV Abs were immobilised on plastic tubes or wells, then
CC	incubated for 30-60 mins with the peptide-oligo product. The vessels were
CC	washed; bound oligo was released with 0.2M glycine and amplified in a
CC	separate tube using as primer AA075025 and AA075026 in 30 cycles of PCR.
CC	The amplification product - AA076031 - was treated with uracil DNA
CC	glycosylase to remove the U18 fragment, and the product captured by
CC	immobilised oligo-dT. (Updated on 25-MAR-2003 to correct FN field.)
XX	
SQ	Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;
XX	
Query Match	1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity	0.0%; Pred.No.1.8e+03;
Matches	0; Conservative 16; Mismatches 2; Indels 0; Gaps 0;
XX	
Oy	428 TTTTATTTTATTTTATTTT 445
Db	1 UUUUUUUUUUUUUUUUU 18
XX	
RESULT 2046	
AA071742/c	
ID	AA071742 standard; DNA; 18 BP.
XX	
AA071742;	
XX	
DT	18-DEC-1995 (first entry)
XX	
DE	Peptide Nucleic acid oligomer targeting ICAM-1 3'-UTR.
XX	
KM	peptide nucleic acid; PNA; intercellular adhesion molecule; ICAM-1;
KW	endothelial leukocyte; ELAM-1; vascular; VCAM-1; anti-inflammatory;
KW	anticancer; antineoplastic; anti-AIDS; anti-rhinoviral; ss.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers

```
FT misc_feature 1..18
FT /*tag= a
FT /note= "at least one (and preferably all) of the backbone
FT subunits are composed of amide units, so that the
FT oligomer consists of the nucleobases attached covalently
FT to a polyamide backbone"
XX
XX WO9504749-A1.
XX
XX 16-FEB-1995.
XX
XX 05-AUG-1994; 94WO-US009026.
XX
XX 05-AUG-1993; 93US-00102650.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Mirabelli CK;
XX
XX WPI; 1995-090842/12.
XX
XX New peptide nucleic acid oligomers hybridising to adhesion molecule genes
XX - are stable anti:sense cpds. of high affinity, partic. for treating
XX inflammation, viral infection, cancer etc.
XX
XX Claim 2; Page 35; 57pp; English.
XX
XX New oligomers are claimed which (A) have at least one peptide nucleic
XX acid (PNA) subunit and (B) have a sequence hybridisable to AUG region,
XX coding region, 5'-untranslated region or 3'-untranslated region of ICM-1
XX or ELAM-1, or hybridisable to AUG region, coding region, 5'- untranslated
XX region, exon/intron junction region or 3'-untranslated region of VCAM-1.
XX The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
XX produce antisense-type gene regulation moieties. Hence they may be used
XX therapeutically for modulating cellular adhesion and thus as
XX antimetastatic agents, anticancer agents, antihinoviral agents, anti-
XX AIDS agents and antiinflammatory agents. They may also be useful as
XX diagnostics, e.g. as probes for specific mRNAs. PNA oligomers have high
XX affinity for complementary single stranded DNA. They are also able to
XX form triple helices in which a first PNA strand binds with RNA or ssDNA
XX and a second PNA strand binds with the resulting double helix or with the
XX first PNA strand. The PNAs possess no significant charge and are water
XX soluble, which facilitates cellular uptake. Further, since they contain
XX amides of non-biological amino acids, they are biostable and resistant to
XX enzymatic degradation by proteases. The present sequence targets human
XX intercellular adhesion molecule-1 (ICAM-1) 3' untranslated region
XX
XX Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 533 TCCTCTGCTCTCAGCCTC 550
XX ||||| ||||| |||||
XX 18 TCCTCCACCTCAGCCTC 1
XX
XX RESULT 2047
XX AAQ95465/c
XX ID AAQ95465 standard; DNA; 18 BP.
XX
XX AAQ95465;
XX
XX 14-FEB-1996 (first entry)
XX
XX Primer A1 (Group 4, set A) for a human chromosomal marker.
XX
XX primer: polymerase chain reaction; PCR; linkage study; locus;
XX microsatellite marker sequence; automated genotyping; allele;
XX polymorphism; detection; Homo sapiens; ss.
XX
XX Synthetic.
OS
```

```
XX
XX PN WO9515400-A1.
XX
XX 08-JUN-1995.
XX
XX 05-DEC-1994; 94WO-US013945.
XX
XX 03-DEC-1993; 93US-00160837.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Levitt RC;
XX
XX WPI; 1995-215278/28.
XX
XX Kit for automated genotyping contg. pairs of PCR primers - designed to
XX amplify polymorphic nucleotide repeat sequences, arranged in sets each
XX with a characteristic fluorescence label, useful e.g. in detection of
XX disease related genetic rearrangement.
XX
XX Disclosure; Fig 7D-2; 104pp; English.
XX
XX The method aims to provide a collection of highly reproducible
XX microsatellite marker sequences (MMS) at approx. 10-50 cm intervals
XX throughout the human genome which can be detectably labelled. The MMS are
XX polymorphic, simple sequence repeats and can be used in automated
XX genotyping, esp. fluorescence-based. The primers correspond to the unique
XX DNA sequence surrounding each marker, and PCR is used to detect each
XX polymorphism. When the MMS show considerable polymorphism (ie. a
XX difference in the number of repeats) between individuals, the markers can
XX be particularly informative. The MMS can be ideal for linkage studies.
XX Kits comprise at least 4 groups, of at least 3 sets, each comprising
XX labelled primers for PCR amplification of the DNA. Group 4 primer pairs
XX are shown in AAQ95465-480 and AAQ95559-590. The chromosomal markers,
XX published size range of the allele and degree of heterozygosity in the
XX population for the markers covered by these primer pairs are not given in
XX the specification
XX
XX Sequence 18 BP; 6 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 702 AAGTATCTCTGCCCC 719
XX ||||| ||||| |||||
XX 18 AAGTGATTCCTGCTCCTC 1
XX
XX RESULT 2048
XX AAT30216/c
XX ID AAT30216 standard; DNA; 18 BP.
XX
XX AAT30216;
XX
XX 20-JAN-1997 (first entry)
XX
XX Antisense oligonucleotide ISIS 1564/1573.
XX
XX Antisense oligonucleotide; human; intracellular adhesion molecule-1;
XX ICM-1; endothelial leukocyte adhesion molecule-1; ELAM-1; B-selectin;
XX vascular cell adhesion molecule-1; VCAM-1; white blood cell; dextran;
XX vascular endothelium; allograft rejection; immunosuppression; rapamycin;
XX anti-lymphocyte serum; monoclonal antibody; cardiac allograft; therapy;
XX renal allograft rejection; donor-specific transplant tolerance; LFA-1;
XX ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..18
XX /*tag= a
XX /note= "phosphorothioate or phosphodiester backbone"
FT
```

```

XX PN WO9615780-A1.
XX PD 30-MAY-1996.
XX PF 22-NOV-1995; 95WO-US015536.
XX PR 23-NOV-1994; 94US-00344155.
XX PA (ISIS-) ISIS PHARM INC.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Bennett CF, Stepkowski SM;
XX DR WPI; 1996-268321/27.
XX PT Oligo:nucleotide targetted to a nucleic acid sequence encoding ICAM-1,
XX PT ELAM-1 or VCAM-1 - useful for treating or preventing allo:graft
XX PT rejection.
XX PS Example 5; Page 45; 92pp; English.
XX CC AAT3021-T30233, AAT3058-T33112 and AAT3667-T36684 represent antisense
XX CC oligonucleotides of the invention. These sequences target regions of the
XX CC coding sequences for human intercellular adhesion molecule-1 (ICAM-1),
XX CC endothelial leukocyte adhesion molecule-1 (ELAM-1, also known as E-
XX CC selectin), or vascular cell adhesion molecule-1 (VCAM-1). This sequence
XX CC targets the 3' untranslated region (nucleotides 2849-2866) of ICAM-1.
XX CC ICAM-1, ELAM-1, and VCAM-1 represent three of the five cell adhesion
XX CC molecules involved in the adherence of white blood cells to vascular
XX CC endothelium. These sequences can be used in a composition for treating
XX CC allograft rejection. The composition contains one of these sequences in
XX CC combination with an immunosuppressive agent. The immunosuppressive agent
XX CC used in the composition is brenigan, rapamycin, anti-lymphocyte serum,
XX CC a monoclonal antibody against LFA-1 or an antisense oligonucleotide. The
XX CC compositions can be used for treating or preventing allograft rejection,
XX CC such as cardiac or renal allograft rejection. By using these
XX CC compositions, allograft survival times are extended, and donor-specific
XX CC transplant tolerance is induced
XX SO Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 533 TCCTCCTGCTCAGCCTC 550
XX DB 18 TCCTCCACCTCAGCCTC 1
XX
XX RESULT 2049
XX AAT94667
XX ID AAT94667 standard; DNA; 18 BP.
XX AC AAT94667;
XX XX
XX DT 27-MAR-1998 (first entry)
XX DE Anchored poly(T) oligonucleotide polyT-Ancha.
XX KM Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
XX KM snapdragon; primer; ss.
XX OS Synthetic.
XX XX
XX PN WO9732023-A1.
XX PD 04-SEP-1997.
XX PF 28-FEB-1997; 97WO-AU000124.
XX PR 01-MAR-1996; 96AU-00008386.

```

```

XX PA (FLOR-) FLORIGENE LTD.
XX PI Brugliera F, Holton TA, Michael MZ;
XX DR WPI; 1997-448691/41.
XX PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
XX PT corresponding DNA, used in the manipulation of pigmentation in plants.
XX PS Example 15; Page 59; 234pp; English.
XX CC Anchored poly(T) oligonucleotides polyT-ancha (AAT94667), polyT-anchC
XX CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
XX CC region of a polyadenylation sequence. They were used to prime cDNA
XX CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
XX CC were also utilised in the PCR amplification of plant cytochrome P450
XX CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
XX CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
XX CC display approach. This can be used to manipulate the pigmentation of
XX CC transgenic plants
XX SO Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 429 TTATTTTATTTTATTTT 446
XX DB 1 TTTTATTTTATTTTATTTT 18
XX
XX RESULT 2050
XX AAV07750/C
XX ID AAV07750 standard; DNA; 18 BP.
XX AC AAV07750;
XX XX
XX DT 02-DEC-1998 (first entry)
XX DE Phosphorothioate oligodeoxynucleotide.
XX KM phosphorothioate; electrospray ionisation-Fourier transform;
XX KM mass spectrometry; off-resonance excitation; ss.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT misc_difference 1..18
XX FT /tag= a
XX FT /note= "phosphorothioate internucleotide linkages"
XX PN WO9840520-A1.
XX PD 17-SEP-1998.
XX PF 12-MAR-1998; 98WO-US004919.
XX PR 14-MAR-1997; 97US-0040717P.
XX PA (HYBR-) HYBRIDON INC.
XX PI Wang BH;
XX XX
XX DR WPI; 1998-520830/44.
XX PT Determining the nucleotide sequence of a nucleic acid analyte - using
XX PT electro-spray ionisation.
XX PS Example 1; Fig 3A; 25pp; English.
XX CC The invention relates to an analytical method for determining the

```


CC nucleotide sequence of nucleic acid analyses, including chemically
CC modified oligonucleotides. This new method utilizes electrospray
CC ionization-Fourier transform mass spectrometry. The ions are excited by
CC sustained off-resonance excitation with single shot excitation, and the
CC target fragmented by collisionally activated dissociation by a neutral
CC gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
CC can be nozzle skimmer dissociation. The method is used in molecular
CC biology and biomedical applications. The method, utilizing electrospray
CC ionization-Fourier transform ion cyclotron resonance mass spectrometry,
CC is extremely rapid and acts directly on the oligonucleotide. The method
CC is effective for a variety of nucleic acid analyses, particularly
CC chemically modified oligonucleotides which have not previously been
CC successfully sequenced. The present sequence represents a
CC phosphorothioate oligodeoxynucleotide
SQ Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX
QY Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 594 ATTTTATTTTATTTT 611
18 ATTTTATTTTATTTT 1
RESULT 2051
AAV21970
ID AAV21970 standard; DNA; 18 BP.
AC
XX AAV21970;
XX
XX 14-JUL-1998 (first entry)
XX
DE Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
XX Nuclease resistant; bacterial infection; antibiotic; target;
XX
XX veterinary medicine; treatment; human; industrial process;
XX
XX bacterial control; ss.
XX
XX Synthetic.
XX
XX WO980533-A1.
XX
XX 29-JAN-1998.
XX
XX 23-JUL-1997; 97WO-US012961.
XX
XX 24-JUL-1996; 96US-00685575.
XX
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
XX Arrow A, Dale RMK, Thompson TL;
XX
XX WPI; 1998-120687/11.
XX
XX
XX Treating bacterial infections in humans or animals with
XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial
XX nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
XX with antibiotics.
XX
XX Claim 49; Page 87; 163pp; English.
XX
XX This antisense oligonucleotide is nuclease resistant and can be used in
XX the treatment of animals, including humans, having a bacterial infection.
XX The treatment comprises administration of such nuclease resistant
XX oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
XX and formulated with a carrier. A compound comprising this nuclease
XX resistant oligonucleotide can be covalently linked to an antibiotic. The
XX method is used to treat infections by a wide variety of Gram-positive and
XX Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
XX The methods are particularly used in immuno-compromised individuals (e.g.
XX patients with acquired immunodeficiency syndrome or those receiving

CC chemotherapy or radiation therapy), optionally in combination with, or
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC therapeutic use, the oligonucleotides can be used to control bacteria in
CC laboratory cultures, foods, beverages and industrial processes. The
CC oligonucleotides are specific for bacteria, without affecting metabolism
CC in mammalian cells. They may also activate RNase H and have a general,
CC non-specific immune-stimulating effect. The oligonucleotides can be
CC administered orally, intranasally, rectally, topically or by injection,
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC enhances cellular uptake
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX
QY Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 428 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 18
RESULT 2052
AAV19943
ID AAV19943 standard; DNA; 18 BP.
AC
XX AAV19943;
XX
XX 14-JUN-1999 (first entry)
XX
XX Primer SEQ ID NO:3 from JP11075880.
XX
XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
XX Synthetic.
XX
XX JP11075880-A.
XX
XX 23-MAR-1999.
XX
XX 10-JUL-1998; 98JP-00195719.
XX
XX 14-JUL-1997; 97JP-00205378.
XX
XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
XX WPI; 1999-257710/22.
XX
XX
XX Labelling of an oligonucleotide - useful for detecting genes.
XX
XX Example 1; Page 7; 10pp; Japanese.
XX
XX A method has been developed for labelling an oligonucleotide having a
XX repeated sequence of (X)n (where X and Y consists of a combination of
XX adenine and thymine or uracil or guanine and cytosine, and n is an
XX integer of 1 or more) at the 3'-terminal side in which the repeated
XX sequence is added and extended using a labelled body of the nucleotide
XX constituting the repeated sequence and a DNA polymerase lacking in 5' to
XX 3' exonuclease activity. The method can be used for detecting a gene. The
XX method can detect a gene in a sensitivity up to ten times higher than
XX prior art methods. The present sequence represents a primer used in an
XX example from the present invention
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX
QY Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 428 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 18

XX	PR	18-JUL-1997;	97JP-00208312.
XX	PA	(TAKI) TAKARA SHUZO CO LTD.	
DR	WIPI,	1999-183822/16.	
PT	Peptides	having at least two new nucleotides - useful as primers in RT-	
PT	PCR.		
XX	PS	Disclosure; Page 11; 19pp; Japanese.	
CC	This	sequence represents a primer of the invention. The invention relates	
CC	to	sequences of at least two nucleotides of formula: (X)m ^{5'} -(alpha)n-beta	
CC	-N3';	or (X)m ^{5'} -(gamma)k-delta-N3'; where X = a labelled compound and/or	
CC	a	nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =	
CC	natural	number indicating the repetition of alpha; beta, delta = V or N;	
CC	V =	adenine, guanine or cytosine; N = adenine, guanine, cytosine or	
CC	thymine;	gamma = thymine; k = natural number of 3 or over, indicating the	
CC	repetition	of gamma, in which thymine expressed by gamma is composed of	
CC	1/3	or less of adenine, guanine and/or cytosine. The new nucleotides are	
CC	useful	as primers for RT-PCR and determination of base sequences. The new	
CC	sequences	allow for reproductive and highly efficient analysis of gene	
CC	sequences		
SQ	Sequence	18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other:	
OY	Query Match	1.5%; Score 14.8; DB 1; Length 18;	
OY	Best Local Similarity	88.9%; Pred. No. 1.8e+03;	
OY	Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
DB	430	TATATTATTTTAAAAA 447	
DB	1	TTTTTTTTTTTTTTAA 18	
RESULT 2055			
ID	AA227846/C		
AC	AA227846 standard; DNA, 18 BP.		
DT	AA227846;		
XX	23-DEC-1999	(first entry)	
XX	PCR	primer for human DNA marker clone S110.	
XX	Tandem	repeat sequence; DNA isolation; intermediate tandem repeat;	
KW	ITR	sequence; pentanucleotide tandem repeat; stutter artifact;	
KW	DNA	typing; DNA profiling; linkage analysis; criminal justice;	
KW	paternity	testing; animal lineage analysis; microsatellite loci;	
KW	polymorphism	detection; PCR primer; ss.	
XX	Synthetic.		
OS	Homo sapiens.		
XX	WO940194-A1.		
XX	12-AUG-1999.		
XX	PF	04-FEB-1999; 99MO-USO02345.	
XX	PR	04-FEB-1998; 98US-00018584.	
XX	(PROM-)	PROMEGA CORP.	
XX	Schumm JW,	Bacher JW;	
XX	WIPI;	1999-590696/50.	
DR	Isolating	DNA containing intermediate tandem repeat sequences, useful in	
PT	DNA	profiling.	
XX	Claim 30;	Page 22; 11pp; English.	

PT Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
PS Example 1; Page 29; 91pp; English.

XX The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AA287160-287164 represent
CC oligonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 0.0%; Pred. No. 1.8e+03;
Matches 0; Conservative 16; Mismatches 2; Indels 0; Gaps 0;

OY 428 TTTTATTTTATTTT 445
::: :::: :::::

Db 1 UUUUUUUUUUUUUUU 18

RESULT 2058

AA287166 standard; DNA; 18 BP.

XX AA287166;

XX 08-MAY-2000. (first entry)

XX Deoxyarabinonucleotide SEQ ID NO:7.

XX 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;

XX transcription; expression; reverse transcription; viral replication;

XX RNase H cleavage; triple helix formation; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..18

XX /tag= a

XX /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-

XX fluoro-beta-D-arabinose"

XX WO967378-A1.

XX 29-DEC-1999.

XX 17-JUN-1999; 99WO-CA000571.

XX 19-JUN-1998; 98CA-02241361.

XX (UWMC-) UNIV MCGILL.

XX Damha M, Parniak M, Noronha A, Wilds C, Borkow G, Arion D;

DR WPI; 2000-160584/14.

XX Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
PS Example 2; Page 31; 91pp; English.

XX The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AA287165-287169 represent
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
CC arabinose used in an exemplification of the present invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 428 TTTTATTTTATTTT 445
||||| ||||| |||||

Db 1 TTTTATTTTATTTT 18

RESULT 2059

AA287167/C

XX AA287167 standard; DNA; 18 BP.

XX AA287167;

XX 08-MAY-2000. (first entry)

XX Deoxyarabinonucleotide SEQ ID NO:8.

XX 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;

XX transcription; expression; reverse transcription; viral replication;

XX RNase H cleavage; triple helix formation; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..18

XX /tag= a

XX /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-

XX fluoro-beta-D-arabinose"

XX WO967378-A1.

XX 29-DEC-1999.

XX 17-JUN-1999; 99WO-CA000571.

XX 19-JUN-1998; 98CA-02241361.

XX (UWMC-) UNIV MCGILL.

PR 09-APR-1999; 99US-0128521P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Smith MM, Shin HD, O'Brien SJ;
XX WPI; 2000-687051/67.
XX
XX
XX Predicting susceptibility to HIV infection or progression useful for
PT selection of therapeutic treatment for persons infected with HIV virus,
PT comprises detecting polymorphism in human interleukin-10 promoter.
XX
XX
XX Example 1; Page 11; 40pp; English.
XX
XX The present invention describes a method for predicting susceptibility to
CC HIV infection or HIV progression in a subject. The method involves
CC detecting a polymorphism in a human interleukin-10 (IL-10) promoter,
CC where the presence of the polymorphism indicates susceptibility to HIV
CC infection or HIV progression. The method provides prognostic information
CC to persons infected with HIV virus and is useful to help select
CC treatments (such as administration of IL-10 or gene therapy with IL-10).
CC The presence of polymorphism is useful as predictor that very aggressive
CC treatment could substantially eradicate the virus from the infected
CC person. The method is useful for the generation of nomograms or other
CC predictive algorithms that can be used, in association with allele
CC status, to prognose probable survival or years to development of AIDS
CC following HIV seroconversion. It indicates that increased expression of
CC the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression
CC and enables a variety of new therapeutic interventions in the treatment
CC of HIV disease. The present sequence represents a short tandem repeat
CC (STR) primer which is used in an example from the present invention
XX
XX
SQ Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 737 GGACTACAGGCGCCACC 754
DB 18 GGATTATAGCGCCACC 1
XX
XX
RESULT 2062
AAD03565
ID AAD03565 standard; DNA; 18 BP.
XX
XX AAD03565;
AC
XX
XX
DT 19-JUN-2001 (first entry)
XX
XX
DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
XX Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
XX antiarthritic; antiatherosclerotic; antidiabetic; nephropathic;
XX antiasthmatic; immunosuppressive; antiatherosclerotic;
XX antidiabetic; osteoprotective; cerebroprotective; vasculoprotective;
XX antineoplastic; neuroprotective; congestive heart failure; myocarditis;
XX hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
XX kidney disease; acute renal failure; renal glucosuria; renal infection;
XX polycystic kidney disease; hereditary nephritis; inflammatory disease;
XX tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
XX stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
XX ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
XX Ratus norvegicus.
XX
XX
XX WO200123564-A1.
XX
XX
XX 05-APR-2001.
XX
XX
XX 27-SEP-2000; 2000WO-US026544.
XX
XX

PR 27-SEP-1999; 99US-0156280P.
XX
XX (SCIO-) SCIOS INC.
XX
XX
XX Stanton LW, Kapoun AM;
XX WPI; 2001-266159/27.
XX
XX
XX Novel secreted factor encoded by clone P00188D12 which is differentially
PT expressed in certain disease states, useful in diagnosing and treating
PT cardiac, renal or inflammatory diseases.
XX
XX
XX Example 1; Page 42; 71pp; English.
XX
XX
XX The patent discloses novel secreted factor protein encoded by clone
CC P00188 D12. The secreted factor is differentially expressed in certain
CC disease states. Secreted protein, its antibodies, antagonists or
CC compositions comprising them are useful in the diagnosis and treatment of
CC cardiac diseases such as congestive heart failure, myocardial infarction,
CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
CC failure, renal glucosuria, renal infarction, nephrogenic diabetes
CC insipidus, polycystic kidney disease, hereditary nephritis and
CC inflammatory diseases such as asthma, autoimmune diabetes, tumour
CC angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
CC protein DNA is useful in antisense-mediated gene inhibition and in gene
CC therapy. An array comprising one or more oligonucleotides complementary
CC to reference RNA or DNA encoding the secreted factor is useful for
CC detecting cardiac, kidney and inflammatory disease. The present DNA
CC sequence is an oligonucleotide which is used in the preparation of a
CC normalised cDNA library containing secreted factor DNAs. The normalised
CC cDNA libraries are used in the identification of differentially expressed
CC rat secreted factor P00188_D12 gene
XX
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 428 TTTTATTATTATTTTTTT 445
DB 1 TTTTATTTTTTTTTTTTTT 18
XX
XX
RESULT 2063
AAD17014/C
ID AAD17014 standard; DNA; 18 BP.
XX
XX
XX AAD17014;
AC
XX
XX
DT 29-NOV-2001 (first entry)
XX
XX
DE Oligonucleotide A18-2PEG linker.
XX
XX Scaffold protein; antibody mimic; fibronectin type III domain;
XX randomised loop; randomised beta-sheet; diagnostic purpose;
XX protein designing; ss.
XX
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
FH msc_feature 18
FT /tag= a
FT /note= "Linked to (PEG)2CCPurromycin"
XX
XX
XX WO200164942-A1.
XX
XX
XX 07-SEP-2001.
XX
XX
XX 28-FEB-2001; 2001WO-US006414.
XX
XX

XX 29-FEB-2000; 2000US-00515260.
XX (PHYL-) PHYLUS INC.
XX
XX Lajovsky D, Wagner RW, Kuimelis RG;
XX WPI; 2001-55782/62.
XX
XX Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX
XX Disclosure; Page 25; 67pp; English.
XX
XX The present invention relates to an array of proteins (antibody mimics)
CC comprising a fibronectin type III domain having a randomized loop, a
CC randomized beta-sheet, or their combination, and has the capacity to bind
CC to a compound that is not bound by a corresponding naturally-occurring
CC fibronectin, immobilised onto a solid support. The antibody mimics is
CC useful for detecting a compound preferably a protein, in a biological
CC sample. It is also useful to detect one or more different analytes
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC is also useful for the purpose of designing proteins capable of binding
CC to virtually any compound of interest. The present sequence is an
CC oligonucleotide A18-2PEG linker used in an exemplification of the
CC invention
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
DB 18 TTTTATTTTATTTT 1
RESULT 2064
AAF9708
ID AAF9708 standard; DNA; 18 BP.
XX
XX AAF9708;
XX
XX 12-JUN-2001 (first entry)
XX
XX Immunostimulatory nucleic acid #824.
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
XX 27-SEP-1999; 99US-0156135P.
XX 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX

PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 56; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 18
RESULT 2065
AAF9734
ID AAF9734 standard; DNA; 18 BP.
XX
XX AAF9734;
XX
XX 12-JUN-2001 (first entry)
XX
XX Immunostimulatory nucleic acid #850.
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO200122972-A2.
XX
XX 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
XX 27-SEP-1999; 99US-0156135P.
XX 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 56; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an

CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone

CC Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

428 TTTTATTTTATTTT 445

1 TTTTATTTTATTTT 18

RESULT 2066

AAF82472

ID AAF82472 standard; DNA; 18 BP.

AAF82472;

29-UTN-2001 (first entry)

Phagemid vector PCR2.1 polylinker oligonucleotide #6.

Phagemid vector; PCR2.1; rat; secreted factor; P00210D09; cardiant;

nephrotropic; antiinflammatory; gene therapy; cardiac disease;

renal disease; inflammatory disease; polylinker; ss.

Synthetic.

MO200123419-A2.

05-APR-2001.

27-SBP-2000; 2000MO-US026582.

27-SBP-1999; 99US-0156277P.

(SCIO-) SCTOS INC.

Stanton LM, Kapoun AM;

WPI; 2001-328177/34.

Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
 treating and/or preventing various cardiac, renal and inflammatory
 diseases.

Example 1; Page 41; 69pp; English.

The present sequence corresponds to polylinker DNA of the phagemid vector
 PCR2.1. It was used in the construction of a normalised rat cDNA library,
 which was used in an example demonstrating differential expression of a
 rat gene referred to as clone P00210D09. The invention relates to a
 polypeptide comprising a sequence of at least 80% identity to residues 22
 -122 of the present sequence, or a sequence encoded by a nucleic acid
 hybridising under stringent conditions to the complement of the coding
 region comprising 1031 nucleotides, and having at least one biological
 activity of the polypeptide encoded by clone P00210D09. The polypeptides
 and polynucleotides of the invention are useful for the treatment of
 cardiac, renal and inflammatory diseases. The polynucleotides are useful
 in antisense mediated gene inhibition and in gene therapy. The
 polypeptides are useful in assays for identifying lead compounds that may
 be used as therapeutic agents in the treatment of cardiac, kidney or

CC inflammatory diseases

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

428 TTTTATTTTATTTT 445

1 TTTTATTTTATTTT 18

RESULT 2067

AAF16625

ID AAF16625 standard; DNA; 18 BP.

AAF16625;

13-MAR-2001 (first entry)

Gastric acid production inhibiting oligonucleotide SEQ ID NO: 112.

Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;

Stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;

DNA-RNA hybrid; ss.

Homo sapiens.

WO200071164-A1.

30-NOV-2000.

24-MAY-2000; 2000MO-AU000498.

24-MAY-1999; 99AU-00000510.

(TACH/) TACHAS G.

Tachas G;

WPI; 2001-025093/03.

Treating gastric acid disturbance by administering an oligonucleotide
 which modulates the activity of a polypeptide involved in gastric acid
 production or secretion.

Example 3; Page 151; 164pp; English.

The present invention provides oligonucleotides, and methods for their
 use, which are useful in modulating the action of proteins involved in
 gastric acid production. The target protein is preferably the histamine
 H2 receptor or one of the proteins which form part of the gastric proton
 pump. The sequences and methods of the invention are useful in the
 treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
 duodenal ulcers and other gastric acid disturbances, most of which are
 caused by Helicobacter pylori

Sequence 18 BP; 5 A; 1 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

777 TTTTATTTTATTTT 794

1 TTTTATTTTATTTT 18

RESULT 2068

AAH40502

ID AAH40502 standard; DNA; 18 BP.

AAH40502

AC AAH40502;
XX
XX 14-AUG-2001 (first entry)
DT
XX
DE SNP specific lower PCR primer SEQ ID 3298.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000MO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 66; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
XX Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 685 CTCTGCTCCCGGTTCA 702
DB 1 CTCGCTCCCGAGTTCA 18

RESULT 2069
AAH38362
ID AAH38362 standard; DNA; 18 BP.

XX
XX AAH38362;
AC
XX 14-AUG-2001 (first entry)
DT
XX
DE SNP specific lower PCR primer SEQ ID 1158.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000MO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 55; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 836 TGATCTGCTCCGCTCGGC 853
DB 1 TGATCTGCTCCGCTCGGC 18

RESULT 2070
AAH40562/c

ID AAH40562 standard; DNA; 18 BP.
 XX
 AC AAH40562;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific lower PCR primer SEQ ID 3358.
 XX
 KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 67; 83pp; English.
 XX
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 394 GCTGGATTACAGCGCTG 411
 Db 18 GCTGGATGACAGCGATG 1
 RESULT 2071

AAH38461
 ID AAH38461 standard; DNA; 18 BP.
 XX
 AC AAH38461;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific upper PCR primer SEQ ID 1257.
 XX
 KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KM Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 56; 83pp; English.
 XX
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX
 SQ Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 249 TCGGCTCCCAAGTCT 266
 Db 1 TCGGCTTCACAGTCT 18

```
RESULT 2072
ABA91529
ID ABA91529 standard; DNA; 18 BP.
XX
XX
AC ABA91529;
XX
XX 23-APR-2002 (first entry)
XX
XX DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
XX
XX DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
XX Synthetic.
XX
XX Key location/Qualifiers
XX FH 8..9
XX FT misc_RNA /*tag= a
XX FT /label= RNA
XX
XX WO200206531-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 12-JUL-2001; 2001WO-US022166.
XX
XX PR 14-JUL-2000; 2000US-00616761.
XX PR 30-MAR-2001; 2001US-00823647.
XX
XX PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
XX PI Dattagupta N;
XX
XX DR WPI; 2002-171819/22.
XX
XX PT Probe for detecting target nucleotide sequence in sample, has sequence
XX PT that forms hairpin structure having a double-stranded segment and single-
XX PT stranded loop collectively forming region complementary to target
XX PT sequence.
XX
XX PS Example 4; Page 49; 72pp; English.
XX
XX CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
XX CC AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
XX CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
XX CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
XX CC the set had a different number of ribonucleotides, 2 in the present case.
XX CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
XX CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
XX CC minutes. The results showed that 4 ribonucleotides were the minimum
XX CC number for RNA cleavage. The invention provides probes for nucleic acid
XX CC hybridisation. The probes form a hairpin structure comprising a double-
XX CC stranded stem and a single-stranded loop, and are capable of both
XX CC intramolecular and intermolecular hybridisation. The double-stranded stem
XX CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
XX CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
XX CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
XX CC can be removed. Arrays and methods for nucleic acid hybridisation using
XX CC the probes are provided
XX
XX SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 899 TATTTTAAATTTTGTTC 916
XX | | | | | | | | | | | | | | | |
XX 1 TTTTAAATTTTGTTC 18
XX
XX RESULT 2073
XX AAD38323/c
XX ID AAD38323 standard; DNA; 18 BP.
```

```
XX
XX AC AAD38323;
XX
XX XX 10-SEP-2002 (first entry)
XX
XX XX Human MONO-15 locus amplifying PCR primer #2.
XX
XX DE Human; microsatellite loci; tumour; familial tumour predisposition;
XX XX microsatellite instability; MSI; cancer; gastrointestinal system;
XX KW endometrium; MONO-15 locus; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2002058265-A1.
XX
XX PD 16-MAY-2002.
XX
XX PF 24-APR-2001; 2001US-00841366.
XX
XX PR 15-SEP-2000; 2000US-00663020.
XX
XX PA (PROM-) PROMEGA CORP.
XX
XX PI Bacher JW, Flanagan L, Nasrif N;
XX
XX DR WPI; 2002-443805/47.
XX
XX XX Analyzing microsatellite loci for detecting microsatellite instability
XX PT that can be used for prognostic tumor diagnosis, comprises coamplifying a
XX PT mononucleotide repeat locus and two tetranucleotide repeat loci.
XX
XX PS Example 4; Page 17; 48pp; English.
XX
XX CC The present invention relates to a method for analysing microsatellite
XX CC loci. The method involves coamplifying a set of 3 microsatellite loci,
XX CC comprising a specific mononucleotide repeat locus selected from the group
XX CC consisting of BAT-25, BAT-26, BAT-40, MONO-11 and MONO-15 and two
XX CC tetranucleotide repeat loci selected from FGA, D1S18, D17S129 etc from
XX CC a sample of genomic DNA and determining the size of the amplified
XX CC fragments. The method is useful for analysing microsatellite loci and for
XX CC detecting microsatellite instability (MSI) in genomic DNA. The
XX CC instability in the set of microsatellite loci are used in prognostic
XX CC tumour diagnosis for the diagnosis of familial tumour predisposition. It
XX CC is also used to detect cancerous tumours in the gastrointestinal system
XX CC and of the endometrium. The cancerous tumours are preferably from a
XX CC colorectal cancer. The present DNA sequence is a PCR primer which is used
XX CC for amplifying human MONO-15 locus. This primer is used in the
XX CC exemplification of the invention
XX
XX SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 674 CTCACCTCAAGCTCTGCC 691
XX | | | | | | | | | | | | | | | |
XX 18 CTCACCTCAAGCTCTGCC 1
XX
XX RESULT 2074
XX ABA86369
XX ID ABA86369 standard; DNA; 18 BP.
XX
XX AC ABA86369;
XX
XX XX 07-OCT-2002 (first entry)
XX
XX DE Secretory leukoprotease inhibitor (SLPI) PCR primer #1.
XX
XX KW Human; secretory leukoprotease inhibitor; SLPI; cystatin A; CSTA; SCCE;
XX KW stratum corneum chymotryptic enzyme; stratum corneum tryptic enzyme; PCR;
XX KW adhesion protein; protease; protease inhibitor; eczema; primer; SCTE;
```


KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 XX scleroderma; hypertrophic scar.
 OS Synthetic.
 XX MO200253141-A2.
 PN 11-JUL-2002.
 PD 14-DEC-2001; 2001MO-US048458.
 PF 14-DEC-2000; 2000US-0255534P.
 XX 14-DEC-2000; 2000US-0255534P.
 XX (COLE-) COLEY PHARM GROUP INC.
 PA Bratzler RL;
 XX WPI; 2002-566690/60.
 DR Inhibiting angiogenesis in a subject, involves administering at least one
 XX antiangiogenic nucleic acid molecule to the subject.
 PT Claim 2; Page 36; 276pp; English.
 PS The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. NO. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTT 445
 DB 1 TTTTATTTTATTTT 18
 RESULT 2077
 ABS78429 standard; DNA; 18 BP.
 ID ABS78429;
 XX ABS78429;
 AC 13-DEC-2002 (first entry)
 DT Angiogenesis inhibitory oligonucleotide #913.
 XX
 DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubecosis; Osler-Weber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX Synthetic.
 OS
 XX
 XX MO200253141-A2.

PD 11-JUL-2002.
 XX 14-DEC-2001; 2001MO-US048458.
 XX 14-DEC-2000; 2000US-0255534P.
 XX (COLE-) COLEY PHARM GROUP INC.
 PA Bratzler RL;
 XX WPI; 2002-566690/60.
 DR Inhibiting angiogenesis in a subject, involves administering at least one
 XX antiangiogenic nucleic acid molecule to the subject.
 PT Claim 2; Page 35; 276pp; English.
 PS The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. NO. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTT 445
 DB 1 TTTTATTTTATTTT 18
 RESULT 2078
 ABL39401 standard; DNA; 18 BP.
 ID ABL39401;
 XX ABL39401;
 AC 16-APR-2002 (first entry)
 DT Immunostimulatory nucleic acid SEQ ID NO: 837.
 XX
 DE Anticancerous agent; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubecosis; Osler-Weber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX Synthetic.
 OS
 XX
 XX MO200197843-A2.
 PD 27-DEC-2001.
 XX 22-JUN-2001; 2001MO-US020154.
 XX 22-JUN-2000; 2000US-0213346P.
 XX (IOWA) UNIV IOWA RES FOUND.

XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 308; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 428 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 18
XX
RESULT 2079
AAD41497
ID AAD41497 standard; DNA; 18 BP.
XX
AC AAD41497;
XX
DT 30-OCT-2002 (first entry)
XX
DE Oligonucleotide used for amplifying sea hare cyplasin L DNA.
XX
OS Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
XX therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
XX Alzheimer's disease; Parkinson's disease; arteriosclerosis;
XX heart disease; stroke; vascular disease; neurotropic; neuroprotective;
XX cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
XX
OS Unidentified.
XX
PN WO200231144-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-EP011837.
XX
PR 13-OCT-2000; 2000EP-00122466.
XX
PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
XX
PI Butzke D, Machuy N, Rudel T, Meyer TF;
XX
DR WPI; 2002-537205/57.
XX
PT Novel polypeptide having cytotoxic activity obtainable from Aplysia,
PT useful for destroying tumors, for identifying novel targets for the
PT development of anti-tumor agents, and as specific ion channel modulators.

XX
PS Example 5; Page 37; 87pp; English.
XX
CC The present invention relates to novel polypeptides having cytotoxic
CC activity obtainable from sea hare Aplysia. Sequences of the invention are
CC useful for the manufacture of cytotoxic agents against apoptosis-
CC resistant cells, where the agents are useful for diagnosis, prevention,
CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
CC protein, factors for generating or detoxifying reactive oxygen species
CC (ROS) and factors for blocking and/or by-passing of caspases. They are
CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
CC for destroying tumours and/or selectively killing cells in tissues, for
CC identifying novel targets for the development of pharmaceutical agents,
CC preferably anti-tumour agents and as specific ion channel modulators,
CC e.g., blockers or openers for therapy, diagnostic or research. They are
CC useful for the diagnosis and therapy of hyperproliferative diseases.
CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.
CC They are also useful for development of drugs for the treatment of
CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
CC present sequence is an oligonucleotide which is used for amplifying sea
CC hare cyplasin L DNA. This sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 428 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 18
XX
RESULT 2080
ABL42967
ID ABL42967 standard; DNA; 18 BP.
XX
AC ABL42967;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:11.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 5; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant

CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention

SO Sequence 18 BP; 3 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 538 CTGCTCAGCTCCAG 555
Db 1 CTGCTCAGCTCCAG 18

RESULT 2081
ABL44445
ID ABL44445 standard; DNA; 18 BP.
XX ABL44445;
DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1489.
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KM PCR primer; ss.
XX Homo sapiens.
OS JP2001321190-A.
PN 20-NOV-2001.
PD 12-MAR-2001; 2001JP-00068285.
PF 10-MAR-2000; 2000JP-00066716.
PR (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
DR Arraying genome clones.
PT Claim 4; Page 34; 528bp; Japanese.
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination Nos. mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals

CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention

SO Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 667 ATCTTGCTCAGCTCAGC 684
Db 1 ATCTTGCTCAGCTCAGC 18

RESULT 2082
ABS53437
ID ABS53437 standard; DNA; 18 BP.
XX ABS53437;
DT 29-NOV-2002 (first entry)
DE Poly d(T) primer.
XX Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
KM poly d(T).
XX Synthetic.
OS WO200265093-A2.
PN 22-AUG-2002.
PD 14-FEB-2002; 2002WO-US005713.
PF 14-FEB-2001; 2001US-0268645P.
PR 14-FEB-2001; 2001US-0268645P.
PR 18-JUL-2001; 2001US-0306216P.
PR 07-NOV-2001; 2001US-0344557P.
PR 07-NOV-2001; 2001US-0348242P.
PR 09-NOV-2001; 2001US-0350176P.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA (REME-) RES FOUND MENTAL HYGIENE INC.
XX Ginsberg SD, Che S;
XX WPI; 2002-567050/60.
DR Increasing efficiency of second strand cDNA synthesis using terminal
PT continuation model before performing further RNA amplification by RNA
PT transcription.
XX Example 7; Page 80; 128bp; English.
XX This invention relates to a novel method for increasing the efficiency of
CC second strand cDNA synthesis through a mechanism of terminal
CC continuation. In the method an RNA molecule is obtained and a first
CC primer is added that comprises a region that hybridises to a
CC complementary region of the molecule before a second primer is added
CC comprising at least one riboguanine at the 3' end of the primer. A first
CC complementary nucleic acid molecule is synthesised, the RNA molecule and
CC second primer are removed and a second complementary nucleic acid
CC molecule is synthesised to form a second hybrid with an extension product
CC of the third primer bound to the first complementary molecule. The method
CC of the invention is useful for increasing the efficiency of second strand
CC cDNA synthesis and may be used for linear amplification of genetic
CC signals from histologically stained tissue. The present sequence

CC represents a poly d(T) PCR primer used in the method of the invention
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTATTTT 445
 |||||
 1 TTTTATTTT 18

RESULT 2083
 AAD36362/c
 ID AAD36362 standard; DNA; 18 BP.

AC AAD36362;

DT 09-AUG-2002 (first entry)

DE Human MONO-15 loci amplifying primer #2.

KW Human; microsatellite locus; microsatellite instability; MSI; tumour;
 cancer; primer; ss.

OS Homo sapiens.

PN MO20022879-A2.

PD 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028647.

PR 15-SEP-2000; 2000US-00663020.

PA (PROM-) PROMEGA CORP.

PI Bacher JW, Flanagan L, Naself N;

DR WPI, 2002-393975/42.

PT Analyzing micro-satellite loci for detecting or diagnosing cancer, by co-
 amplifying set of three microsatellite loci from DNA sample in multiplex
 reaction using primers, and determining size of amplified fragments.

PS Claim 6; Page 60; 73pp; English.

CC The present invention relates to a method of analysing microsatellite
 CC loci. The method involves co-amplifying a set of three microsatellite
 CC loci comprising at least one mononucleotide repeat locus and at least two
 CC tetra-nucleotide repeat loci from a sample of genomic DNA in a multiplex
 CC amplification reaction using primers and determining the size of the
 CC amplified DNA fragments obtained. The method is useful for analysing
 CC microsatellite loci and for detecting microsatellite instability (MSI) in
 CC genomic DNA microsatellite loci of the second genomic DNA, where the MSI
 CC results are useful in prognostic tumour diagnosis, in diagnosis of
 CC familial tumour predisposition, to detect cancerous tumours of the
 CC gastrointestinal system and of the endometrium, where the cancerous
 CC tumours are tumours from a colorectal cancer. The method is useful for
 CC detecting or diagnosing diseases associated with MSI such as certain
 CC types of cancer and predisposition for cancer and in diagnostic assays to
 CC be used to determine treatment and prognosis of disease. The present DNA
 CC sequence is a primer which is used for amplifying human MONO-15 locus.
 CC This primer is used in the method of the invention

SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 674 CTCACGTGCAACTCTGCC 691

DB 18 CTCACGTGCAACTCTGCC 1
 |||||

RESULT 2084

ABA93239
 ID ABA93239 standard; DNA; 18 BP.

AC ABA93239;

DT 18-APR-2002 (first entry)

DE Adaptor oligonucleotide SEQ ID NO:2.

KW Detection; comparative detection; adaptor; ss.

OS Synthetic.

PN JP200133800-A.

PD 04-DEC-2001.

PF 30-MAY-2000; 2000JP-00160324.

PR 30-MAY-2000; 2000JP-00160324.

PA (UNIT-) UNITECH CO LTD.

DR WPI, 2002-135950/18.

PT Comparative detection of the amounts of RNA and DNA.

PS Disclosure; Page 9; 9pp; Japanese.

CC The present invention describes a method for the comparative detection of
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
 CC transcribing respectively from at least two tissue RNAs are respectively
 CC fragmented by using a same restriction enzyme; (b) each different adaptor
 CC and a common adaptor are added to each of the cDNA fragments derived from
 CC the same or different tissues by the step (a); (c) the resultant adaptor-
 CC added cDNAs are mixed together; (d) an adaptor primer having the common
 CC sequence to said different adaptor and a gene-specific adaptor are used
 CC to amplify said adaptor-added cDNAs containing no region derived from
 CC polyadenylic acid of the mRNA before the addition of the adaptor among
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected
 CC from the measured result; (g) each different adaptor and a common adaptor
 CC are added to each of the genomic DNA fragments derived from a same or
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
 CC an adaptor primer having the common sequence to the different adaptor and
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
 CC of the genomic DNAs are measured between the individuals. The method is
 CC used for the detection of the amounts of RNA and DNA. The present
 CC sequence represents an oligonucleotide which is used in the
 CC exemplification of the present invention

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTATTTT 445
 |||||
 1 TTTTATTTT 18

RESULT 2085
 AB210473/c
 ID AB210473 standard; DNA; 18 BP.

AC AB210473;


```
XX 16-JAN-2003 (first entry)
DT
XX Haematopoietic cell proliferation disorder related oligonucleotide #613.
XX
DE
XX Human; haematopoietic cell proliferation disorder; cytostatic;
XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002MO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E, Pelet C;
PI Lewin A, Lipscher E, Mater S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 45; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used; for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SO Sequence 18 BP; 4 A; 1 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1055 ACCACACCCCGCTAATTT 1072
DB 18 ACCACACCCCGCTAATTT 1
RESULT 2086
ABZ10474/C
ID ABZ10474 standard; DNA; 18 BP.
XX
```

```
AC ABZ10474;
XX
XX 16-JAN-2003 (first entry)
DT
XX Haematopoietic cell proliferation disorder related oligonucleotide #614.
XX
DE
XX Human; haematopoietic cell proliferation disorder; cytostatic;
XX gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002MO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E, Pelet C;
PI Lewin A, Lipscher E, Mater S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 45; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used; for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SO Sequence 18 BP; 4 A; 0 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1055 ACCACACCCCGCTAATTT 1072
DB 18 ACCACACCCCGCTAATTT 1
RESULT 2087
ABV76822/C
ID ABV76822 standard; DNA; 18 BP.
XX
```

```
XX AC ABV76822;
XX
XX DT 12-FEB-2003 (first entry)
XX DE PCR primer used to amplify a human cDNA sequence.
XX
XX KM Rheumatoid arthritis; onset risk; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200279466-A1.
XX
XX PD 10-OCT-2002.
XX
XX PF 29-MAR-2002; 2002WO-0P001191.
XX
XX PR 30-MAR-2001; 2001JP-00102006.
XX
XX PA (SHIO/) SHIOZAWA S.
XX
XX PI Shiozawa S, Komai K, Yagi H, Matsura N;
XX
XX DR WPI; 2003-046814/04.
XX
XX PT Genomic DNAs participating in rheumatoid arthritis, applicable in
XX diagnosis as well as judging onset risks of and screening drugs for the
XX disease based on gene mutation.
XX
XX PS Example 1; Page 7; 25pp; Japanese.
XX
XX CC The specification describes a genomic DNA sequence which participates in
XX CC rheumatoid arthritis. The DNA is applicable in diagnosis as well as
XX CC judging onset risks of, and screening drugs for treating or preventing,
XX CC rheumatoid arthritis. The present PCR primer was used in the course of
XX CC the invention
XX
XX SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 870 ATTACAGCGCTGAGCCAC 887
Db 18 ATTACAGCGCATGCGCCAC 1

RESULT 2088
AAD56466/c
ID AAD56466 standard; RNA; 18 BP.
XX
XX AC AAD56466;
XX
XX DT 07-AUG-2003 (first entry)
XX
XX DE Target RNA #1 used in the exemplification of the invention.
XX
XX KM Acyclic linker; gene expression; gene therapy; ss.
XX
XX OS Unidentified.
XX
XX PN WO2003037909-A1.
XX
XX PD 08-MAY-2003.
XX
XX PF 29-OCT-2002; 2002WO-CA001628.
XX
XX PR 29-OCT-2001; 2001US-0330719P.
XX
XX PA (UYMC-) UNIV MCGILL.
XX
XX PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
```

```
XX DR WPI; 2003-421516/39.
XX
XX PT Novel acyclic linker-containing oligonucleotide useful for preventing or
XX PT decreasing translation, reverse transcription and/or replication of a
XX PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX PS Example 2; Fig 5; 104pp; English.
XX
XX CC The invention relates to an acyclic linker-containing oligonucleotide
XX CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX CC the invention are useful for preventing or decreasing translation,
XX CC reverse transcription and/or replication of a target RNA in a system.
XX CC They are useful for selectively preventing gene expression in a sequence-
XX CC specific manner, for hybridising to complementary RNA such as cellular
XX CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
XX CC RNA. They are also useful therapeutically in formulations or medicaments
XX CC to prevent or treat a disease characterised by the expression of a
XX CC particular target RNA. The invention is used in gene therapy. The present
XX CC sequence is a target RNA, used in the exemplification of the invention
XX
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 445
Db 18 TTTTATTTTATTTT 1

RESULT 2089
AAD56440
ID AAD56440 standard; DNA; 18 BP.
XX
XX AC AAD56440;
XX
XX DT 07-AUG-2003 (first entry)
XX
XX DE Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX KM antisense; ss.
XX
XX OS Unidentified.
XX
XX PN WO2003037909-A1.
XX
XX PD 08-MAY-2003.
XX
XX PF 29-OCT-2002; 2002WO-CA001628.
XX
XX PR 29-OCT-2001; 2001US-0330719P.
XX
XX PA (UYMC-) UNIV MCGILL.
XX
XX PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
XX DR WPI; 2003-421516/39.
XX
XX PT Novel acyclic linker-containing oligonucleotide useful for preventing or
XX PT decreasing translation, reverse transcription and/or replication of a
XX PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX PS Example 2; Fig 9; 104pp; English.
XX
XX CC The invention relates to an acyclic linker-containing oligonucleotide
XX CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
XX CC the invention are useful for preventing or decreasing translation,
XX CC reverse transcription and/or replication of a target RNA in a system.
XX CC They are useful for selectively preventing gene expression in a sequence-
XX CC specific manner, for hybridising to complementary RNA such as cellular
```

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 18
DB
RESULT 2090
AADS6446
ID AADS6446 standard; DNA; 18 BP.
AC AADS6446;
XX
XX 07-AUG-2003 (first entry)
XX
DE 2'-F-RNA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KM antisense; ss.
XX
XX Unidentified.
OS
FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluororabinothymidine"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX PA
XX
XX PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention

XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 18
DB
RESULT 2091
ACH03247
ID ACH03247 standard; DNA; 18 BP.
AC ACH03247;
XX
XX 25-SEP-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #882.
DE
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
XX antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
OS
XX
XX US2003050268-A1.
XX
XX 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
XX (KRIE/) KRIEG A M.
XX PA (BERG/) BERG D J.
XX
XX Krieg AM, Berg DJ;
XX
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 33; 229pp; English.
XX
XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 445
1 TTTTATTTTATTTT 18
DB
RESULT 2092
AADS7871
ID AADS7871 standard; DNA; 18 BP.

```
XX AAD57871;
AC 20-NOV-2003 (first entry)
XX
DE Antisense oligo #1 used in the exemplification of the invention.
XX
XX Antisense oligo #1 used in the exemplification of the invention.
XX
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX hepatitis B; gene therapy; vincristine; anti-HIV; antisense; ss.
XX
XX Unidentified.
XX
XX WO2003064441-A2.
XX
XX 07-AUG-2003.
XX
XX 31-JAN-2003; 2003WO-CA000129.
XX
XX 01-FEB-2002; 2002US-0352873P.
XX
XX (UYNMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA;
XX
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related
XX to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX Example 2; Page 35; 73pp; English.
XX
XX The present invention relates to a new oligonucleoside which comprises
XX alternating first and second segments. The first segment comprises at
XX least one sugar modified nucleoside. The second segment comprises at
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX each of the first and second segments, so that it comprises at least 4
XX alternating segments. The oligonucleoside is useful for preparing a
XX composition for inducing RNase H-mediated cleavage of a target RNA in a
XX system, preventing or decreasing translation, transcription or
XX replication of a target RNA in a system, detecting the presence of a
XX target RNA in a system, validating a gene target corresponding to a
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX or hepatitis B. The invention is useful in gene therapy. The present
XX sequence is an antisense oligonucleotide used in the exemplification of
XX the invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 8.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 428 TTTTATTTTATTTT 445
XX ||||| ||||| |||||
XX 1 TTTTATTTTATTTT 18
XX
XX
XX RESULT 2093
XX AAD57878
XX ID AAD57878 standard; DNA; 18 BP.
XX
XX AAD57878;
XX
XX 20-NOV-2003 (first entry)
XX
XX Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX hepatitis B; gene therapy; vincristine; anti-HIV; antisense; DNA-RNA hybrid;
XX ss.
XX
XX Unidentified.
```

```
XX Key Location/Qualifiers
XX PH 1..3
XX FT /*tag= a
XX FT /label= RNA
XX FT /note= "2'-O-methyl-D-uridine"
XX
XX FT misc_RNA
XX FT 7..9
XX FT /*tag= b
XX FT /label= RNA
XX FT /note= "2'-O-methyl-D-uridine"
XX
XX FT misc_RNA
XX FT 13..15
XX FT /*tag= c
XX FT /label= RNA
XX FT /note= "2'-O-methyl-D-uridine"
XX
XX
XX WO2003064441-A2.
XX
XX 07-AUG-2003.
XX
XX 31-JAN-2003; 2003WO-CA000129.
XX
XX 01-FEB-2002; 2002US-0352873P.
XX
XX (UYNMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA;
XX
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related
XX to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX Example 2; Page 35; 73pp; English.
XX
XX The present invention relates to a new oligonucleoside which comprises
XX alternating first and second segments. The first segment comprises at
XX least one sugar modified nucleoside. The second segment comprises at
XX least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX each of the first and second segments, so that it comprises at least 4
XX alternating segments. The oligonucleoside is useful for preparing a
XX composition for inducing RNase H-mediated cleavage of a target RNA in a
XX system, preventing or decreasing translation, transcription or
XX replication of a target RNA in a system, detecting the presence of a
XX target RNA in a system, validating a gene target corresponding to a
XX target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX or hepatitis B. The invention is useful in gene therapy. The present
XX sequence is an antisense oligonucleotide used in the exemplification of
XX the invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
XX
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 38.9%; Pred. No. 1.8e+03;
XX Matches 7; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 428 TTTTATTTTATTTT 445
XX ::||| ::||| ::|||
XX 1 UUUUUUUUUUUUUU 18
XX
XX
XX RESULT 2094
XX AAD57879
XX ID AAD57879 standard; DNA; 18 BP.
XX
XX AAD57879;
XX
XX 20-NOV-2003 (first entry)
XX
XX Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX hepatitis B; gene therapy; vincristine; anti-HIV; antisense; DNA-RNA hybrid;
XX ss.
XX
XX Unidentified.
```

KM	ss.
XX	Unidentified.
OS	
XX	
FH	Key
FT	misc_RNA
FT	Location/Qualifiers 1..6 /*tag= a /label= RNA
FT	/note= "2'-O-methyl-D-uridine"
FT	13..18 /*tag= b /label= RNA /note= "2'-O-methyl-D-uridine"
FN	
XX	MO200306441-A2.
FD	
XX	07-AUG-2003.
PB	
XX	31-JAN-2003; 2003WO-CA000129.
PR	
XX	01-FEB-2002; 2002US-0352873P.
PA	(UYMC-) UNIV MCGILL.
PI	Damha MJ, Parniak MA;
DR	WPI; 2003-689523/65.
PT	New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.
PS	Example 2; Page 35; 73pp; English.
CC	The present invention relates to a new oligonucleoside which comprises alternating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of each of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleotide is useful for preparing a composition for inducing RNase H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or replication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS) or hepatitis B. The invention is useful in gene therapy. The present sequence is an antisense DNA-RNA hybrid used in the exemplification of the invention
SQ	Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;
OY	Query Match 1.5%; Score 14.8; DB 1; Length 18; Best Local Similarity 27.8%; Pred No. 1.8e+03; Matches 5; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
DB	428 TTTTATTTATTTTTTT 445 ::: ::: 1 UUUUUUTTTTTTUUUU 18
RESULT 2095	
AAD57877	
ID	AAD57877 standard; DNA; 18 BP.
XX	
AC	AAD57877;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
KM	Sugar-modified nucleosides; acquired immune deficiency syndrome; AIDS;
KW	hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW	ss.

XX	OS:	unidentified.
XX		
PH	Key	Location/Qualifiers
FT	misc_RNA	1
FT		/tag= a
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	3
FT		/tag= b
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	5
FT		/tag= c
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	7
FT		/tag= d
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	9
FT		/tag= e
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	11
FT		/tag= f
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	13
FT		/tag= g
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	15
FT		/tag= h
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
FT	misc_RNA	17
FT		/tag= i
FT		/label= RNA
FT		/note= "2'-O-methyl-D-uridine"
PN	WO2003064441-A2.	
XX		
PD	07-AUG-2003.	
XX		
PX	31-JAN-2003; 2003WO-CA000129.	
XX		
PR	01-FEB-2002; 2002US-0352873P.	
XX	(UWMC-) UNIV MCGILL.	
PA		
PI	Damha MJ, Parniak MA;	
XX		
DR	WPI; 2003-689523/65.	
PT	New oligonucleotide, useful for preventing or treating a disease related	
XX	to a target RNA in a system, e.g., AIDS or hepatitis B.	
PS	Example 2; Page 35; 73pp; English.	
XX		
CC	The present invention relates to a new oligonucleoside which comprises	
CC	alternating first and second segments. The first segment comprises at	
CC	least one sugar modified nucleoside. The second segment comprises at	
CC	least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of	
CC	each of the first and second segments, so that it comprises at least 4	
CC	alternating segments. The oligonucleotide is useful for preparing a	
CC	composition for inducing RNase H-mediated cleavage of a target RNA in a	
CC	system, preventing or decreasing translation, transcription or	
CC	replication of a target RNA in a system, detecting the presence of a	
CC	target RNA in a system, validating a gene target corresponding to a	
CC	target RNA in a system, or preventing or treating a disease related to a	
CC	target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)	
CC	or hepatitis B. The invention is useful in gene therapy. The present	

CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 8; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTATTTT 445
DB 1 UTUTUTUTUTUTUTUT 18
RESULT 2096
AAD57890/c
ID AAD57890 standard; RNA; 18 BP.
XX
AC AAD57890;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target RNA #1 used in RNase H assay.
XX
KM Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KM hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS Unidentified.
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CAN000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 4; Page 38; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system, or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is a target RNA used in RNase H assay. This sequence is used in
CC the exemplification of the invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTATTTT 445
DB 18 TTTTATTTT 1

RESULT 2097
ID AAL60006
AAL60006 standard; DNA; 18 BP.
XX
AC AAL60006;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human GH-1 gene amplifying PCR primer, CRV156.1el.
XX
KM Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;
KM gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003042226-A2.
XX
PD 22-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US035719.
XX
PR 09-NOV-2001; 2001US-0347448P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Wood LS, Wagner S, Parodi LA;
XX
DR WPI; 2003-449555/42.
XX
PT New growth hormone 1 (GH-1) diagnostic polynucleotide, useful as markers
PT for the analysis of a disease, or of susceptibility to drug treatment for
PT GH-1 dysfunction or other diseases.
XX
PS Example 2; Page 30; 74pp; English.
XX
CC The invention relates to growth hormone 1 (GH-1) gene including single
CC nucleotide polymorphisms (SNP). The GH-1 diagnostic polynucleotide is
CC useful as markers for the analysis of a disease, of susceptibility to
CC drug treatment for GH-1 dysfunction or other diseases, or may be included
CC in any complete or partial genetic map of the human genome. GH-1 mutant
CC polypeptides are useful as antagonists of GH-1 hormone action.
CC CC polynucleotides encoding these polypeptides are useful in gene therapy.
CC The present sequence is a PCR primer used for amplifying human GH-1 gene
XX
SQ Sequence 18 BP; 4 A; 9 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1051 TGCACACACCCGCTA 1068
DB 1 TGCACACACCCGCTA 18
RESULT 2098
ADB37210
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KM ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KM hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.

XX 08-MAY-2003.
XX 02-FEB-2001; 2001US-00776479.
XX 03-FEB-2000; 2000US-0179991P.
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX (FOUR/) FOURON Y.
XX Bratzler RL, Petersen DM, Fouron Y;
XX WPI; 2003-657977/62.
XX Treating and/or preventing allergy or asthma using an immunostimulatory
XX nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Disclosure; Page 17; 221pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
XX asthma which comprises administering to a subject a poly-G nucleic acid
XX in an aerosol formulation. The methods and compositions of the present
XX invention are useful for diagnosing and/or treating asthma and allergy
XX especially in a hypo-responsive subject. The present sequence represents
XX an immunostimulatory nucleic acid of the invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 428 TTTTATTTATTTT 445
XX 1 TTTTATTTT 18
XX
XX RESULT 2099
XX ADB37236
XX ID ADB37236 standard; DNA; 18 BP.
XX
XX ADB37236;
XX 04-DEC-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #850.
XX
XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX hypo-responsive subject; immunostimulatory.
XX
XX Synthetic.
XX
XX US2003087848-A1.
XX
XX 08-MAY-2003.
XX
XX 02-FEB-2001; 2001US-00776479.
XX
XX 03-FEB-2000; 2000US-0179991P.
XX
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y;
XX
XX WPI; 2003-657977/62.
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
XX nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Disclosure; Page 18; 221pp; English.

XX the invention relates to a method of treating or preventing allergy or
XX asthma which comprises administering to a subject a poly-G nucleic acid
XX in an aerosol formulation. The methods and compositions of the present
XX invention are useful for diagnosing and/or treating asthma and allergy
XX especially in a hypo-responsive subject. The present sequence represents
XX an immunostimulatory nucleic acid of the invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 428 TTTTATTTATTTT 445
XX 1 TTTTATTTT 18
XX
XX RESULT 2100
XX ADC38978/c
XX ID ADC38978 standard; DNA; 18 BP.
XX
XX ADC38978;
XX 18-DEC-2003 (first entry)
XX
XX Human ICAM-1 targeted primer #4.
XX
XX se; primer; immunosuppressive; antisense therapy;
XX corneal allograft rejection; intercellular adhesion molecule-1; ICAM-1;
XX extracellular adhesion molecule-1; ELAM-1;
XX vascular cell adhesion molecule-1; VCAM-1; corneal explant.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX misc_difference 1.18
XX /*tag= a
XX /note= "internucleotide linkages are optionally
XX phosphodiester bonds"
XX
XX WO2003032920-A2.
XX
XX 24-APR-2003.
XX
XX 16-OCT-2002; 2002WO-US033236.
XX
XX 18-OCT-2001; 2001US-00982262.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Mirabelli CK;
XX
XX WPI; 2003-403142/38.
XX
XX Inhibiting corneal allograft rejection, by contacting an allograft with a
XX formulation having an oligonucleotide targeted to intercellular adhesion
XX molecule-1, extracellular adhesion molecule-1 or vascular cell adhesion
XX molecule-1.
XX
XX Example 5; SEQ ID NO 4; 106pp; English.
XX
XX The invention relates to a method of inhibiting corneal allograft
XX rejection, by contacting the allograft with a topical formulation
XX comprising an antisense oligonucleotide targeted to intercellular
XX adhesion molecule-1 (ICAM-1), extracellular adhesion molecule-1 (ELAM-1)
XX or vascular cell adhesion molecule-1 (VCAM-1). The oligonucleotide is
XX useful for inhibiting corneal allograft rejection or for preserving a
XX corneal explant ex vivo, where the explant is human. This sequence
XX corresponds to one of the oligonucleotide of the invention.
XX

SQL Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 533 TCCTCTGCTGCTGAGCCTC 550

18 TCCTCCACCTCAGCCTC 1

DB

RESULT 2101

ADD31139/c

ID ADD31139 standard; DNA; 18 BP.

XX

AC ADD31139;

DE 15-JAN-2004 (first entry)

XX Human microsatellite locus PCR primer #8.

XX ss; PCR; primer; human; microsatellite locus;

XX prognostic tumour diagnosis; familial tumour predisposition;

XX colorectal cancer; gastrointestinal cancer; endometrial cancer;

XX colorectal cancer.

XX Homo sapiens.

XX US2003180758-A1.

XX 25-SEP-2003.

XX 09-DEC-2002; 2002US-00314810.

XX 15-SEP-2000; 2000US-00663020.

XX 24-APR-2001; 2001US-00841366.

XX (PROM-) PROMEGA CORP.

XX PI Bacher JW, Flanagan L, Nassif N;

XX WPI; 2003-830985/77.

XX Analyzing microsatellite instability by amplification of multiple loci

XX including mono-nucleotide and tetra-nucleotide repeats useful to detect

XX PT cancerous gastrointestinal or endometrium tumors particularly colorectal

XX PT cancer.

XX Claim 4; SEQ ID NO 8; 48bp; English.

XX The invention relates to a method of analysing microsatellite loci. The

XX CC invention is used to detect microsatellite instability in prognostic

XX CC tumour diagnosis, particularly a familial tumour predisposition,

XX CC especially to detect cancerous tumors of the gastrointestinal system or

XX CC endometrium, most particularly colorectal cancer. The present sequence

XX CC represents a human microsatellite locus PCR primer.

XX SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

QY 674 CTCACGCAACCTCTGCTC 691

18 CTCACGCAACCTCTGCTC 1

DB

RESULT 2102

ADE14006

ID ADE14006 standard; DNA; 18 BP.

XX

AC ADE14006;

XX 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #115.

XX Human; optineurin; db; ophthalmological; single nucleotide polymorphism;

XX SNV; glaucoma; progressive ocular hypertensive disorder;

XX glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

XX US2003190617-A1.

XX 09-OCT-2003.

XX 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

XX (SIEE/) SI E.

XX (RAYM/) RAYMOND V.

XX (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;

XX WPI; 2003-864168/80.

XX New nucleic acid sequences of the optineurin gene are useful to detect

XX polymorphisms particularly single nucleotide polymorphisms in the

XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related

XX PT disorders.

XX Claim 11; SEQ ID NO 117; 159bp; English.

XX The invention relates to an isolated nucleic acid (N1) comprising at

XX least 20 but not more than 1500 consecutive nucleotides of the optineurin

XX CC promoter appearing as ADE13890. Also included are the optineurin promoter

XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of

XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin

XX CC promoter, a host cell comprising the promoter operably linked to a

XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample

XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism

XX CC in a promoter region of the optineurin gene, associated with a glaucoma

XX CC phenotype), detecting a SNP sequence variation in a sample containing

XX CC DNA, detecting the presence of an optineurin promoter sequence variation

XX CC in a sample containing DNA, determining the presence or increased

XX CC susceptibility to glaucoma or to a progressive ocular hypertensive

XX CC disorder resulting in loss of visual field in a patient (or the severity

XX CC or progression of glaucoma in a patient, comprising providing

XX CC amplification reaction primers that direct amplification of a selected

XX CC nucleic acid region containing the variation within the optineurin

XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising

XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid

XX CC capable of detecting a SNP located within an optineurin promoter, and

XX CC detecting the polymorphism). The invention is used to diagnose and

XX CC prognose glaucoma and also to treat glaucoma related disorders. The

XX CC present sequence is an optineurin promoter motif, repeat element or

XX CC putative regulatory region.

QY 668 TCTTGCTCAGTCAAC 685

1 TCTTGCTCAGTCAAC 18

DB

RESULT 2103

ADE14244

ID ADE14244 standard; DNA; 18 BP.

XX

XX AC ADE14244;
 XX DT 29-JAN-2004 (first entry)
 XX DE Optineurin promoter motif, repeat element or regulatory region #353.
 XX DE Optineurin promoter motif, repeat element or regulatory region #353.
 XX DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 XX DE SNP; glaucoma; progressive ocular hypertensive disorder;
 XX DE glaucoma related disorder; motif, repeat element; regulatory region.
 XX OS Homo sapiens.
 XX OS US2003190617-A1.
 XX PN 09-OCT-2003.
 XX PD 06-MAR-2002; 2002US-00091281.
 XX PF 06-MAR-2002; 2002US-00091281.
 XX PR 06-MAR-2002; 2002US-00091281.
 XX PA (SITE/) SI E.
 XX PA (RAYM/) RAYMOND V.
 XX PA (MORI/) MORISSETTE J.
 XX PI Raymond V, Morissette J, Si E;
 XX PI WPI; 2003-864168/80.
 XX DR WPI; 2003-864168/80.
 XX PT New nucleic acid sequences of the optineurin gene are useful to detect
 XX PT polymorphisms particularly single nucleotide polymorphisms in the
 XX PT optineurin promoter to diagnose, prognosis and treat glaucoma and related
 XX PT disorders.
 XX PS Claim 11; SEQ ID NO 355; 159pp; English.
 XX CC The invention relates to an isolated nucleic acid (NI) comprising at
 XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 XX CC promoter appearing as ADE13890. Also included are the optineurin promoter
 XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 XX CC promoter, a host cell comprising the promoter operably linked to a
 XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 XX CC in a promoter region of the optineurin gene, associated with a glaucoma
 XX CC phenotype), detecting a SNP sequence variation in a sample containing
 XX CC DNA, detecting the presence of an optineurin promoter sequence variation
 XX CC in a sample containing DNA, determining the presence or increased
 XX CC susceptibility to glaucoma or to a progressive ocular hypertensive
 XX CC disorder resulting in loss of visual field in a patient (or the severity
 XX CC or progression of glaucoma in a patient, comprising providing
 XX CC amplification reaction primers that direct amplification of a selected
 XX CC nucleic acid region containing the variation within the optineurin
 XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 XX CC capable of detecting a SNP located within an optineurin promoter, and
 XX CC detecting the polymorphism). The invention is used to diagnose and
 XX CC prognose glaucoma and also to treat glaucoma related disorders. The
 XX CC present sequence is an optineurin promoter motif, repeat element or
 XX CC putative regulatory region.
 XX SQ Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 795 TTCAACCATGTTGCCAGG 812
 Db 1 TTCAACCATGTTGCCAGG 18

XX AC ADE14203/C
 XX ID ADE14203 standard; DNA; 18 BP.
 XX AC ADE14203;
 XX DT 29-JAN-2004 (first entry)
 XX DE Optineurin promoter motif, repeat element or regulatory region #312.
 XX DE Optineurin promoter motif, repeat element or regulatory region #312.
 XX DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 XX DE SNP; glaucoma; progressive ocular hypertensive disorder;
 XX DE glaucoma related disorder; motif, repeat element; regulatory region.
 XX OS Homo sapiens.
 XX OS US2003190617-A1.
 XX PN 09-OCT-2003.
 XX PD 06-MAR-2002; 2002US-00091281.
 XX PF 06-MAR-2002; 2002US-00091281.
 XX PR 06-MAR-2002; 2002US-00091281.
 XX PA (SITE/) SI E.
 XX PA (RAYM/) RAYMOND V.
 XX PA (MORI/) MORISSETTE J.
 XX PI Raymond V, Morissette J, Si E;
 XX PI WPI; 2003-864168/80.
 XX DR WPI; 2003-864168/80.
 XX PT New nucleic acid sequences of the optineurin gene are useful to detect
 XX PT polymorphisms particularly single nucleotide polymorphisms in the
 XX PT optineurin promoter to diagnose, prognosis and treat glaucoma and related
 XX PT disorders.
 XX PS Claim 11; SEQ ID NO 314; 159pp; English.
 XX CC The invention relates to an isolated nucleic acid (NI) comprising at
 XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 XX CC promoter appearing as ADE13890. Also included are the optineurin promoter
 XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 XX CC promoter, a host cell comprising the promoter operably linked to a
 XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 XX CC in a promoter region of the optineurin gene, associated with a glaucoma
 XX CC phenotype), detecting a SNP sequence variation in a sample containing
 XX CC DNA, detecting the presence of an optineurin promoter sequence variation
 XX CC in a sample containing DNA, determining the presence or increased
 XX CC susceptibility to glaucoma or to a progressive ocular hypertensive
 XX CC disorder resulting in loss of visual field in a patient (or the severity
 XX CC or progression of glaucoma in a patient, comprising providing
 XX CC amplification reaction primers that direct amplification of a selected
 XX CC nucleic acid region containing the variation within the optineurin
 XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 XX CC capable of detecting a SNP located within an optineurin promoter, and
 XX CC detecting the polymorphism). The invention is used to diagnose and
 XX CC prognose glaucoma and also to treat glaucoma related disorders. The
 XX CC present sequence is an optineurin promoter motif, repeat element or
 XX CC putative regulatory region.
 XX SQ Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 638 TGTCAACCCAGGCTGAGT 655
 Db 18 TGTCAACCCAGGCTGAGT 1

RESULT 2105
ADE7617/C
ID ADE7617 standard; DNA; 18 BP.
XX
AC ADE7617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW genotyping; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
KW cystic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033012.
XX
PR 15-OCT-2001; 2001US-0329427P.
PR 15-OCT-2001; 2001US-0329428P.
PR 15-OCT-2001; 2001US-0329619P.
PR 15-OCT-2001; 2001US-0329620P.
PR 14-MAR-2002; 2002US-0364416P.
XX
PA (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI Li AX, Hashmi G, Seul M;
XX
DR WPI; 2003-393553/37.
XX
PT Concurrent interrogation of a number of polymorphic sites, useful for
PT genetic testing, carrier screening, genetic profiling, and identity
PT testing, comprises conducting a multiplexed elongation assay using
PT probes.
XX
PS Example 9; Page 46; 143pp; English.
XX
CC This invention relates to a novel method for the concurrent interrogation
CC of a number of polymorphic sites in the presence of, and without
CC interference from, non-designated polymorphic sites. Specifically, it
CC comprises conducting a multiplexed elongation assay by applying one or
CC more temperature cycles to achieve linear amplification of the target or
CC a combination of annealing and elongation steps under temperature-
CC controlled conditions. Furthermore, this detection method uses probe
CC extension or elongation and relies on enzymatic recognition, a superior
CC technique that no longer depends on differential hybridisation. The
CC present invention describes probes and methods useful for identifying or
CC detecting polymorphisms at one or more designated sites, such that they
CC can identify mutations within the cystic fibrosis conductance
CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC genes. In addition, concurrent interrogation of a multiplicity of
CC polymorphic sites is useful for genetic testing, carrier screening,
CC genotyping or genetic profiling, and identity testing. This
CC oligonucleotide is the negative control probe used for the elongation
CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTTATTTT 445
DB 18 TTTTATTTTATTTTATTTT 1

RESULT 2106
ADE84357/C
ID ADE84357 standard; DNA; 18 BP.
XX
AC ADE84357;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human lymphoid cell proliferative disorder gene Cpg analysis oligo #63.
XX
KW lymphoid cell proliferative disorder; methylation;
KW methylated Cpg dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003044226-A2.
XX
PD 30-MAY-2003.
XX
PF 25-NOV-2002; 2002WO-EP013265.
XX
PR 23-NOV-2001; 2001DE-01057491.
PR 28-DEC-2001; 2001DE-01064501.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Caldwell C, Genc B, Becker E, Walter S, Nimrich I;
XX
DR WPI; 2003-457621/43.
XX
PT Detecting and differentiating between lymphoid cell proliferative
PT disorders comprises contacting a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated Cpg
PT dinucleotides.
XX
PS Claim 30; SEQ ID NO 353; 448pp; English.
XX
CC The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated Cpg dinucleotides within the target nucleic
CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, BSR4, AR, CDK4, RB2, CDC25A, GP1b beta, MYO1, CDH3,
CC MYC1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, FOS,
CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,
CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOKA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC Cpg dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting of a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents an oligonucleotide used to analyse of Cpg positions within the
CC above mentioned genes.
XX
SQ Sequence 18 BP; 4 A; 1 C; 7 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1055 ACCACACCCCGCTAATTT 1072

Db 18 ACCACACCCGACTAATT 1

RESULT 2107

AD84358/C
ID ADE84358 standard; DNA; 18 BP.

AC ADE84358;

XX 29-JUN-2004 (first entry)

DE Human lymphoid cell proliferative disorder gene Cpg analysis oligo #64.

XX Lymphoid cell proliferative disorder; methylation;

KM methylated Cpg dinucleotide; single nucleotide polymorphism; SNP;

KM diffuse large B-cell lymphoma; mantle cell lymphoma;

KM chronic lymphocytic leukemia; small lymphocytic lymphoma;

KM follicular lymphoma; diagnosis; prognosis; primer; ss.

XX Homo sapiens.

OS Homo sapiens.

PN W02003044226-A2.

PD 30-MAY-2003.

PF 25-NOV-2002; 2002MO-EP013265.

PR 23-NOV-2001; 2001DE-01057491.

PR 28-DEC-2001; 2001DE-01064501.

XX (EPIC-) EPICENOMICS AG.

PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;

DR WPI; 2003-457621/43.

XX Detecting and differentiating between lymphoid cell proliferative

PT disorders comprising contacting a target nucleic acid with at least one

PT reagent that distinguishes between methylated and non-methylated Cpg

PT dinucleotides.

PS Claim 30; SEQ ID NO 354; 448bp; English.

XX The invention relates to a method of detecting and differentiating

CC between lymphoid cell proliferative disorders associated with at least

CC one gene and/or their regulatory regions in a subject by contacting a

CC target nucleic acid in a biological sample obtained from the subject with

CC at least one reagent or series of reagents that distinguish between

CC methylated and non-methylated Cpg dinucleotides within the target nucleic

CC acid. The genes and/or their regulatory regions are preferably selected

CC from MDR1, CSNK2B, BGR4, AR, CDK4, RB2, CDC35A, GRPb beta, MYO1, CDH3,

CC MYCL1, ELK1, ABUL, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,

CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic

CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences

CC of the genes are useful for detecting the methylation state of all the

CC Cpg dinucleotides within one or more the sequences, or their complements,

CC for determining the cytosine methylation state and/or single nucleotide

CC polymorphisms (SNPs), and for differentiating at least two of the medical

CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,

CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular

CC lymphoma. They are also useful for detecting of a predisposition to,

CC monitoring of lymphoid cell proliferative disorder. This sequence

CC represents an oligonucleotide used to analyse or Cpg positions within the

CC above mentioned genes.

XX Sequence 18 BP; 4 A; 0 C; 7 G; 7 T; 0 U; 0 Other;

XX SQ

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1055 ACCACACCCCGCTAATT 1072

RESULT 2108

ADFI789/C
ID ADFI7789 standard; DNA; 18 BP.

AC ADFI7789;

XX 12-FEB-2004 (first entry)

DE PCR primer 1274_C396G_ER for amplifying a human CA gene.

XX beta-migrating plasmidogen activator inhibitor 1; PCR; primer; ss;

KM cardiovascular associated; CA; atherosclerosis; ischaemia; hypertension;

KM stenosis; cardiac; cerebroprotective; antiatherosclerotic;

KM hypotensive; human.

XX Homo sapiens.

OS Homo sapiens.

PN EP1327639-A1.

PD 16-JUL-2003.

PF 15-JAN-2002; 2002EP-00000253.

PR 15-JUN-2002; 2002EP-00000253.

XX (FARB) BAYER AG.

PI Stroop U, Schwes S, Kallabis H, Schmitz G;

DR WPI; 2003-714408/68.

XX Novel isolated polynucleotide encoded by cardiovascular associated gene,

PT useful for treating cardiovascular disease e.g., high blood pressure,

PT myocardial infarction, stroke, atherosclerosis.

XX Example; Page 20; 40pp; English.

PS This invention relates to novel isolated polynucleotides with allelic

CC variations that encode cardiovascular associated (CA) polypeptides, which

CC are useful for the identification of therapeutic agents for the treatment

CC of cardiovascular disease. Specifically, it refers to methods for

CC assessing cardiovascular risks in humans by describing genetic variations

CC that diagnose a predisposition or susceptibility for cardiovascular

CC diseases including atherosclerosis, ischaemia, hypertension and

CC reterosclerosis. The present invention describes specific CA genes that can be

CC used as probes for the detection of genetic polymorphisms. Furthermore,

CC they can be used for treating cardiovascular disease such as elevated low

CC density lipoprotein (LDL)-cholesterol levels, high blood pressure,

CC abnormal electrocardiographic profile, myocardial infarction or strokes.

CC As such, they can be described as having cardiac, cerebroprotective,

CC antiatherosclerotic or hypotensive activities. This oligonucleotide

CC sequence is a PCR primer used for amplifying human beta-migrating

CC plasmidogen activator inhibitor 1 (Seqid 2) DNA, a CA gene of the

CC invention.

XX Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

XX SQ

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 2109

QY 871 TTACAGGCGTGAGCCACC 888

DB 18 TTACAGGCGATGAGCTACC 1

ADG89548
ID ADG89548 strand; DNA; 18 BP.
XX
AC ADG89548;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human matrilin-3 PCR primer REMAT3.7E.F SEQ ID NO:123.
XX
XX human; matrilin-3; osteopathic; gene therapy; osteoarthritis; MATN3; EGF;
XX se; PCR; primer.
XX
XX Homo sapiens.
XX
OS WO2003062469-A2.
XX
PD 31-JUL-2003.
XX
XX 23-JAN-2003; 2003WO-1B000342.
XX
PR 25-JAN-2002; 2002US-0453705P.
XX
PR 05-DEC-2002; 2002US-0431538P.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson SE;
XX
PI WPI; 2003-646073/61.
XX
DR New nucleic acid molecule for diagnosing, prognosing or treating
PT osteoarthritis comprises a matrilin-3 gene or its fragment or variant,
PT and at least one polymorphism.
XX
XX Disclosure; SEQ ID NO 123; 190pp; English.
XX
XX The invention relates to a novel nucleic acid molecule comprising a
CC matrilin-3 gene, or its fragment or variant, a sequence of 137870 bp
CC fully defined in the specification, and at least one polymorphism given
CC in the specification. A protein of the invention has osteopathic
CC activity. A polynucleotide of the invention may have a use in gene
CC therapy. The composition and methods of the invention are useful in
CC diagnosing, prognosing or treating osteoarthritis using polymorphisms in
CC the matrilin-3 gene. The present sequence is used in the exemplification
CC of the invention.
XX
XX Sequence 18 BP; 5 A; 7 C; 5 G; 1 T; 0 U; 0 Other;
SO
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 873 ACAGGCGTGGAGCCACAC 890
DB 1 ACAGGCGATGGGCCACAC 18
RESULT 2110
ACAG8892/C
ID ACAG8892 standard; DNA; 18 BP.
XX
AC ACAG8892;
XX
XX 08-JUL-2003 (first entry)
XX
XX Selection and amplification of genetic markers PCR related primer #3.
XX
XX Genetic marker selection; multiplex PCR amplification;
XX prenatal diagnostic testing; foetal sex determination;
XX genetic identification; DNA profiling; DNA fingerprinting;
XX forensic analysis; PCR; primer; ss.
XX
XX Homo sapiens.
XX
OS

PN WO2003031646-A1.
XX
XX 17-APR-2003.
XX
XX 14-OCT-2002; 2002WO-AU001388.
XX
XX 12-OCT-2001; 2001AU-00008234.
XX
XX 12-OCT-2001; 2001AU-00008235.
XX
XX (UYGU) UNIV QUEENSLAND.
XX
XX Findlay I, Matthews PL, Mulcahy BK;
XX
XX WPI; 2003-381725/36.
XX
XX Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.
XX
XX Claim 36; Page 39; 64pp; English.
XX
XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 943 CCCAGGCTGGAGTGCAT 960
DB 18 CCCAGGATGGGCTGCAT 1
RESULT 2111
ADG31947/C
ID ADG31947 standard; DNA; 18 BP.
XX
XX ADG31947;
XX
XX 26-FEB-2004 (first entry)
XX
XX RNA/DNA hybrid PCR primer used to amplify human CYP1A1 gene Segid 21.
XX
XX DNA/RNA hybrid; ss; genotyping; gene polymorphism;
XX single nucleotide polymorphism; SNP; cytochrome CYP2C19;
XX cytochrome CYP1A1; glutathione-S-transferase; aldehyde dehydrogenase;
XX ALDH2; PCR; primer; GSTM1; GSTT1.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO2003102178-A1.
XX
XX 11-DEC-2003.
XX
XX 30-MAY-2003; 2003WO-JP006804.
XX
XX 31-MAY-2002; 2002JP-00158853.
XX
XX 12-JUL-2002; 2002JP-00204143.
XX
PR

PR 19-JUL-2002; 2002JP-00211813.
PR 25-OCT-2002; 2002JP-00310862.
PR 19-NOV-2002; 2002JP-00335830.
XX
XX (TAKI) TAKARA BIO INC.
PI Kobayashi E, Enoki T, Tanabe M, Ueda Y, Okuda S, Sagawa H;
PI Kato I;
XX WPI; 2004-043111/04.
XX
PT Isothermal chimeric primer initiated nucleic acid amplification detection
PT of base substitution, deletion or insertion for typing of gene
PT polymorphisms such as SNP.
XX
PS Claim 2; SEQ ID NO 21; 115bp; Japanese.
XX
CC This invention relates to a novel method of typing gene polymorphisms.
CC Specifically, it refers to the identification of the single nucleotide
CC polymorphism G636A in human cytochrome gene CYP2C19, the T6235C SNP in
CC human cytochrome gene CYP1A1, as well as various polymorphisms in the
CC human glutathione-S-transferase gene and the human aldehyde dehydrogenase
CC gene ALDH2. Furthermore, gene polymorphisms in several target nucleic
CC acids may be detected in a single sample by successive amplification of
CC the individual targets. The present invention describes a fast, accurate
CC and highly reproducible method of detecting a base substitution e.g. SNP,
CC insertion or deletion mutation for diagnosis of genetic diseases,
CC detection of sensitivity to drugs and other substances, as well as other
CC genomic investigations. This oligonucleotide sequence is a PCR primer
CC used to amplify a human CYP1A1 gene, in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 992 TCCCGGCTCAAGCATT 1009
Db 18 TCCCGGCTCAAGCATT 1
XX
RESULT 2112
AD134489
ID AD134489 standard; DNA; 18 BP.
XX
AC AD134489;
XX
DT 22-APR-2004 (first entry)
XX
DE Nucleotide sequence of an oligo dT18.
XX
KW Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
OS Synthetic.
XX
XX WO2003102243-A1.
XX
XX 11-DEC-2003.
XX
XX 30-MAY-2003; 2003WO-US017103.
XX
XX 31-MAY-2002; 2002US-0384454P.
XX
XX (JANC) JANSSEN PHARM NV.
XX
XX Kamme FC, Zhu YJ;
XX
XX WPI; 2004-035466/03.
XX
XX Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating

PT single-stranded oligonucleotide from the transcription sample.
XX
XX Example 1; SEQ ID NO 8; 26pp; English.
XX
PS The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction.
CC Sequences AD134483-AD134489 represent oligonucleotides used in a T7 RNA
CC transcription reaction.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 428 TTTTATTATTATTTT 445
Db 1 TTTTATTATTATTTT 18
XX
RESULT 2113
ADH76761
ID ADH76761 standard; DNA; 18 BP.
XX
AC ADH76761;
XX
DT 22-APR-2004 (first entry)
XX
DE MCHRI genomic sequence analysis primer #70.
XX
KW melanin-concentrating hormone receptor 1; MCHRI; anorectic; gene therapy;
KW obesity; primer; ss.
XX
OS Unidentified.
XX
XX WO2003104489-A2.
XX
XX 18-DEC-2003.
XX
XX 05-JUN-2003; 2003WO-EP005917.
XX
XX 05-JUN-2002; 2002EP-00012569.
XX
XX (UYPH-) UNIV PHILIPPS MARBURG.
XX
XX Platzner M, Platzner C, Gudermann T, Hebebrand J, Hinney A;
XX
XX Reichwald K;
XX
XX WPI; 2004-062377/06.
XX
XX
XX New diagnostic composition, useful for diagnosing obesity related to the
PT presence of a molecular variant of the MCHRI gene or a susceptibility to
PT the disorder.
XX
XX Example 2; Page 43; 76pp; English.
XX
CC The invention relates to a novel diagnostic polynucleotide composition.
CC The polynucleotide composition comprises: a sequence encoding a
CC polypeptide with defined sequences given in the specification; a sequence
CC capable of hybridizing to a melanin-concentrating hormone receptor 1
CC (MCHRI) gene; a polynucleotide encoding an MCHRI polypeptide; or a
CC sequence comprising one or more of the nucleotide exchanges (SNP's) given
in the specification and at least 8 bases of surrounding sequence of the

CC MCHRI gene. The composition has anorectic activity. The polynucleotide
CC composition may be used in gene therapy to treat the disorders of the
CC invention. The composition is useful for diagnosing obesity related to
CC the presence of a molecular variant of the MCHRI gene or a susceptibility
CC to the disorder. The MCHRI protein or polynucleotide is useful for
CC preparing a medicament for treating or preventing obesity related to the
CC presence of a molecular variant of the MCHRI gene. This polynucleotide
CC represents an MCHRI primer of the invention.
XX
SQ Sequence 18 BP; 4 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGCTGAGC 884
DB 1 GGTATTACAGCTGTGAGC 18

RESULT 2114
ADH76763
XX ADH76763 standard; DNA; 18 BP.
XX
AC ADH76763;
XX
DT 22-APR-2004 (first entry)
XX
DE MCHRI genomic sequence analysis primer #72.
XX
XX melanin-concentrating hormone receptor 1; MCHRI; anorectic; gene therapy;
KM obesity; primer; ss.
XX
OS Unidentified.
XX
XX WO2003104489-A2.
XX
XX 18-DEC-2003.
XX
PD 05-JUN-2003; 2003WO-EP005917.
XX
PF 05-JUN-2002; 2002EP-00012569.
XX
PR 05-JUN-2002; 2002EP-00012569.
XX
PA (UYPH-) UNIV PHILIPPS MARBURG.
XX
XX
PI Plutzer M, Plutzer C, Gudermann T, Hebebrand J, Hinney A;
PI Reichwald K;
XX
XX WPI; 2004-062377/06.
XX
DR
XX
PT New diagnostic composition, useful for diagnosing obesity related to the
PT presence of a molecular variant of the MCHRI gene or a susceptibility to
PT the disorder.
XX
XX Example 2; Page 43; 76pp; English.
XX
PS The invention relates to a novel diagnostic polynucleotide composition.
XX The polynucleotide composition comprises: a sequence encoding a sequence
CC polypeptide with defined sequences given in the specification; a sequence
CC capable of hybridizing to a melanin-concentrating hormone receptor 1
CC (MCHRI) gene; a polynucleotide encoding an MCHRI polypeptide; or a
CC sequence comprising one or more of the nucleotide exchanges (SNP's) given
CC in the specification and at least 8 bases of surrounding sequence of the
CC MCHRI gene. The composition has anorectic activity. The polynucleotide
CC composition may be used in gene therapy to treat the disorders of the
CC invention. The composition is useful for diagnosing obesity related to
CC the presence of a molecular variant of the MCHRI gene or a susceptibility
CC to the disorder. The MCHRI protein or polynucleotide is useful for
CC preparing a medicament for treating or preventing obesity related to the
CC presence of a molecular variant of the MCHRI gene. This polynucleotide
CC represents an MCHRI primer of the invention.
XX
SQ Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1114 GGTGCTTCAACTCTCG 1131
DB 1 GGTGCTTCAACTCTCG 18

RESULT 2115
ADH78590/C
XX ADH78590 standard; DNA; 18 BP.
XX
AC ADH78590;
XX
DT 22-APR-2004 (first entry)
XX
DE Test element oligonucleotide #2.
XX
XX Fluid functional property; fluid flow pattern;
KM fluid reagent distribution; time dependent fluid reactivity; ss.
XX
XX Synthetic.
XX
XX US2003232343-A1.
XX
PD 18-DEC-2003.
XX
PF 14-JUN-2002; 2002US-00172675.
XX
PR 14-JUN-2002; 2002US-00172675.
XX
XX 14-JUN-2002; 2002US-00172675.
XX
PA (LEPROUST) LEPROUST E M.
PA (AMORSE) AMORSE D A.
PA (PECK/) PECK B J.
XX
XX Leproust EM, Amorse DA, Peck BJ;
PI
XX
XX WPI; 2004-061269/06.
XX
DR
XX
PT Determining a functional property of fluid in chamber by introducing a
PT support comprising test elements having reaction and detection domains,
PT introducing a test fluid, and detecting locations not reactive with the
PT fluid.
XX
XX Example 2; SEQ ID NO 2; 22pp; English.
XX
PS The invention relates to a method of determining a functional property of
XX a fluid in a chamber comprising introducing into the chamber a support to
CC which is bound several test elements, each of the test elements
CC comprising a reaction domain and a detection domain, introducing into the
CC chamber a fluid that is interactive with the reaction domains, removing
CC the fluid from the chamber, determining by means of the detection domains
CC the locations at which the fluid has not interacted with the reaction
CC domains, and relating the locations to the functional property of the
CC fluid. The reaction domains involves nucleotides. The detection domain
CC comprises a member of a specific binding pair. The determining of the
CC step involves treating the test elements to modify only those reaction
CC domains that have interacted with the fluid. The functional property is
CC chosen from the flow pattern of the fluid, reagent distribution within
CC the fluid and time dependent reactivity of the fluid. The method is
CC useful for determining a functional property of a fluid in a chamber and
CC for synthesising arrays of biopolymers e.g., arrays of polynucleotides.
CC The method provides for the characterisation of a new fluid in a known
CC flow cell, a known fluid in a new flow cell or a new fluid/flow cell
CC combination. This sequence represents a test element used in the method
CC of the invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTT 445
 Db 18 TTTTATTTTATTTT 1

RESULT 2116
 ADI20814
 ID ADI20814 standard; DNA; 18 BP.

AC ADI20814;

DT 06-MAY-2004 (first entry)

DE Hybridisation detection oligonucleotide #12.

KW DD3; Cpg dinucleotide; cell proliferative disorder; ss.

OS Synthetic.

PN W02004005543-A1.

PD 15-JAN-2004.

PF 25-JUN-2003; 2003WO-EP006690.

PR 08-JUL-2002; 2002DE-01030692.

XX (EPIG-) EPIGENOMICS AG.

PI Horns T;

DR WPI; 2004-091385/09.

PT Detecting methylation of 5' and promoter region of DD3 gene for
 PT diagnosing proliferative disorders comprising contacting target nucleic
 PT acid with a reagent that distinguishes between methylated and non-
 PT methylated Cpg dinucleotide.

PS Claim 6; SEQ ID NO 17; 56pp; English.

XX The present invention relates to detecting the methylation state of the
 CC 5' and promoter region of the gene DD3 within a subject comprising
 CC contacting a target nucleic acid having one or more sequences selected
 CC from 5 3531 base pair sequences in a biological sample with at least one
 CC reagent or a series of reagents. The method is useful for detecting the
 CC methylation state of the 5' and promoter region of the gene DD3 within a
 CC subject. The set of oligonucleotides comprising at least three of the
 CC oligomers is useful for detecting the cytosine methylation state and/or
 CC single nucleotide polymorphisms (SNPs) within SEQ. ID NO. 1-5 and its
 CC complementary sequences. The set of oligomers is also useful for
 CC detecting the methylation state of all Cpg dinucleotides within SEQ ID
 CC NO. 1 and its complementary sequences. The set of at least two
 CC oligonucleotides can be used as primer oligonucleotides for the
 CC amplification of DNA sequences selected from SEQ ID NO. 1-5 and its
 CC complementary sequences. The DNA- and/or PNA-array is useful for
 CC analyzing diseases associated with the methylation state of the gene DD3
 CC comprising at least one nucleic acid. The methods, nucleic acids,
 CC oligonucleotide or PNA-oligomer, kit, array or the set of
 CC oligonucleotides is useful for the characterization, classification,
 CC differentiation, grading, staging, and/or diagnosis of cell proliferative
 CC disorders, or the predisposition to cell proliferative disorders. It can
 CC also be used for the therapy of cell proliferative disorders. The present
 CC sequence represents a detection oligonucleotide of the invention.

XX Sequence 18 BP; 3 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 161 AATTTTGTATTTT 178

Db 1 AATTTTGTATTTT 18

RESULT 2117
 ADM46455/c
 ID ADM46455 standard; DNA; 18 BP.

AC ADM46455;

DT 03-JUN-2004 (first entry)

DE Antisense oligonucleotide targeting human ICAM-1 #4.

XX Antisense; ss; human; intercellular adhesion molecule; ICAM-1;
 KW vascular cell adhesion molecule; VCAM-1;
 KW endothelial leukocyte adhesion molecule; ELAM-1;
 KW inflammatory ophthalmological disorder; redness; inflammation;
 KW corneal explant; corneal allograft rejection.

OS Homo sapiens.

PN US2004033977-A1.

PD 19-FEB-2004.

PF 04-JUN-2003; 2003US-0045463.

PR 14-AUG-1990; 90US-00567286.

PR 02-SEP-1992; 92US-00939855.

PR 21-JAN-1993; 93US-00007997.

PR 10-FEB-1993; 93US-00969151.

PR 17-MAY-1993; 93US-00063167.

PR 12-MAY-1995; 95US-00440740.

PR 03-AUG-1998; 98US-00128496.

PR 12-SEP-2000; 2000US-00659288.

PR 18-OCT-2001; 2001US-00982262.

PA (BENN/) BENNETT C F.

PA (MIRA/) MIRABELLI C.

PI Bennett CF, Mirabelli C;

DR WPI; 2004-180090/17.

PT New antisense oligonucleotide, useful for diagnosing, as research
 PT reagents and for treating disease states, which respond to modulation of
 PT the synthesis or metabolism of cell adhesion molecules.

PS Example 5; SEQ ID NO 4; 72pp; English.

XX The invention relates to an antisense oligonucleotide targeting human
 CC intercellular adhesion molecule (ICAM-1) having a sequence appearing as
 CC ADM46473. In the oligonucleotide, at least one adenosine nucleotide is
 CC replaced with a thymidine, cytidine or guanosine nucleotide, at least one
 CC thymidine nucleotide is replaced with an adenosine, cytidine or guanosine
 CC nucleotide, at least one guanosine nucleotide is replaced with an
 CC adenosine, thymidine or cytidine nucleotide or at least one cytidine
 CC nucleotide is replaced with an adenosine, cytidine or guanosine
 CC nucleotide. The oligonucleotide is one of 88 disclosed antisense
 CC oligonucleotides targeting ICAM-1, vascular cell adhesion molecule (VCAM-
 CC 1) or endothelial leukocyte adhesion molecule (ELAM-1). Also included are
 CC an RNA compound 8-80 nucleobases in length targeted to human ICAM-1 mRNA
 CC (where the compound specifically hybridises with the human ICAM-1 mRNA
 CC and inhibits the expression of human ICAM-1 mRNA), and a double stranded
 CC RNA compound having the RNA equivalent sequence of ADM46473. The
 CC oligonucleotide is useful for modulating the activity of the RNA and DNA
 CC and the modulation of the synthesis and metabolism of specific cell
 CC adhesion molecules. It is also useful for the diagnosis, as research
 CC reagents and for treating disease states, which respond to modulation of
 CC the synthesis or metabolism of cell adhesion molecules. The
 CC oligonucleotide is suitable for treating inflammatory ophthalmological
 CC disorders including redness and inflammation caused by allergens and

CC allergic reactions. The oligonucleotides can also be used to preserve
CC corneal explants ex vivo and to prevent corneal allograft rejections. The
CC specific hybridisation exhibited by the oligonucleotides may be used for
CC assays, purifications or cellular product preparations. The present
CC sequence is an antisense oligonucleotide targeting ICAM-1.

XX Sequence 18 BP; 4 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 533 TCCTCCTGCTCAGCTC 550

Db 18 TCCTCCACCTCAGCTC 1

RESULT 2118

ID ADN08321 standard; DNA; 18 BP.

XX ADN08321;

DT 15-JUL-2004 (first entry)

DE 3T3 cell transformation promoting human DNA primer, SEQ ID NO 21.

XX transformation; 3T3 cell; genetic engineering; cytostatic;

KM recombinant protein; gene therapy; cancer; human; ss; primer.

XX Homo sapiens.

XX WO2004033493-A1.

XX 22-APR-2004.

PF 07-AUG-2003; 2003WO-CN000636.

XX 07-AUG-2002; 2002CN-00136401.

PR 16-SEP-2002; 2002CN-00136998.

PR 16-SEP-2002; 2002CN-00136999.

XX (NEMO-) NEMOGEN LTD.

PI Yang S, Gu J;

XX WPI; 2004-330446/30.

XX Human protein for promoting transformation of 3T3 cells and its encoded
PT polynucleotide, applicable in producing recombinant proteins and in gene
PT therapy of e.g. cancer.

XX Example 2; SEQ ID NO 21; 68bp; Chinese.

XX The invention relates to a novel isolated human protein for promoting the
CC transformation of 3T3 cells and contains any of the 31 amino acid
CC sequences defined in the specification. The invention further provides:

CC an isolated polynucleotide that encodes any of the proteins described
CC above; a vector containing any of the said polynucleotides; a host cell
CC for genetic engineering, which is transformed or transduced by the
CC polynucleotide or vector described above; a process for producing the
CC human protein by culturing such transformed cells for expression and
CC collecting the product; and an antibody binding specifically with the
CC human protein. The 3T3 transformation promoting human protein has
CC cytostatic activity. The protein and its encoded polynucleotide are
CC useful for promoting the transformation of 3T3 cells, together with
CC expression vectors and transfectants for the application in producing
CC recombinant proteins and in gene therapy for the treatment of disorders,
CC such as cancer. This polynucleotide sequence represents a primer for the
CC DNA encoding one of the 3T3 transformation promoting human proteins of
CC the invention.

XX Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 661 GGCGCAATCTTGCTCAG 678

Db 1 GGCGCAATCAGCGCTCAC 18

RESULT 2119
ID ADN02345/C standard; DNA; 18 BP.

XX ADN02345;

DT 15-JUL-2004 (first entry)

DE PCR primer 64 used during linkage analysis of human D-amino acid oxidase.

XX late-onset neurodegenerative disease; D-amino acid oxidase; DAO;

KM flavin dinucleotide; FAD-dependent oxidase;

KM D-amino acid oxidative deamination; EC.1.4.3.3; neuroprotective;

KM antiparkinsonian; amyotrophic lateral sclerosis; ALS; Parkinson's;

KM Alzheimer's; gene therapy; human; ss; PCR; primer; linkage analysis;

XX chromosome 12.

OS Homo sapiens.

XX WO2004033723-A2.

XX 22-APR-2004.

PF 06-OCT-2003; 2003WO-GB004337.

XX 09-OCT-2002; 2002GB-00023424.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Mitchell J, De Bellerche J;

XX WPI; 2004-348204/32.

XX Determining an increased risk of a late-onset neurodegenerative disease
PT to a patient comprises analyzing a sample from the patient to determine
PT whether the patient has a D-amino acid oxidase (DAO) abnormality.

XX Example 1; SEQ ID NO 73; 209bp; English.

XX The invention relates to a novel method for determining an increased risk
CC of a late-onset neurodegenerative disease to a patient which comprises
CC analysing a sample from the patient to determine whether the patient has

CC a D-amino acid oxidase (DAO) abnormality, where the presence of a DAO
CC abnormality is an indication that the patient has an increased risk of
CC the late-onset neurodegenerative disease. DAO is a flavin dinucleotide
CC (FAD)-dependent oxidase which catalyses the oxidative deamination of D-
CC amino acids (EC.1.4.3.3). The method of the invention has neuroprotective
CC and antiparkinsonian applications and may be useful in determining an
CC increased risk of a late-onset neurodegenerative disease to a patient, as
CC well as in preparing a medicament for treating a late-onset
CC neurodegenerative disease, such as amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease (PD) or Alzheimer's disease (AD), possibly via gene
CC therapy. The current sequence is that of a PCR primer of the invention
CC which was used during linkage analysis of human D-amino acid oxidase.

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CCCGGCTCAGCGATTC 1010

|| ||| ||||| ||||| |||||

Db 18 CTGGGTTCAAGCATTC 1

RESULT 2120

ADO28710/C

ID ADO28710 standard, DNA; 18 BP.

AC ADO28710;

XX

DT 15-JUL-2004 (first entry)

XX

DE Single stranded cDNA production poly-A-tail seqid 6.

XX

XX single stranded cDNA; adaptor-mediated process; cDNA synthesis;

KM poly-A-tail; ss.

OS Synthetic.

XX

PN US6706476-B1.

XX

PD 16-MAR-2004.

XX

PF 09-MAR-2001; 2001US-00803263.

XX

PR 22-AUG-2000; 2000US-0226954P.

XX

PA (AZIG-) AZIGM BIOSCIENCE AS.

PI Thirstrup K, Warthoe P, Petersson NB;

DR WPI; 2004-326403/30.

XX

PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis primer to RNA and synthesizing first cDNA strand, ligating adaptor to single stranded cDNA using DNA ligase, and amplifying ligated single stranded cDNA fragment.

PT

PS

XX

XX Example 1; SEQ ID NO 6; 22pp; English.

CC The invention describes a method of synthesizing single stranded cDNA by a 5'-ligated adaptor-mediated process involving: annealing a cDNA synthesis primer to RNA, separating the cDNA strand from the RNA, purifying the cDNA, contacting the cDNA with an adaptor, ligating the adaptor through 5'-phosphate on strand (II) of the adaptor to single stranded using DNA ligase, and amplifying the obtained ligated single stranded fragment in an molecular amplification procedure. The method is useful for: synthesizing a single stranded cDNA by a 5'-ligated adaptor-mediated process, where the source of nucleic acid is chosen from blood, serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and saliva. The tissue sample comprises a cell population which may be single cell, 100-1000000 cells or more as desired; making a cDNA library from a collection of mRNA molecules in a sample, where the method is applied to amplify the cDNAs corresponding to the mRNAs by annealing one or more cDNA synthesis primers to several mRNAs in the sample; producing a subtractive hybridisation probe which involves synthesizing a double-stranded cDNA collection from a first mRNA population by the method, where primer 1 is modified by biotin in the 5' end, isolating the biotin-containing single stranded cDNA (sense) by use of streptavidin coated magnetic beads, synthesizing a double-stranded cDNA collection from a second mRNA population according to the method, isolating the non-biotin-containing single stranded cDNA (anti-sense) by use of streptavidin coated magnetic beads, hybridising the sense to the anti-sense cDNA, where an unhybridised sub-population of the anti-sense cDNA is found, isolating the unhybridised sub-population of the anti-sense cDNA by use of streptavidin coated cDNA, and generating a second double-stranded cDNA collection from the unhybridised sub-population by PCR using primer 1 and primer 2; and detecting expression of a gene in a pre-selected cell population. The method is an improved method for producing amplified heterogeneous populations of cDNA from limited quantities of RNA or other nucleic acid. This sequence represents a poly-A-tail used to in the production single stranded cDNA.

CC

XX

XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 445

Db 18 TTTTATTTTATTTT 1

RESULT 2121

ADO28711

ID ADO28711 standard, DNA; 18 BP.

AC ADO28711;

XX

DT 15-JUL-2004 (first entry)

XX

DE Single stranded cDNA production poly-A-tail complement seqid 7.

XX

XX single stranded cDNA; adaptor-mediated process; cDNA synthesis;

KM poly-A-tail; ss.

OS Synthetic.

XX

PN US6706476-B1.

XX

PD 16-MAR-2004.

XX

PF 09-MAR-2001; 2001US-00803263.

XX

PR 22-AUG-2000; 2000US-0226954P.

XX

PA (AZIG-) AZIGM BIOSCIENCE AS.

PI Thirstrup K, Warthoe P, Petersson NB;

DR WPI; 2004-326403/30.

XX

PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis primer to RNA and synthesizing first cDNA strand, ligating adaptor to single stranded cDNA using DNA ligase, and amplifying ligated single stranded cDNA fragment.

PT

PS

XX

XX Example 1; SEQ ID NO 7; 22pp; English.

CC The invention describes a method of synthesizing single stranded cDNA by a 5'-ligated adaptor-mediated process involving: annealing a cDNA synthesis primer to RNA, separating the cDNA strand from the RNA, purifying the cDNA, contacting the cDNA with an adaptor, ligating the adaptor through 5'-phosphate on strand (II) of the adaptor to single stranded using DNA ligase, and amplifying the obtained ligated single stranded fragment in an molecular amplification procedure. The method is useful for: synthesizing a single stranded cDNA by a 5'-ligated adaptor-mediated process, where the source of nucleic acid is chosen from blood, serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and saliva. The tissue sample comprises a cell population which may be single cell, 100-1000000 cells or more as desired; making a cDNA library from a collection of mRNA molecules in a sample, where the method is applied to amplify the cDNAs corresponding to the mRNAs by annealing one or more cDNA synthesis primers to several mRNAs in the sample; producing a subtractive hybridisation probe which involves synthesizing a double-stranded cDNA collection from a first mRNA population by the method, where primer 1 is modified by biotin in the 5' end, isolating the biotin-containing single stranded cDNA (sense) by use of streptavidin coated magnetic beads, synthesizing a double-stranded cDNA collection from a second mRNA population according to the method, isolating the non-biotin-containing single stranded cDNA (anti-sense) by use of streptavidin coated magnetic beads, hybridising the sense to the anti-sense cDNA, where an unhybridised sub-population of the anti-sense cDNA is found, isolating the unhybridised sub-population of the anti-sense cDNA by use of streptavidin coated cDNA, and generating a second double-stranded cDNA collection from the unhybridised sub-population by PCR using primer 1 and

CC primer 2; and detecting expression of a gene in a pre-selected cell
 CC population. The method is an improved method for producing amplified
 CC heterogeneous populations of cDNA from limited quantities of RNA or other
 CC nucleic acid. This sequence represents the complement of a poly-A-tail
 CC used to in the production single stranded cDNA.

XX Sequence 18 BP; 0 A; 0 C; 18 T; 0 U; 0 Other;

QY Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 428 TTTTATTATTATTATT 445
 1 TTTTATTATTATTATT 18

RESULT 2122
 ADO81024/c
 ID ADO81024 standard; DNA; 18 BP.

XX ADO81024;

XX 29-JUL-2004 (first entry)

XX Human prion protein microsatellite locus primer #20.

XX gene typing; polymorphic microsatellite loci; PMU;
 XX disease predisposition; microsatellite marker; prion disease;
 XX cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
 XX milk protein; hormone; transcription factor; p17-blue-vector; human;
 XX microsatellite; PCR; primer; ss.

XX Homo sapiens.

XX DE10236711-A1.

XX 26-FEB-2004.

XX 09-AUG-2002; 2002DE-01036711.

XX 09-AUG-2002; 2002DE-01036711.

XX (UYHO-) UNIV HOHENHEIM.

XX Geldermann H, Preuss S, Han Y;

XX WPI; 2004-215730/21.

XX Typing genes that contain polymorphic microsatellite loci, useful for
 PT identifying predisposition to disease, by amplification and determining
 PT length of amplicons.

XX Example 3; Page 34; 64pp; German.

XX The invention describes a method of typing (M1) a gene (I) that has one
 CC or more polymorphic microsatellite loci (PMU). The method comprises: PCR
 CC amplification of at least one DNA region of (I) that includes PMU, using
 CC as template a DNA sample containing at least one segment of (I); and
 CC determining the length of the resulting amplicon(s). Also described are:
 CC a method of determining (M2) microsatellite markers (MM) for
 CC predisposition to a disease, associated with a gene that includes one or
 CC more PMU; and predisposition (M3) of diseases associated with gene that
 CC include PMU. The method is used to identify microsatellite markers, in a
 CC disease-related gene, that are associated with a predisposition to
 CC diseases and for predisposition of such diseases, especially prion diseases
 CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
 CC metabolic diseases; also to type genes that encode milk proteins,
 CC hormones or transcription factors. The method is simpler, quicker and
 CC particularly less expensive than known methods based on sequencing. This
 CC sequence represents a primer used to genotype a region of the human prion
 CC protein (Prp) comprising a polymorphic microsatellite locus.

SQ Sequence 18 BP; 3 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

QY Query Match 1.5%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 632 CAACTCTGTACCCAGGC 649
 Db 18 CCACTCTGTACCCAGAC 1

RESULT 2123
 ADO26684
 ID ADO26684 standard; DNA; 18 BP.

XX ADO26684;

XX 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:77.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYOU) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

XX P-PSDB; ADO26685.

XX Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.
 XX Example 1; SEQ ID NO 77; 86pp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism or interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism or interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part

CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.

CC Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 428 TTTTATTTTATTTT 445
Db 1 TTTTATTTTATTTT 18

RESULT 2124
ADO26682/c
ID ADO26682 standard; DNA; 18 BP.

AC ADO26682;
XX
DT 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:75.

KW phenotype; phenotypic preference; phenotype modulation; leader; ds.

OS Synthetic;

PN WO2004042059-A1.

PD 21-MAY-2004.

PF 10-NOV-2003; 2003WO-AU001487.

PR 08-NOV-2002; 2002US-0425163P.

PA (UYOU) UNIV QUEENSLAND.

PI Frazer IH;

DR WPI; 2004-411519/38.

DR P-PSDB; ADO26683.

PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.

PS Example 1; SEQ ID NO 75; 86bp; English.

XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of

CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism of interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism of interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.

CC Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 428 TTTTATTTTATTTT 445
Db 18 TTTTATTTTATTTT 1

RESULT 2125
ADP45818
ID ADP45818 standard; DNA; 18 BP.

AC ADP45818;

DT 26-AUG-2004 (first entry)

DE Extend primer 10 used to genotype human ICM-1/ICAM-4/ICAM-5 SNP.

KW breast cancer; cytostatic; gene therapy; human;

KW intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;

KW CD54; cell surface glycoprotein p3.58; ICAM-4;

KW Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;

XX ss; primer; PCR; SNP; single nucleotide polymorphism; probe.

OS Homo sapiens.

PN WO2004047623-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037948.

PR 25-NOV-2002; 2002US-0429136P.

PR 24-JUN-2003; 2003US-0490234P.

PA (SEQU-) SEQUENOM INC.

PI Roth RB, Nelson MR, Braun A, Kammerer SM, Remeland R;
WPI; 2004-441051/41.

PT Identifying a subject at risk of breast cancer by detecting the presence
PT of polymorphic variations in the ICM, MAPK10, KIAA061, NMA1 or GALE
PT regions which are associated with breast cancer in a nucleic acid sample

PT from a subject.
XX
XX
PS Example 4; Page 83; 289pp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of one or
CC more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a subject at risk of
CC breast cancer, for early diagnosis, prevention and treatment of breast
CC cancer, possibly via gene therapy, as well as to analyse and predict a
CC response to a breast cancer treatment and in clinical drug trials. The
CC current sequence is that of an extend primer (also described as probe) of
CC the invention which was used to genotype human intercellular adhesion
CC molecule ICAM-1/ICAM-4/ICAM-5 gDNA. ICAM-1 (human rhinovirus receptor, BB2
CC /CD54; cell surface glycoprotein P3.58) has been mapped to chromosomal
CC position 19p13.3-p13.2, ICAM-4 (Landsteiner-Wiener blood group, LW) has
CC been mapped to chromosomal position 19p13.2-cen and ICAM-5
CC (telencephalin) has been mapped to chromosomal position 19p13.2.
XX
SQ Sequence 18 BP; 4 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 394 GCTGGATTACAGCGCTG 411
DB 1 GCTGGATTACAGCGCTG 18
RESULT 2126
ADP86130
ID ADP86130 standard; DNA; 18 BP.
XX
AC ADP86130;
XX
DT 09-SEP-2004 (first entry)
XX
DE Cpg immunostimulatory oligonucleotide #1.
XX
KW Cpg immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO2004053104-A2.
XX
PD 24-JUN-2004.
XX
PF 11-DEC-2003; 2003WO-US039775.
XX
PR 11-DEC-2002; 2002US-0432409P.
PR 25-SEP-2003; 2003US-0506108P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann B;
XX
DR WPI; 2004-487902/46.
XX
PT New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.

XX
XX Example; SEQ ID NO 1; 104pp; English.
XX
CC The invention relates to a class of Cpg immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastoma, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, esophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a Cpg
CC immunostimulatory oligonucleotide.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 428 TTTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 18
RESULT 2127
ADQ30328
ID ADQ30328 standard; DNA; 18 BP.
XX
AC ADQ30328;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human VRI exon 1d transcription factor binding fragment #47.
XX
KW $\frac{3}{4}$ Human VRI receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZP1; NFKappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hyperalgesia; hyperalgesia; neuralgia; myalgia; human.
XX
OS Homo sapiens.
XX
FH WO2004053120-A2.
XX
PN 24-JUN-2004.
XX
PD 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENTHAL GMBH.
XX
PI Weine E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 52; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VRI
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VRI modulator is derived from one or more of
CC positions 221931-223944 of Genbank AF670399, 31673-36359 of AF653116, or

44731-43231 or 36616-33151 of AF166787 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also describes a vector that contains the VR1 modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VR1 receptor by introducing the modulator or the vector into a cell that contains the VR1 gene. The products of the invention are used for detecting a transcription factor from its binding to a regulatory sequence (or a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzyme-linked immunosorbent assay, particularly for diagnosis of diseases associated with overexpression or underexpression of the transcription factor. The region that modulates VR1 receptor expression includes a binding site for a transcription factor, e.g. MZ1, NFkappaB, NFAT or GATA1. The nucleic acids of the invention, or vectors containing them, are used for prevention or treatment of pain, also for treating sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also neuralgia and myalgia, that are associated with activity of the VR1 receptor. This sequence represents a fragment of human VR1 exon 1d DNA which is capable of binding to a transcription factor.

Sequence 18 BP; 1 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

Query Match	1.5%	Score 14.8	DB 1	length 18
Best Local Similarity	88.9%	Pred No. 1.8e+03		
Matches 16	Conservative	0	Mismatches 2	Indels 0
			Gaps	0

QY	200	TGTTGGTCAGGCTGGTCT	217
Db	1	TGTTGGCTAGGCTGGTCT	18

RESULT 2128

ID ABZ45509 standard; DNA; 41 BP

AC ABZ45509

DT 26-JUN-2003 (first entry)

DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2293.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19.

genetic profiling; therapeutic customisation; adverse reaction

XX

XX
XX

FT variation

FT	standard_name= "Single nucleotide polymorphism (SNP)"
FT	

PN WO200252044-A2

PD 04-JUL-2002.

PF 27-DEC-2001; 2001WO-JP011592.

PR 27-DEC-2000; 2000JP-00399443

PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.
 22

PI Nakamura Y, Sekine A, Iida A, Sato S,
yy

WPI; 2002-583571/62.

PT	Identifying individual
PT	of factiveness or

PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.

XX
PS Claim 23; Page 102; 2785pp; English

Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other;

Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other,

Query Match	1.5%;	Score 14.8;	DB 1;	Length 41;
Best Local Similarity	64.7%;	Pred. No. 2.2e+03;		
Matches 22;	Conservative	0;	Mismatches 12;	Indels 0;
			Gaps	0

```

Qy      ;      619 TGAGACAGAGTCTTCAACTCTGTGCACCCCAAGCTGG 652
          |||||  |||||  |||||  |||||  |||||
Db      35  TGAGCCAAGATCTGCCCACTGCAAGTCCAGCTGG 2

```

ABZ46915/c

XX

XX

100

XX

KW polymorphic site; drug evaluation; drug screening; genotyping;

KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds

05 Homo sapiens.

FH Key

FT

FT	variation	replace(21,T)
1		44.22
2		44.22
3		44.22
4		44.22
5		44.22
6		44.22
7		44.22
8		44.22
9		44.22
10		44.22
11		44.22
12		44.22
13		44.22
14		44.22
15		44.22
16		44.22
17		44.22
18		44.22
19		44.22
20		44.22
21		44.22
22		44.22
23		44.22
24		44.22
25		44.22
26		44.22
27		44.22
28		44.22
29		44.22
30		44.22
31		44.22
32		44.22
33		44.22
34		44.22
35		44.22
36		44.22
37		44.22
38		44.22
39		44.22
40		44.22
41		44.22
42		44.22
43		44.22
44		44.22
45		44.22
46		44.22
47		44.22
48		44.22
49		44.22
50		44.22
51		44.22
52		44.22
53		44.22
54		44.22
55		44.22
56		44.22
57		44.22
58		44.22
59		44.22
60		44.22
61		44.22
62		44.22
63		44.22
64		44.22
65		44.22
66		44.22
67		44.22
68		44.22
69		44.22
70		44.22
71		44.22
72		44.22
73		44.22
74		44.22
75		44.22
76		44.22
77		44.22
78		44.22
79		44.22
80		44.22
81		44.22
82		44.22
83		44.22
84		44.22
85		44.22
86		44.22
87		44.22
88		44.22
89		44.22
90		44.22
91		44.22
92		44.22
93		44.22
94		44.22
95		44.22
96		44.22
97		44.22
98		44.22
99		44.22
100		44.22

```

/standard_name= "Single nucleotide polymorphism (SNP)"
FT
....

```

PN WO200252044-A2.
 XX
 PD 04-JUL-2002.
 XX
 PF 27-DEC-2001; 2001WO-JP011592.
 XX
 PR 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX
 PA (RIKE) RIKEN KK.
 PI Nakamura Y, Sekine A, Iida A, Saito S;
 XX
 DR WPI; 2002-583571/62.
 XX
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 PS Claim 23; Page 129; 2785pp; English.
 XX
 CC Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolizing enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy
 CC
 XX
 SQ Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.8; DB 1; Length 41;
 Best Local Similarity 64.7%; Pred. No. 2.2e+03;
 Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 QY 619 TGAGACAGACTCTCAACTGTGTACCCAGGCTGG 652
 DB 35 TGAGCCAAAGATCTCGCAGCTGACGTCAAGCTGG 2
 XX
 RESULT 2130
 AB245508/c
 ID AB245508 standard; DNA; 41 BP.
 XX
 AC AB245508;

XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2292.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 KW genetic profiling; therapeutic customisation; adverse reaction;
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX FH replace(21,A)
 XX FT /*tag= a
 XX FT /standard_name= "single nucleotide polymorphism (SNP)"
 XX
 PN WO200252044-A2.
 XX
 PD 04-JUL-2002.
 XX
 PF 27-DEC-2001; 2001WO-JP011592.
 XX
 PR 27-DEC-2000; 2000JP-00399443.
 PR 02-MAY-2001; 2001JP-00135256.
 PR 27-AUG-2001; 2001JP-00256862.
 XX
 PA (RIKE) RIKEN KK.
 PI Nakamura Y, Sekine A, Iida A, Saito S;
 XX
 DR WPI; 2002-583571/62.
 XX
 PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.
 XX
 PS Claim 23; Page 102; 2785pp; English.
 XX
 CC Sequences AB243217-AB250887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from AB243217-AB250887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolizing enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy
 CC

XX Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.8; DB 1; Length 41;
Best Local Similarity 64.7%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 619 TGAGACGAGTCTCAACTCTGTCCAGGCTGG 652
DB 39 TGAGCCAGATCTCGCCACTGCAGTCCAGCTGG 6
RESULT 2131
ABZ46914/c
ID ABZ46914 standard; DNA; 41 BP.
XX ABZ46914;
AC
DT 26-JUN-2003 (first entry)
XX
DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3698.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction; SNP; ds.
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT variation replace(21,A)
FT /*tag= a
FT /strand name= "Single nucleotide polymorphism (SNP)"
FT replace(25,T)
FT /*tag= b
FT /strand_name= "Single nucleotide polymorphism (SNP)"
FT
FT
PN WO200252044-A2.
XX
PD 04-JUL-2002.
XX
PE 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
PA (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
PI WPI; 2002-563571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 129; 2785pp; English.
PS
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes

CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.8; DB 1; Length 41;
Best Local Similarity 64.7%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 619 TGAGACGAGTCTCAACTCTGTCCAGGCTGG 652
DB 39 TGAGCCAGATCTCGCCACTGCAGTCCAGCTGG 6
RESULT 2132
AAD20847/c
ID AAD20847 standard; DNA; 15 BP.
XX
AC AAD20847;
XX
XX 03-JAN-2002 (first entry)
XX
XX Human CHRN3 gene polymorphism detecting ASO primer #11.
DE
XX Human; cholinergic receptor, nicotinic, beta polypeptide 3; CHRN3;
KW single nucleotide polymorphism; SNP; drug screening; Alzheimer's disease;
KW neurological disorder; gene therapy; genotyping; haplotyping; primer;
XX allele-specific oligonucleotide; ASO; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200175063-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US010277.
XX
XX 03-APR-2000; 2000US-0194162P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA (CHEW/) CHEW A.
PA (CHOI/) CHOI J Y.
PA (KOSH/) KOSH B.
PA (STEP/) STEPHENS J C.
PI Chew A, Choi JY, Koshy B, Stephens JC;
XX
XX WPI; 2001-626425/72.
XX
XX New polynucleotide, useful for studying expression and function of
FT CHRN3, comprises polymorphic variant of cholinergic receptor, nicotinic,
FT beta polypeptide 3 (CHRN3) gene, containing one of polymorphic sites P51
PT -P58.
XX
XX Claim 15; Page 15; 68pp; English.
PS

XX The invention relates to methods for haplotyping cholinergic receptor,
CC nicotinic, beta polypeptide 3 (CHRN3) gene. The invention also provides
CC single nucleotide polymorphisms (SNP) in the human CHRN3 gene.
CC Polymorphic variants of CHRN3 gene is used for screening for candidate
CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3
CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is an allele-specific
CC oligonucleotide (ASO) primer used to detect human CHRN3 gene
CC polymorphisms. Human CHRN3 gene includes 8 polymorphic sites P51-P58
XX

Sequence 15 BP; 3 A; 3 C; 5 G; 3 T; 0 U; 1 Other;

Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 670 TTGGCTCACTGCAC 684
|:|||||
DB 15 TTGGCTCACTGCAC 1

RESULT 2133
AAD20695
ID AAD20695 standard; DNA; 15 BP.
XX
AC AAD20695;
XX
DT 03-JAN-2002 (first entry)
XX

ASO primer #5 used to detect human GPIBA gene polymorphism.

Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;
KM Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;
KM Alzheimer's disease; allele-specific oligonucleotide; polymorphism;
KM primer; human immunodeficiency virus; ASO; ss.

OS Homo sapiens.
XX
PN WO200175065-A2.
XX
PD 11-OCT-2001.
XX

03-APR-2001; 2001WO-US010671.
XX
PR 03-APR-2000; 2000US-0194341P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX

Bentivegna SC, Choi JY, Kliew SE, Koshy B, Parks KE,
PI
XX
DR WPI; 2001-626427/72.
XX

New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are
PT useful for diagnosis and drug discovery for treating Bernard Soulier
PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's
PT disease.
XX
PS Claim 16; Page 14; 66pp; English.
XX

The invention relates to methods for haplotyping glycoprotein Ib
CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method
CC involves determining if the individual has one of the GPIBA haplotypes or
CC haplotype pairs. The methods of the invention are useful for disease
CC diagnosis and in the discovery and development of drugs for treating
CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,
CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The
CC present sequence is allele-specific oligonucleotide (ASO) primer used for
CC detecting human GPIBA gene polymorphisms

XX Sequence 15 BP; 4 A; 6 C; 1 G; 3 T; 0 U; 1 Other;
SQ

Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 379 TCAGCCTCCCAAGT 393
|:|||||
DB 1 TCAGCCTCCCAAGT 15

RESULT 2134
ABL01115
ID ABL01115 standard; DNA; 15 BP.
XX
AC ABL01115;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human AKR1B1 gene polymorphism detection ASO probe SEQ ID NO:12.
XX

Human; aldo-keto reductase family 1 member B1; aldose reductase; sr;
KM AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
KM allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
XX

OS Homo sapiens.
XX
PN WO200179223-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011944.
XX
PR 12-APR-2000; 2000US-0196315P.
XX

(GENA-) GENAISSANCE PHARM INC.
XX
PA
XX
PI Choi JY, Nandabalan K, Rounds E, Sanchis A;
XX
DR WPI; 2002-075056/10.
XX

Novel polymorphic variants of aldo-keto reductase family 1, member b1
PT gene useful in studying expression and function of the protein, useful
PT for screening drugs to treat diseases e.g. diabetes.
XX
PS Claim 16; Page 14; 103pp; English.
XX

The present invention describes an isolated polynucleotide (1) comprising
CC a sequence which is a polymorphic variant (PV) of a reference sequence
CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
CC fragment, having the 22214 base pair sequence given in ABL01105. AKR1B1
CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
CC used in the treatment of diabetes. The human AKR1B1 gene is located on
CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific
CC oligonucleotide (ASO) probes used in the detection of polymorphisms in
CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
CC ABL01221 represent preferred primers used in the detection of
CC polymorphisms in the human AKR1B1 gene
XX

Sequence 15 BP; 3 A; 3 C; 5 G; 3 T; 0 U; 1 Other;
SQ

Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 871 TTACAGGCGTGAACC 885
|:|||||
DB 1 TTACAGGCGTGAACC 15

RESULT 2135

ABL01146
ID ABL01146 standard; DNA; 15 BP.
XX
AC ABL01146;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human AKR1B1 gene polymorphism detection ASO primer SEQ ID NO:43.
XX
KM Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;
KM AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;
KM allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.
XX
OS Homo sapiens.
XX
PN WO200179223-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011944.
XX
PR 12-APR-2000; 2000US-0196315P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Nandabalan K, Rounds E, Sanchis A;
XX WPI; 2002-075056/10.
XX
PT Novel polymorphic variants of aldo-keto reductase family 1, member B1
PT gene useful in studying expression and function of the protein, useful
PT for screening drugs to treat diseases e.g. diabetes.
XX
PS Claim 16; Page 14; 103pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a sequence which is a polymorphic variant (PV) of a reference sequence
CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its
CC fragment, having the 2224 base pair sequence given in ABL01105. AKR1B1
CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be
CC used in the treatment of diabetes. The human AKR1B1 gene is located on
CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific
CC oligonucleotide (ASO) probes used in the detection of polymorphisms in
CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in
CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to
CC ABL01221 represent preferred primers used in the detection of
CC polymorphisms in the human AKR1B1 gene
XX
SQ Sequence 15 BP; 3 A; 2 C; 6 G; 3 T; 0 U; 1 Other;
XX
Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 395 CTGGGATTACAGCG 409
Db 1 CTGGGATTACAGG 15
XX
RESULT 2136
AAD26858
ID AAD26858 standard; DNA; 15 BP.
XX
AC AAD26858;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human GPR4 gene polymorphism detecting ASO primer #17.
XX
KM Human; G-protein coupled receptor 4; GPR4; haplotyping; polymorphism;
KM allele-specific oligonucleotide; ASO; primer; ss.
XX
OS Homo sapiens.

XX
PN WO200187904-A2.
XX
PD 22-NOV-2001.
XX
PF 09-MAY-2001; 2001WO-US015097.
XX
PR 17-MAY-2000; 2000US-0204928P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Duda AE, Kazemi A, Koshy B;
XX WPI; 2002-097579/13.
XX
PT Haplotyping, (H1), the G-protein coupled receptor 4 (GPR4) gene of an
PT individual, comprising determining which haplotype an individual.
XX
PS Claim 15; Page 13; 61pp; English.
XX
CC The invention relates to G-protein coupled receptor 4 (GPR4) gene
CC variants. The data about the GPR4 polynucleotides and polypeptides and
CC the polymorphisms associated with them are useful for haplotyping at the
CC GPR4 locus. Allele-specific oligonucleotide (ASO) is useful as probes and
CC primers for assaying a polymorphism in GPR4 gene. The present sequence is
CC an ASO primer used to detect human GPR4 gene polymorphism
XX
SQ Sequence 15 BP; 4 A; 2 C; 6 G; 2 T; 0 U; 1 Other;
XX
Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 728 GAGTACTGGGACTA 742
Db 1 GAGTACTGGGACTA 15
XX
RESULT 2137
ABV99766/c
ID ABV99766 standard; DNA; 15 BP.
XX
AC ABV99766;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human PKFB2 allele specific oligonucleotide probe #4.
XX
KM Human; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2; PKFB2;
KM cytosolic; antidiabetic; gene therapy; cancer; diabetes; ss; ASO;
KM allele specific oligonucleotide; probe; polymorphism.
XX
OS Homo sapiens.
XX
PN WO200194363-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018458.
XX
PR 07-JUN-2000; 2000US-0209935P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kazemi A, Koshy B;
XX WPI; 2002-566434/60.
XX
PT New 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (PKFB2) gene
PT variants, for improving efficiency and reliability in the development of
PT drugs for treating diseases associated with PKFB2 activity e.g. cancer.
XX
PS Claim 16; Page 13; 95pp; English.

XX The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose
 CC -2,6-biphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has
 CC cytosolic and antidiabetic activity. The polynucleotides may have a use
 CC in gene therapy. The identified candidate agents targeting PFKFB2, are
 CC useful for treating cancer and diabetes. The methods of the invention are
 CC useful for improving the efficiency and reliability of several steps in
 CC the discovery and development of drugs for treating diseases associated
 CC with PFKFB2 activity. The present sequence represents a allele specific
 CC oligonucleotide (ASO) probe used in the invention to detect PFKFB2 gene
 CC polymorphisms
 XX
 SQ Sequence 15 BP; 2 A; 1 C; 9 G; 2 T; 0 U; 1 Other;
 XX
 Query Match 1.5%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.6e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 681 CAACCTCTGCTCTCC 695
 DB 15 CAACCTCTGCTCTCC 1
 RESULT 2138
 ABL51983/C
 ID ABL51983 standard; DNA; 15 BP.
 XX
 AC ABL51983;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:31.
 XX
 KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
 KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
 KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
 KW haplotyping; genotyping; respiratory inflammatory disease;
 KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 14
 FT /tag= a
 FT /note= "polymorphic site indicated by an ambiguity base"
 XX
 PN WO200222652-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 17-SEP-2001, 2001WO-US042217.
 XX
 PR 15-SEP-2000, 2000US-0232895P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Han J, Kliehm SE, Sausker EA;
 XX
 DR WPI, 2002-393942/42.
 XX
 PT Novel genetic variants of soluble carrier family 18 (vesicular
 PT monamine), member 2 gene useful for screening drugs to treat diseases
 PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.
 XX
 PS Claim 17; Page 14; 183pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (1) having a
 CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
 CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
 CC sequence (SS) of 40023 bp (see ABL51983), and defined by a corresponding
 CC set of polymorphisms whose locations and identities are given in the
 CC specification; or a sequence (S2) complementary to (S1). (1) has
 CC antiinflammatory and neuroleptic activities, and can be used in gene

CC therapy. Methods from the present invention can be used for haplotyping
 CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
 CC as the vesicular monoamine transporter (VMAT2). (1) is useful in studying
 CC the expression and function of SLC18A2, and in expressing the SLC18A2
 CC protein for use in screening for candidate drugs to treat diseases
 CC related to SLC18A2 activity and in studying the effect of the variation
 CC on the biological activity of SLC18A2 as well as on the binding affinity
 CC of candidate drugs targeting SLC18A2 for the treatment of respiratory
 CC inflammatory diseases such as neuropsychiatric disorders involving
 CC monoaminergic brain systems. The present sequence represents an allele
 CC specific oligonucleotide (ASO) primer for human SLC18A2, which is given
 CC in the present invention
 XX
 SQ Sequence 15 BP; 4 A; 4 C; 4 G; 2 T; 0 U; 1 Other;
 XX
 Query Match 1.5%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.6e+03;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 209 GGCTGTCTCGAACT 223
 DB 15 GGCTGTCTCGAACT 1
 RESULT 2139
 ABR32790/C
 ID ABR32790 standard; DNA; 15 BP.
 XX
 AC ABR32790;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human APPBP1 gene, allele-specific oligonucleotide #20.
 XX
 KW Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;
 KW Alzheimer's disease; transgenic animal; platelet aggregation;
 KW single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200202820-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 02-JUL-2001, 2001WO-US020951.
 XX
 PR 30-JUN-2000, 2000US-021551P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Anastasio AE, Chew A, Choi JV, Kazemi A, Koshy B, Sausker EA;
 XX
 DR WPI, 2002-164539/21.
 XX
 PT Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene
 PT polymorphic variants, useful e.g. in studying the expression and function
 PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.
 XX
 PS Claim 17; Page 13; 104pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a sequence
 CC which is a polymorphic variant of a reference sequence for the amyloid
 CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its
 CC fragment. The polymorphic variants are useful in studying the expression
 CC and function of APPBP1, in expressing APPBP1 protein for use in screening
 CC for candidate drugs to treat diseases related to APPBP1 activity, in
 CC studying the effect of the variation on the biological activity of
 CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for
 CC the treatment of disorders such as Alzheimer's disease. The haplotyping
 CC methods are useful in validating APPBP1 as a candidate target for
 CC treating a specific condition or disease predicted to be associated with
 CC APPBP1 activity, or in the design of clinical trials of candidate drugs

CC for treating a specific condition or disease associated with APPBP1
CC activity. The transgenic animals are useful for studying expression of
CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against APPBP1 protein, and for testing the efficacy of
CC therapeutic agents and compounds for disorders related to platelet
CC aggregation in a biological system. ABK32771-ABK32327 represent human
CC APPBP1 gene allele-specific oligonucleotides used in the method of the
CC invention

SO Sequence 15 BP; 2 A; 2 C; 7 G; 3 T; 0 U; 1 Other;

Query Match 1.5%; Score 14.6; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.6e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 376 GCCTGAGCTCCCAA 390
Db 15 GCTCAGCTCCCAA 1

RESULT 2140

ABK81778
ID ABK81778 standard; DNA; 15 BP.

AC ABK81778;

DT 13-AUG-2002 (first entry)

DE Human CHRM5 gene polymorphism detection ASO primer #4.

XX Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;

KM single nucleotide polymorphism; SNP; allele-specific oligonucleotide;

KW ASO; primer; ss.

XX Homo sapiens.

OS WO200232924-A2.

PN 25-APR-2002.

PF 11-OCT-2001; 2001WO-US032022.

PR 19-OCT-2000; 2000WO-US029071.

XX (GENA-) GENAISANCE PHARM INC.

PI Bieganski KM, Chew A, Choi JY, Denton RR, Nandabalan K;

PI Sausker EA, Stephens JC;

XX WPI; 2002-435523/46.

DR Novel cholinergic receptor, muscarinic 5 polynucleotide useful

PT therapeutically and in screening for candidate drug to treat diseases

PT related to the receptor activity.

PS Claim 14; Page 13; 72pp; English.

XX The present invention relates to a new cholinergic receptor, muscarinic 5

CC (CHRM5) polynucleotide comprising a sequence which is a polymorphic

CC variant for a reference sequence for the CHRM5 gene or its fragment, or a

CC polymorphic variant of a reference sequence for a CHRM5 cDNA or its

CC fragment. The invention is useful in drug screening assays. The molecules

CC of the invention are useful in studying the expression and function of

CC CHRM5, and in expressing CHRM5 protein for use in screening for candidate

CC drugs to treat diseases related to CHRM5 activity. The methods of the

CC invention are useful in developing diagnostic tests and therapeutic

CC treatments. The method is also useful in the design of clinical trials of

CC candidate drugs for treating specific condition or disease associated

CC with CHRM5 activity and is useful in determining whether an individual

CC has one of the haplotypes or one of the haplotype pairs. The invention is

CC useful in a variety of diagnostic and prognostic formats and therapeutic

CC methods. The invention is also useful in genotyping and/or haplotyping

CC the CHRM5 gene in an individual. The present nucleic acid sequence

CC represents one of a collection of allele-specific oligonucleotide (ASO)

CC primers (ABK81775-ABK81794) that were used in the invention to detect

CC polymorphisms in the human CHRM5 gene

XX

SO Sequence 15 BP; 2 A; 8 C; 2 G; 2 T; 0 U; 1 Other;

Query Match 1.5%; Score 14.6; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.6e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 847 CCTGGCCTCCCAA 861
Db 1 CCTGGCCTCCCAA 15

RESULT 2141

ABK81766/c
ID ABK81766 standard; DNA; 15 BP.

AC ABK81766;

DT 13-AUG-2002 (first entry)

DE Human CHRM5 gene polymorphism detection ASO probe #2.

XX Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;

KM single nucleotide polymorphism; SNP; allele-specific oligonucleotide;

KW ASO; probe; ss.

XX Homo sapiens.

OS WO200232924-A2.

PN 25-APR-2002.

PF 11-OCT-2001; 2001WO-US032022.

PR 19-OCT-2000; 2000WO-US029071.

XX (GENA-) GENAISANCE PHARM INC.

PI Bieganski KM, Chew A, Choi JY, Denton RR, Nandabalan K;

PI Sausker EA, Stephens JC;

XX WPI; 2002-435523/46.

DR Novel cholinergic receptor, muscarinic 5 polynucleotide useful

PT therapeutically and in screening for candidate drug to treat diseases

PT related to the receptor activity.

PS Claim 14; Page 13; 72pp; English.

XX The present invention relates to a new cholinergic receptor, muscarinic 5

CC (CHRM5) polynucleotide comprising a sequence which is a polymorphic

CC variant for a reference sequence for the CHRM5 gene or its fragment, or a

CC polymorphic variant of a reference sequence for a CHRM5 cDNA or its

CC fragment. The invention is useful in drug screening assays. The molecules

CC of the invention are useful in studying the expression and function of

CC CHRM5, and in expressing CHRM5 protein for use in screening for candidate

CC drugs to treat diseases related to CHRM5 activity. The methods of the

CC invention are useful in developing diagnostic tests and therapeutic

CC treatments. The method is also useful in the design of clinical trials of

CC candidate drugs for treating specific condition or disease associated

CC with CHRM5 activity and is useful in determining whether an individual

CC has one of the haplotypes or one of the haplotype pairs. The invention is

CC useful in a variety of diagnostic and prognostic formats and therapeutic

CC methods. The invention is also useful in genotyping and/or haplotyping

CC the CHRM5 gene in an individual. The present nucleic acid sequence

CC

Query Match 1.5%; Score 14.6; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 383 CCTCCCAAGTCTG 397
DB 15 CCTCCCAAGTCTG 1

RESULT 2142
ABK81777/c
ID ABK81777 standard; DNA; 15 BP.

XX ABK81777;

XX 13-AUG-2002 (first entry)

XX Human CHRMS gene polymorphism detection ASO primer #3.

XX Human; cholinergic receptor muscarinic 5; CHRMS; genotyping; haplotyping;

XX single nucleotide polymorphism; SNP; allele-specific oligonucleotide;

XX ASO; primer; ss.

XX Homo sapiens.

XX MO200232924-A2.

XX 25-APR-2002.

XX 11-OCT-2001; 2001WO-US032022.

XX 19-OCT-2000; 2000WO-US029071.

XX (GENA-) GENA155555 PHARM INC.

XX Blegiecki KM, Chew A, Choi JY, Denton RR, Nandabalan K;

XX Saubner EA, Stephens JC;

XX WPI; 2002-435523/46.

XX Novel cholinergic receptor, muscarinic 5 polynucleotide useful

XX therapeutically and in screening for candidate drug to treat diseases

XX related to the receptor activity.

XX Claim 14; Page 13; 72pp; English.

XX The present invention relates to a new cholinergic receptor, muscarinic 5

XX (CHRMS) polynucleotide comprising a sequence which is a polymorphic

XX variant for a reference sequence for the CHRMS gene or its fragment, or a

XX polymorphic variant of a reference sequence for a CHRMS cDNA or its

XX fragment. The invention is useful in drug screening assays. The molecules

XX of the invention are useful in studying the expression and function of

XX CHRMS, and in expressing CHRMS protein for use in screening for candidate

XX drugs to treat diseases related to CHRMS activity. The methods of the

XX invention are useful in developing diagnostic tests and therapeutic

XX treatments. The method is also useful in the design of clinical trials of

XX candidate drugs for treating specific condition or disease associated

XX with CHRMS activity and is useful in determining whether an individual

XX has one of the haplotypes or one of the haplotype pairs. The invention is

XX useful in a variety of diagnostic and prognostic formats and therapeutic

XX methods. The invention is also useful in genotyping and/or haplotyping

XX the CHRMS gene in an individual. The present nucleic acid sequence

XX represents one of a collection of allele-specific oligonucleotide (ASO)

XX primers (ABK81775-ABK81794) that were used in the invention to detect

XX polymorphisms in the human CHRMS gene

XX Sequence 15 BP; 4 A; 5 C; 1 G; 4 T; 0 U; 1 Other;

XX Query Match 1.5%; Score 14.6; DB 1; Length 15;

XX Best Local Similarity 93.3%; Pred. No. 1.6e+03;

XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 389 AAAGTCTGGGATTA 403
DB 15 AAAGTCTGGGATTA 1

RESULT 2143
AAQ45257
ID AAQ45257 standard; DNA; 35 BP.

XX AAQ45257;

XX 25-MAR-2003 (revised)

XX 28-OCT-1994 (first entry)

XX Alu primer PDJ34 to amplify Yeast Artificial Chromosome DNA.

XX Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR;

XX sequence tagged site; genetic disorder; diagnosis; abnormality;

XX Prader-Willi; Angelman; Beckwith-Wiedemann; syndrome; ss.

XX Synthetic.

XX WO9406936-A1.

XX 31-MAR-1994.

XX 10-SEP-1993; 93WO-US008501.

XX 11-SEP-1992; 92US-00943639.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Althart SD, Multirangura A, Ledbetter DH;

XX WPI; 1994-118484/14.

XX Diagnosis of genetic disorders associated with chromosomal abnormalities

XX and uniparental disomy, e.g. Prader-Willi; Angelman syndrome - using in

XX situ hybridisation using probes spanning the IR4-3R or GABRB3 regions.

XX Example 5; Page 32; 91pp; English.

XX The Alu primers PDJ34 and 2484 (AAQ45257 and AAQ45258) were used to

XX amplify DNA from Yeast artificial chromosomes as part of a cloning

XX procedure to isolate probes for specific chromosomal abnormalities. In

XX particular, probes to diagnose Prader-Willi; Angelman Syndrome were

XX identified. The majority of PWS/Angelman patients are deleted for a

XX common set of markers including MDJ4, IR4-3R, TD189-1 and TD3- 21.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;

XX Query Match 1.5%; Score 14.6; DB 1; Length 35;

XX Best Local Similarity 51.5%; Pred. No. 2.3e+03;

XX Matches 17; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 392 GTCGTGGATTCACAGCGTCGCTGCTGG 424

DB 2 GAGCTRWGATYRRCAYTGACCTCAGCTCG 34

RESULT 2144

ABK93847

ID ABK93847 standard; DNA; 35 BP.

XX ABK93847;

XX 02-MAY-2002 (first entry)

XX Human GAS1 PCR primer SEQ ID NO:5.

XX Human; GAS1; gene amplified in squamous cell carcinoma 1; cancer;

XX chromosome 9; chromosome 9p23-24; cell differentiation; gene therapy;

XX

KW cell proliferation; PCR primer; ss.
XX Homo sapiens.
XX
XX WO200196566-A1.
XX
XX 20-DEC-2001.
XX
XX 12-JUN-2001; 2001WO-JP004959.
XX
XX 12-JUN-2000; 2000JP-00174946.
XX
XX (SAKA) OTSUKA PHARM CO LTD.
XX
XX Inazawa J, Imoto I;
XX
XX WPI; 2002-090209/12.
XX
XX Gene GAS1 amplified in squamous cell carcinoma and its expression
PT product for diagnosis investigation and treatment of disorders involving
PT cell proliferation such as cancer.
XX
XX Example 1; Page 77; 82pp; Japanese.
XX
XX The present invention describes human GAS1 (gene amplified in squamous
CC cell carcinoma 1). GAS1 has been located to the p23-24 region of human
CC chromosome 9. GAS1 can be used in the diagnosis and investigation of
CC diseases with which cell differentiation and proliferation are
CC associated, such as cancer. It can also be used in gene therapy of these
CC diseases, and screening substances for their ability to modify the
CC expression of GAS1 and for use as drugs. The present sequence represents
CC a PCR primer for human GAS1, which is used in an example from the
CC present invention
XX
XX Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;
SQ
Query Match 1.5%; Score 14.6; DB 1; Length 35;
Best Local Similarity 51.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
OY 392 GTGCTGGATTACAGCGCTGACGCCGCTGG 424
DB 2 GAGCYRWGATYRRCAYTGCACTCCAGCCTGG 34
RESULT 2145
ADK41334
ID ADK41334 standard; DNA; 40 BP.
XX
XX ADK41334;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human chromosome 19 single nucleotide polymorphism detecting probe #22.
DE
XX
XX sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;
KW single nucleotide polymorphism; SNP; probe.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key location/Qualifiers
FH variation replace(20,G)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
XX WO2004003229-A2.
XX
XX 08-JAN-2004.
XX
XX 27-JUN-2003; 2003WO-DK000448.
XX
XX 27-JUN-2002; 2002DK-00001005.

PR 07-OCT-2002; 2002DK-00001500.
PR 25-FEB-2003; 2003DK-00000289.
PR 29-APR-2003; 2003DK-00000639.
XX
XX (UYAA-) UNIV AARHUS.
PA (ARBE-) ARBEJDSMILJO INST NAT INST OCCUPA.
XX
XX Nexo BA, Vogel U, Rockenbauer E, Bukowy ZK,
XX
XX WPI; 2004-142878/14.
XX
XX Estimating the disease risk or prognosis of an individual by sequence
PT polymorphism analysis.
XX
XX Claim 18; SEQ ID NO 92; 145pp; English.
XX
XX The invention relates to a novel method of estimating disease risk or
CC prognosis of an individual by sequence polymorphism analysis, especially
CC polymorphisms in the human chromosome 19q. The invention further relates
CC to: estimating a treatment response of an individual suffering from
CC cancer to a disease treatment; a primer or probe for use in the method of
CC estimating the disease risk or prognosis of an individual or for
CC estimating a treatment response of an individual suffering from cancer to
CC a disease treatment; an antibody directed to an epitope of a RAI gene
CC product; and a kit for use in the method of estimating the disease risk
CC or prognosis of an individual or for estimating a treatment response of
CC an individual suffering from cancer to a disease treatment, comprising at
CC least one primer or probe and optionally amplifying means for nucleic
CC acid amplification. The novel method is useful for estimating the disease
CC risk or prognosis of an individual or for estimating a treatment response
CC of an individual suffering from cancer to a disease treatment. This
CC polynucleotide sequence represents a probe used for detecting single
CC nucleotide polymorphisms in the DNA of human chromosome 19 of the
CC invention.
XX
XX Sequence 40 BP; 8 A; 13 C; 12 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.6; DB 1; Length 40;
Best Local Similarity 62.2%; Pred. No. 2.2e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY 388 CAAAGTGTGGATTACAGCGGTGACGCCGCTGG 424
DB 3 CAGTGAAGTGAATGCGCACCACTGCACTCCAGCCTGG 39
RESULT 2146
ABZ43589
ID ABZ43589 standard; DNA; 41 BP.
XX
XX ABZ43589;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human cerebroside transferase CST gene polymorphic site, #373.
DE
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FH variation replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.
PR 02-MAY-2001; 2001JP-00135256.
PR 27-AUG-2001; 2001JP-00256862.
XX
PA (RIKEN) RIKEN KK.
XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2002-583571/62.
DR
XX
PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 70; 27855p; English.
XX
CC Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.6; DB 1; Length 41;
Best Local Similarity 69.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 260 AAGTCTAGATACAGACTGCGCAACATG 288
DB 13 AGGAGTTGCGAGACCAGCTGCGCAACATG 41
RESULT 2147
AB249741
ID AB249741 standard; DNA; 41 BP.
XX
AC AB249741;
XX
DT 26-JUN-2003 (first entry)
XX
DX Human cerebroside transferase CST gene polymorphic site, #6523.
XX

KW Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(21,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN) RIKEN KK.
XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX WPI; 2002-583571/62.
XX
PT Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 197; 27855p; English.
XX
CC Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphism data, particularly that relating to single nucleotide
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolizing enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.6; DB 1; Length 41;
Best Local Similarity 69.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

XX
DR WPI; 2004-180052/17.
XX
PT New nucleic acid comprising a single nucleotide polymorphism at a
PT specific location, useful in paternity testing, genetic analysis or
PT diagnosing, preventing or treating cardiovascular diseases e.g.
PT angioedema or angina pectoris.
XX
PS Claim 3; SEQ ID NO 59; 376pp; English.
XX
CC The invention relates to an isolated nucleic acid (I) derived from a
CC human gene encoding a protein, such as the C1, S subcomponent protein
CC (C1S), the alanyl aminopeptidase protein (ANPEP), the mepirin A, beta
CC protein (MEP1B), the aminopeptidase P-like protein (XPN-PPPL), the tissue
CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein
CC (XPNPEP2), the soluble guanylate cyclase 1, alpha-2 subunit protein
CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
CC including the alleles, reference alleles and alternate alleles of the
CC single nucleotide polymorphisms, listed in the specification. The
CC polymorphic position resides in a (non)coding position within the genomic
CC sequence of the gene. The polymorphic position residing in a coding
CC position results in a missense or silent mutation of the translated
CC product of the gene. The polymorphic position residing in a non-coding
CC position resides within the untranslated region or an intronic region of
CC the gene. Constructing haplotypes using the nucleic acids above further
CC comprises using the haplotypes to identify an individual for the presence
CC of a disease phenotype, and correlating the presence of the disease
CC phenotype with the haplotype. The disease phenotype is angioedema or an
CC angioedema-like disorder. The nucleic acids, primers and probes are
CC useful in phenotype correlations, paternity testing, medicine and genetic
CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
CC preventing or treating cardiovascular diseases, e.g. angioedema, angina
CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
CC stroke, embolism, thrombosis, coronary artery disease or
CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
CC present sequence represents a human single nucleotide polymorphism (SNP)
CC of the invention.
XX
SQ Sequence 41 BP; 9 A; 13 C; 11 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.6; DB 1; Length 41;
Best Local Similarity 62.2%; Pred. No. 2.2e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 388 CAAAGTCTGGGATTACAGCGTCGACGCTGCTGG 424
DB 5 CAGTGAGCTGAGATCGACCACTGCACCTCGAGCTGG 41
RESULT 2150
AA176192
ID AA176192 standard; DNA; 51 BP.
XX
AC AA176192;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3133.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
OS Homo sapiens.
XX
OS
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US032758.
XX

PR 30-NOV-1999; 99US-0168138P.
PR 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
PS Claim 1; Page 1009; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175332 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 14 A; 16 C; 12 G; 9 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.6; DB 1; Length 51;
Best Local Similarity 69.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 260 AAGTCTAGATRCAGAGCTGGCCACCATG 288
DB 2 AGGAGTTCGAGACCGAGCTGGCCACCATG 30
RESULT 2151
AAH89507/c
ID AAH89507 standard; DNA; 51 BP.
XX
AC AAH89507;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 288.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000322.
XX
PR 07-JAN-2000; 2000US-0174962P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
XX

DR P-PSDB; AAM00390.
 XX
 XX Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes.
 XX
 XX Claim 1; Page 186; 475bp; English.
 XX
 XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC scleroderma, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a polymorphism-containing
 CC oligonucleotide fragment of the invention
 XX
 SQ Sequence 51 BP; 11 A; 13 C; 15 G; 12 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.6; DB 1; Length 51;
 Best Local Similarity 69.0%; Pred. No. 2.1e+03;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 260 AAGTGTAGATACGAGCTGCGCCACATG 288
 Db 48 AGGAGTTTGAGACCGCTGCGCCACATG 20
 RESULT 2152
 AAI76193
 ID AAI76193 standard; DNA; 51 BP.
 XX
 AC AAI76193;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:3134.
 XX
 KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KM protein therapy; vaccine; probe; diagnostic assay; detection;
 KM quantitation; restorative therapy; polymorphic; de.
 XX
 OS Homo sapiens.
 OS
 PN WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US032758.
 XX
 PR 30-NOV-1999; 99US-0168138P.
 PR 29-NOV-2000; 2000US-00726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 PI
 XX WPI; 2001-356160/37.
 DR
 XX Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy.
 PT
 XX Claim 1; Page 1009; 2653bp; English.
 PS
 XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For
 CC example, (I) may be used to treat disorders by rectifying mutations or
 CC deletions in a patient's genome that affect the activity of polypeptides
 CC by expressing inactive proteins or to supplement the patient's own
 CC production of polypeptide. Additionally, (I) and its complementary
 CC sequences may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The
 CC polypeptides encoded by (I) may be used as antigens in the production of
 CC antibodies specific for polymorphic polypeptides. The antibodies may also
 CC be used to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of polymorphic
 CC polypeptides in samples
 XX
 SQ Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.6; DB 1; Length 51;
 Best Local Similarity 69.0%; Pred. No. 2.1e+03;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 260 AAGTGTAGATACGAGCTGCGCCACATG 288
 Db 2 AGGAGTTTGAGACCGCTGCGCCACATG 30
 RESULT 2153
 AAQ95283
 ID AAQ95283 standard; DNA; 16 BP.
 XX
 AC AAQ95283;
 XX
 DT 09-FEB-1996 (first entry)
 XX
 DE Simple tandem repeat (STR) PCR primer WG294B.
 XX
 KM Simple tandem repeat; STR; treatment; genetic; diagnosis;
 KM characterisation; mapping; linkage studies; analysis; alleles;
 KM PCR primer WG294B; wg294; ss.
 XX
 OS Synthetic.
 OS
 PN WO9517522-A2.
 XX
 PD 29-JUN-1995.
 XX
 PF 21-DEC-1994; 94WO-GB002789.
 XX
 PR 21-DEC-1993; 93GB-00026052.
 XX
 PA (UYLE-) UNIV LEICESTER.
 XX
 PI Jeffreys AJ, Armour J;
 PI
 XX WPI; 1995-240682/31.
 DR
 XX Identifying simple tandem repeat loci in DNA - by screening DNA library
 PT to enrich for fragments contg. the repeats before cloning and
 PT rescreening, also simple tandem repeats for treatment or diagnosis.
 XX
 XX Claim 25; Page 39; 51pp; English.
 PS
 XX AAQ95282 and AAQ95283 are a primer pair for the PCR amplification of the
 CC simple tandem repeat (STR) corresponding to wg294. The STR can be used
 CC for treatment and diagnosis in human and veterinary medicine, partic. for
 CC genetic characterisation, mapping, linkage studies and analysis/diagnosis
 CC of acquired disease alleles
 XX
 SQ Sequence 16 BP; 1 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGG 852
 DB 1 GATCTGCTGCTCGG 16

RESULT 2154
 AAD12238/c
 ID AAD12238 standard; DNA; 16 BP.

XX AAD12238;

DT 25-SEP-2001 (first entry)

XX Human CYP450 2C19 CDNA upper strand sequencing primer 1064U.

XX Human; gene structure; phenotypic expression; guanosine cofactor;

KM germline variation analysis; exon-intron boundary; Tetrahymena rRNA;

KW cytochrome P450 2C19; CYP450 2C19; primer; ss.

XX Homo sapiens.

PN WO200153529-A2.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US001461.

XX 20-JAN-2000; 2000US-00488127.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Thomann H, Fitzgerald MS;

XX WPI; 2001-465380/50.

XX Determining structure of genes whose sequence is not known from CDNA, by

XX sequencing the gene or gene across exon-intron boundaries using evenly

XX spaced primers comprising nucleic acids that hybridize to the CDNA of

XX gene.

XX Example 2; Page 27; 81pp; English.

XX The present invention relates to a method for determining gene structure

XX when the genomic sequence is unknown. The method involves sequencing the

XX gene across exon-intron boundaries using evenly spaced primers or tiled

XX primers. The tiled primers comprises nucleic acids that hybridize to the

XX known CDNA sequence of the gene at about 100-300 base intervals and the

XX gene comprises the template. Gene structure can be determined without the

XX need to sequence the entire gene. The method provides information

XX necessary to determine gene structure and phenotypic expression without

XX the need to sequence entire chromosomal copy of the gene or fragment. The

XX methods are useful in genome sequence variation analysis. The method is

XX also useful for determining the boundaries between regions of nucleic

XX acids that were separated by intervening sequence, and also for

XX determining boundaries present in genes containing group 1 type introns

XX such as Tetrahymena rRNA, where self-splicing occurs in the presence of

XX guanosine cofactor. The present sequence is a primer used for sequencing

XX human CYP450 2C19 CDNA related to the invention

XX Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 822 ATCTCTGACCTGTG 837

DB 16 ATCTCTGACCTGTG 1

RESULT 2155

ADD28838/c

ID ADD28838 standard; DNA; 16 BP.

XX ADD28838;
 AC 15-JAN-2004 (first entry)
 XX
 DT
 XX

DE Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:457.

XX molecular sub-typing system; Escherichia coli;

KM variable number tandem repeat; VNTR; genetic data;

XX epidemiological database; research; gene; de.

XX Escherichia coli.

XX WO2003050269-A2.

XX 19-JUN-2003.

XX 11-DEC-2002; 2002WO-US039914.

XX 11-DEC-2001; 2001US-0339687P.

XX (UNIV-) UNIV ARIZONA.

XX (KEIM/) KEIM P.

XX (KEYS/) KEYS C.

XX Keim P, Keys C;

XX WPI; 2003-864934/80.

XX Molecular sub-typing system for Escherichia coli, comprises observing and

XX recording variable number tandem repeat arrays in an Escherichia coli DNA

XX sample.

XX Claim 7; SEQ ID NO 457; 166pp; English.

XX The present invention describes a molecular sub-typing system (S) for

XX Escherichia coli, which comprises observing and recording variable number

XX tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also

XX described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers

XX (II) for amplifying (1); (3) amplicon comprising (II) and a locus

XX comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails

XX (III) for multiplex amplification of (1) comprising two or more primers

XX of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR

XX comprising primers for VNTR loci in E. coli, and amplifying reagents for

XX maintaining hybridisation and amplification condition in a PCR instrument

XX with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.

XX coli O157:H7 strains by multiplex, comprising (III), and amplifying

XX reagents for maintaining hybridisation and amplification condition in a

XX multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub

XX -typing (MT) an E. coli strain, comprising: (a) obtaining one or more

XX primers for amplifying loci comprising VNTR, where the primers have an

XX observable indicator; (b) obtaining single-stranded sample DNA from the

XX E. coli sample to be subtyped; (c) combining the primers, the sample DNA

XX and amplifying reagents under hybridising and amplifying conditions in a

XX PCR instrument to form amplicons comprising the primers and the VNTR; (d)

XX separating the amplicons by size; (e) evaluating the numbers and sizes of

XX separated amplicons; and (f) comparing the evaluation to an evaluation of

XX amplicons obtained by PCR from a known E. coli strain. Mt is useful for

XX producing discrete genetic data for an epidemiological database. (1) is

XX useful as a research tool. (S) is useful for subtyping pathogenic E.

XX coli. The present sequence represents an E. coli VNTR loci related

XX amplicon sequence which is used in the exemplification of the present

XX invention.

XX Sequence 16 BP; 13 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 443

DB 16 TTTTATTTTATTTT 1

RESULT 2157
ADD28836/c
ID ADD28836 standard; DNA; 16 BP.
XX
AC ADD28836;
XX
DT 15-JAN-2004 (first entry)
XX
DE Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:458.
XX
KW molecular sub-typing system; Escherichia coli;
KM variable number tandem repeat; VNTR; genetic data;
KW epidemiological database; research; gene; ds.
XX
OS Escherichia coli.
XX
PN W02003050269-A2.
XX
PD 19-JUN-2003.
XX
PF 11-DEC-2002; 2002MO-US039914.
XX
PR 11-DEC-2001; 2001US-0339687P.
XX
PA (UYAR-) UNIV ARIZONA.
PA (KEIM/) KEIM P.
PA (KEYS/) KEYS C.
XX
PI Keim P, Keys C;
PI
DR WPI; 2003-864934/80.
XX
PT Molecular sub-typing system for Escherichia coli, comprises observing and
PT recording variable number tandem repeat arrays in an Escherichia coli DNA
PT sample.
XX
PS Claim 7; SEQ ID NO 458; 166pp; English.
XX
CC The present invention describes a molecular sub-typing system (S) for
CC Escherichia coli, which comprises observing and recording variable number
CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers
CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
CC (III) for multiplex amplification of (I) comprising two or more primers
CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
CC maintaining hybridisation and amplification condition in a PCR instrument
CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying
CC reagents for maintaining hybridisation and amplification condition in a
CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub
CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
CC primers for amplifying loci comprising VNTR, where the primers have an
CC observable indicator; (b) obtaining single-stranded sample DNA from the
CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
CC and amplifying reagents under hybridising and amplifying conditions in a
CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
CC separating the amplicons by size; (e) evaluating numbers and sizes of
CC separated amplicons; and (f) comparing the evaluation to an evaluation of
CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
CC producing discrete genetic data for an epidemiological database. (I) is
CC useful as a research tool. (S) is useful for subtyping pathogenic E.
CC coli. The present sequence represents an E. coli VNTR loci related
CC amplicon sequence which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 16 BP; 3 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. NO. 1.7e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 428 TTTTATTTTATTTT 443
DB 1 TTTTATTTTATTTTAT 16
RESULT 2157
ADD28836/c
ID ADD28836 standard; DNA; 16 BP.
XX
AC ADD28836;
XX
DT 15-JAN-2004 (first entry)
XX
DE Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:455.
XX
KW molecular sub-typing system; Escherichia coli;
KM variable number tandem repeat; VNTR; genetic data;
KW epidemiological database; research; gene; ds.
XX
OS Escherichia coli.
XX
PN W02003050269-A2.
XX
PD 19-JUN-2003.
XX
PF 11-DEC-2002; 2002MO-US039914.
XX
PR 11-DEC-2001; 2001US-0339687P.
XX
PA (UYAR-) UNIV ARIZONA.
PA (KEIM/) KEIM P.
PA (KEYS/) KEYS C.
XX
PI Keim P, Keys C;
PI
DR WPI; 2003-864934/80.
XX
PT Molecular sub-typing system for Escherichia coli, comprises observing and
PT recording variable number tandem repeat arrays in an Escherichia coli DNA
PT sample.
XX
PS Claim 7; SEQ ID NO 455; 166pp; English.
XX
CC The present invention describes a molecular sub-typing system (S) for
CC Escherichia coli, which comprises observing and recording variable number
CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers
CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
CC (III) for multiplex amplification of (I) comprising two or more primers
CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
CC maintaining hybridisation and amplification condition in a PCR instrument
CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying
CC reagents for maintaining hybridisation and amplification condition in a
CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub
CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
CC primers for amplifying loci comprising VNTR, where the primers have an
CC observable indicator; (b) obtaining single-stranded sample DNA from the
CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
CC and amplifying reagents under hybridising and amplifying conditions in a
CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
CC separating the amplicons by size; (e) evaluating numbers and sizes of
CC separated amplicons; and (f) comparing the evaluation to an evaluation of
CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
CC producing discrete genetic data for an epidemiological database. (I) is
CC useful as a research tool. (S) is useful for subtyping pathogenic E.
CC coli. The present sequence represents an E. coli VNTR loci related
CC amplicon sequence which is used in the exemplification of the present
CC invention.

XX Sequence 16 BP; 13 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
 SQ Query Match 1.5%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 428 TTTTATTTTATTTT 443
 16 TTTTATTTTATTTT 1
 Db

RESULT 2158
 ADD28837
 ID ADD28837 standard; DNA; 16 BP.
 AC ADD28837;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:456.
 XX
 KW molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX
 OS Escherichia coli.
 XX
 PN WO2003050269-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 11-DEC-2002; 2002WO-US039914.
 XX
 PR 11-DEC-2001; 2001US-0339687P.
 XX
 PA (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX
 PI Keim P, Keys C;
 XX
 DR WPI; 2003-864934/80.
 XX
 PT Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX
 PS Claim 7; SEQ ID NO 456; 166pp; English.
 XX
 CC The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC (III) for multiple amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (MI) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. MI is useful for

CC producing discrete genetic data for an epidemiological database. (1) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 16 BP; 3 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.7e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 428 TTTTATTTTATTTT 443
 1 TTTTATTTTATTTT 16
 Db

RESULT 2159
 ADE14208
 ID ADE14208 standard; DNA; 16 BP.
 AC ADE14208;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Optineurin promoter motif, repeat element or regulatory region #317.
 XX
 KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX
 OS Homo sapiens.
 XX
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 PA (SIEB/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 DR WPI; 2003-864168/80.
 XX
 PT New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 XX
 XX Claim 11; SEQ ID NO 319; 159pp; English.
 XX
 CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin

CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
XX Sequence 16 BP; 4 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 869 GATTACAGCGGTGAGC 884
XX 1 GATTACAGGTGTGAGC 16
XX
XX RESULT 2160
XX ADE14014/c
XX ID ADE14014 standard; DNA; 16 BP.
XX
XX ADE14014;
XX
XX 29-JAN-2004 (first entry)
XX
XX DE Optineurin promoter motif, repeat element or regulatory region #123.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX KM SNP; glaucoma; progressive ocular hypertensive disorder;
XX KM glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
XX
XX US2003190617-A1.
XX
XX 09-OCT-2003.
XX
XX PF 06-MAR-2002; 2002US-00091281.
XX
XX PR 06-MAR-2002; 2002US-00091281.
XX
XX PA (STEE/) SI E.
XX PA (RAYM/) RAYMOND V.
XX PA (MORI/) MORISSETTE J.
XX
XX PI Raymond V. Morissette J, Si E;
XX
XX DR WPI; 2003-864168/80.
XX
XX PT New nucleic acid sequences of the optineurin gene are useful to detect
XX PT polymorphisms particularly single nucleotide polymorphisms in the
XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
XX PT disorders.
XX
XX PS Claim 11; SEQ ID NO 125; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (NI) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as ADE13890. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient or the severity
XX or progression of glaucoma in a patient, comprising providing

CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
XX Sequence 16 BP; 9 A; 2 C; 1 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Db 588 TGGCTAATTTTATTT 603
XX 16 TGGCTAATTTTATTTAT 1
XX
XX RESULT 2161
XX AAD63061/c
XX ID AAD63061 standard; DNA; 16 BP.
XX
XX AAD63061;
XX
XX 12-FEB-2004 (first entry)
XX
XX DE Human NADH dehydrogenase Fe-S protein 8 (NDUFS8) tandem tag DNA #1.
XX
XX Tandem tag; concatenated tag; human; NADH dehydrogenase; Fe-S; ds.
XX
XX Homo sapiens.
XX
XX US2003190618-A1.
XX
XX 09-OCT-2003.
XX
XX PF 06-MAR-2002; 2002US-00092885.
XX
XX PR 06-MAR-2002; 2002US-00092885.
XX
XX PA (SAMA/) SAMAL B.
XX PA (LIY/) LI Y.
XX PA (HERM/) HERMIDA L C.
XX PA (HOPP/) HOPPA N L.
XX PA (JOHE/) JOHE K K.
XX
XX PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;
XX
XX DR WPI; 2003-831617/77.
XX
XX PT Generating five prime biased tandem tag libraries of cDNAs by isolating a
XX PT sample of mRNAs, amplifying the released tags, concatenating the
XX PT amplified tags to form concatenated tags, amplifying and isolating the
XX PT concatenated tags.
XX
XX PS Disclosure; Page 4; opp; English.
XX
XX The present invention discloses a method for generating five prime biased
XX tandem tag libraries of cDNAs. The step involves isolating a sample of
XX mRNAs, amplifying the released tags, concatenating the amplified tags to
XX form concatenated tags, amplifying and isolating the concatenated tags.
XX The present sequence is human NADH dehydrogenase (ubiquinone) Fe-S
XX protein 8 (NADH-coenzyme Q reductase; NDUFS8) tandem tag DNA
XX
XX Sequence 16 BP; 3 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 689 GCCTCCCGGTTCAAG 704
|||
DB 16 GCCTCCGAGTTCAAG 1

RESULT 2162
AAD63093/C
ID AAD63093 standard; DNA; 16 BP.

AC AAD63093;

DT 12-FEB-2004 (first entry)

DE Human tandem tag DNA #27.

XX Tandem tag; concatenated tag; human; ds.

XX Homo sapiens.

PN US2003190618-A1.

PD 09-OCT-2003.

PF 06-MAR-2002; 2002US-00092885.

PR 06-MAR-2002; 2002US-00092885.

XX (SAMA/) SAMAL B.

PA (LIYY/) LI Y.

PA (HERM/) HERMIDA L C.

PA (HOPP/) HOPPA N L.

PA (JOHE/) JOHE K K.

XX Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;

XX WPI; 2003-831617/77.

XX Generating five prime biased tandem tag libraries of cDNAs by isolating a

XX sample of mRNAs, amplifying the released tags, concatenating the

XX amplified tags to form concatenated tags, amplifying and isolating the

XX concatenated tags.

XX Disclosure; Page 6; 0pp; English.

XX The present invention discloses a method for generating five prime biased

XX tandem tag libraries of cDNAs. The step involves isolating a sample of

XX mRNAs, amplifying the released tags, concatenating the amplified tags to

XX form concatenated tags, amplifying and isolating the concatenated tags.

XX The present sequence is human tandem tag DNA

XX Sequence 16 BP; 5 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 778 TTTAGTAGAGATGG 793

DB 16 TTTAGTAGAGATGG 1

RESULT 2163

AAD63047/C

XX AAD63047 standard; DNA; 16 BP.

AC AAD63047;

DT 12-FEB-2004 (first entry)

DE Human ribosomal protein S21 (RPS21) tandem tag DNA #1.

XX Tandem tag; concatenated tag; human; ds.

OS Homo sapiens.

PN US2003190618-A1.

PD 09-OCT-2003.

PF 06-MAR-2002; 2002US-00092885.

PR 06-MAR-2002; 2002US-00092885.

XX (SAMA/) SAMAL B.

PA (LIYY/) LI Y.

PA (HERM/) HERMIDA L C.

PA (HOPP/) HOPPA N L.

PA (JOHE/) JOHE K K.

XX Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;

XX WPI; 2003-831617/77.

XX Generating five prime biased tandem tag libraries of cDNAs by isolating a

XX sample of mRNAs, amplifying the released tags, concatenating the

XX amplified tags to form concatenated tags, amplifying and isolating the

XX concatenated tags.

XX Disclosure; Page 4; 0pp; English.

XX The present invention discloses a method for generating five prime biased

XX tandem tag libraries of cDNAs. The step involves isolating a sample of

XX mRNAs, amplifying the released tags, concatenating the amplified tags to

XX form concatenated tags, amplifying and isolating the concatenated tags.

XX The present sequence is human ribosomal protein tandem tag DNA

XX Sequence 16 BP; 1 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1051 TGCCACACACCGCGC 1066

DB 16 TGCCACACACCGCGC 1

RESULT 2164

AAD63083/C

XX AAD63083 standard; DNA; 16 BP.

AC AAD63083;

DT 12-FEB-2004 (first entry)

DE Human tandem tag DNA #17.

XX Tandem tag; concatenated tag; human; ds.

XX Homo sapiens.

PN US2003190618-A1.

PD 09-OCT-2003.

PF 06-MAR-2002; 2002US-00092885.

PR 06-MAR-2002; 2002US-00092885.

XX (SAMA/) SAMAL B.

PA (LIYY/) LI Y.

PA (HERM/) HERMIDA L C.

PA (HOPP/) HOPPA N L.

PA (JOHE/) JOHE K K.

XX Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;

XX WPI; 2003-831617/77.
XX
XX Generating five prime biased tandem tag libraries of cDNAs by isolating a
PT sample of mRNA, amplifying the released tags, concatenating the
PT amplified tags to form concatenated tags, amplifying and isolating the
PT concatenated tags.
XX
XX Disclosure; Page 5; Opp; English.
XX
XX The present invention discloses a method for generating five prime biased
CC tandem tag libraries of cDNAs. The step involves isolating a sample of
CC mRNA, amplifying the released tags, concatenating the amplified tags to
CC form concatenated tags, amplifying and isolating the concatenated tags.
CC The present sequence is human tandem tag DNA
XX
SQ Sequence 16 BP; 4 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 396 TGGGATTACGCGCTG 411
16 TGGGATTACGCGCTG 1
DB
RESULT 2165
ADH59611
ID ADH59611 standard; DNA; 16 BP.
XX
XX AC ADH59611;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Non-nucleotide probe of the invention #15.
XX
XX KM non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
XX probe.
XX
XX OS Synthetic.
XX
XX PN WO2003027328-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 24-SEP-2002; 2002WO-US030573.
XX
XX PR 24-SEP-2001; 2001US-0324499P.
XX
XX PA (BOST-) BOSTON PROBES INC.
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX PI Kirtsen NV, Hyldig-Nielsen JU, Williams BF;
XX WPI; 2003-421160/39.
XX
XX DR Non-nucleotide probe for suppressing binding of detectable nucleic acid
PT probes to undesired sequences, has aggregate nucleobase sequence
PT homologous to randomly distributed repeat sequence of genomic nucleic
PT acid.
XX
XX PS Claim 10; SEQ ID NO 17; 103bp; English.
XX
XX CC The present sequence represents a non-nucleotide probe. The probe is
CC useful for suppressing the binding of one or more detectable nucleic acid
CC probes, that are greater than 100 base pairs and that have been derived
CC from genomic nucleic acid, to one or more undesired sequences in an assay
CC for determining target genomic nucleic acid of a sample. The method
CC comprises contacting the sample with the mixture of probes (preferably
CC comprising 5-50 probes), contacting the sample with the one or more
CC detectable nucleic acid probes, and determining the target genomic
CC nucleic acid of the sample by determining the hybridization of the one or

CC more detectable nucleic acid probes to the target genomic nucleic acid of
CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
CC cell, and the sample is metaphase spread, interphase nucleic or nucleic
CC found in paraffin embedded tissue material or frozen tissue sections. The
CC probe is also useful in comparing a sample of genomic nucleic acid with
CC that of a control sample using a genomic nucleic acid reference array.
CC The method comprises treating a sample of genomic nucleic acid and
CC control genomic nucleic acid, which are differentially labelled, the
CC array or both the sample and control genomic nucleic acid and the array
CC with the mixture of the probe under suitable hybridization conditions,
CC contacting the array with treated mixture of sample and control genomic
CC nucleic acid under suitable hybridization conditions, and comparing the
CC intensities of the signals from the differential labels of the array to
CC that caused by hybridization of the probes to genomic nucleic acid, thus
CC determining one or more variations in copy numbers of sequences in the
CC sample as compared with the relative copy numbers of substantially
CC identical sequences in the control. The hybridization of the genomic
CC array is determined using an intercalating dye or a detectable antibody,
CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
CC The sample of genomic nucleic acid to be tested and the reference of
CC nucleic acid are labelled with detectable moiety such that hybridization
CC of the genomic array is determined by determining the presence, absence,
CC amount or location of the detectable label on the one or more genomic
CC arrays. The genomic array comprises nucleic acid that is prepared from
CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
CC represents a non-nucleotide probe of the invention.
XX
SQ Sequence 16 BP; 0 A; 11 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 843 CCGCCTCGGCTCC 858
1 CCGCCTCGGCTCC 16
DB
RESULT 2166
ADH59599/c
ID ADH59599 standard; DNA; 16 BP.
XX
XX AC ADH59599;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Non-nucleotide probe of the invention #3.
XX
XX KM non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
XX probe.
XX
XX OS Synthetic.
XX
XX PN WO2003027328-A2.
XX
XX PD 03-APR-2003.
XX
XX PF 24-SEP-2002; 2002WO-US030573.
XX
XX PR 24-SEP-2001; 2001US-0324499P.
XX
XX PA (BOST-) BOSTON PROBES INC.
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX PI Kirtsen NV, Hyldig-Nielsen JU, Williams BF;
XX WPI; 2003-421160/39.
XX
XX DR Non-nucleotide probe for suppressing binding of detectable nucleic acid
PT probes to undesired sequences, has aggregate nucleobase sequence
PT homologous to randomly distributed repeat sequence of genomic nucleic
PT acid.
XX

PS Claim 10; SEQ ID NO 5; 103bp; English.

CC The present sequence represents a non-nucleotide probe. The probe is
CC useful for suppressing the binding of one or more detectable nucleic acid
CC probes, that are greater than 100 base pairs and that have been derived
CC from genomic nucleic acid, to one or more undesired sequences in an assay
CC for determining target genomic nucleic acid of a sample. The method
CC comprises contacting the sample with the mixture of probes (preferably
CC comprising 5-50 probes), contacting the sample with the one or more
CC detectable nucleic acid probes, and determining the target genomic
CC nucleic acid of the sample by determining the hybridization of the one or
CC more detectable nucleic acid probes to the target genomic nucleic acid of
CC the sample. The genomic nucleic acid is contained in a fixed tissue or a
CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic
CC found in paraffin embedded tissue material or frozen tissue sections. The
CC probe is also useful in comparing a sample of genomic nucleic acid with
CC that of a control sample using a genomic nucleic acid reference array.
CC The method comprises treating a sample of genomic nucleic acid and
CC control genomic nucleic acid, which are differentially labelled, the
CC array or both the sample and control genomic nucleic acid and, the array
CC with the mixture of the probe under suitable hybridization conditions,
CC contacting the array with treated mixture of sample and control genomic
CC nucleic acid under suitable hybridization conditions, and comparing the
CC intensities of the signals from the differential labels of the array to
CC that caused by hybridization of the probes to genomic nucleic acid, thus
CC determining one or more variations in copy numbers of sequences in the
CC sample as compared with the relative copy numbers of substantially
CC identical sequences in the control. The hybridization of the genomic
CC array is determined using an intercalating dye or a detectable antibody,
CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.
CC The sample of genomic nucleic acid to be tested and the reference of
CC nucleic acid are labelled with detectable moiety such that hybridization
CC of the genomic array is determined by determining the presence, absence,
CC amount or location of the detectable label on the one or more genomic
CC arrays. The genomic array comprises nucleic acid that is prepared from
CC Bacterial Artificial Chromosome (BAC) clones. The present sequence
CC represents a non-nucleotide probe of the invention.

XX Sequence 16 BP; 2 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 843 CCGGCTCGGCTCC 858

DB 16 CCGGCTCGGCTCC 1

RESULT 2167

ID ABR34281/C

ABX14989 standard; DNA; 16 BP.

AC ABR34281;

DT 14-MAR-2003 (first entry)

DE Human delta opioid receptor OPRD1-1 SNP genotyping PCR primer #1.

XX Human, delta opioid receptor; OPRD1-1; ss; PCR; primer; SNP;
XX single nucleotide polymorphism; eating disorder; anorexia nervosa;
XX energy homeostasis disorder; chromosome 1.

OS Homo sapiens.

PN WO200292838-A2.

PD 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014940.

PR 11-MAY-2001; 2001US-0290016P.

PA (BIOI-) BIOINVEST LTD.

XX Bergen AM;

XX WPI; 2003-129306/12.

PT New isolated nucleic acid molecule encoding a delta opioid receptor
PT variant associated with an eating or energy homeostasis disorder, useful
PT for diagnosing a genetic predisposition to such disorder, e.g. anorexia
PT nervosa.

XX Example; Page 19; 39pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a
CC delta opioid receptor variant associated with an eating or energy
CC homeostasis disorder. Also included are a delta opioid receptor variant
CC encoded by the nucleic acid, an isolated antibody that specifically
CC recognizes the delta opioid receptor variant, a vector comprising the
CC nucleic acid, a host cell transformed to contain the vector, producing
CC the polypeptide by culturing the host cell, identifying an agent which
CC modulates the expression of the nucleic acid, diagnosing a genetic
CC predisposition to an eating or energy homeostasis disorder by detecting
CC the presence or absence of the variant nucleic acid in a patient sample,
CC an allele specific primer that detects a polymorphism in the gene
CC encoding a delta opioid receptor associated with an eating or energy
CC homeostasis disorder and a non-human transgenic animal modified to
CC contain the variant nucleic acid. The variants are named OPRD1-1 to
CC OPRD1-8. The human opioid receptor gene is located on chromosome 1. The
CC nucleic acid molecules and delta opioid receptor variant are useful for
CC diagnosing a genetic predisposition to an eating or energy homeostasis
CC disorder, such as anorexia nervosa. The allele specific primer is useful
CC for detecting polymorphism in the gene encoding a delta opioid receptor
CC associated with the disorder cited. The present sequence is a genotyping
CC PCR primer for detecting the presence of a particular SNP (single
CC nucleotide polymorphism) in a sample

XX Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 16;

XX Best Local Similarity 93.8%; Pred. No. 1.7e+03;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 871 TTACAGGCGTGAGCCA 886

DB 16 TTACAGGCGTGAGCCA 1

RESULT 2168

ID ABR34281/C

ABT34281 standard; DNA; 16 BP.

AC ABR34281;

DT 12-JUN-2003 (first entry)

DE Opioid receptor D1 PCR primer SEQ ID NO 67.

XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;
XX serotonin receptor ID; delta-opioid receptor; dopamine receptor D2;
XX anorexia nervosa; bulimia nervosa; PCR; primer; ss.

OS Unidentified.

PN WO2003012143-A1.

PD 13-FEB-2003.

PF 16-JUL-2002; 2002WO-US022555.

PR 16-JUL-2001; 2001US-0305153P.

PR 20-JUL-2001; 2001US-0306440P.

PR 13-NOV-2001; 2001US-0331285P.

PR 19-DEC-2001; 2001US-0340843P.

PR 19-DEC-2001; 2001US-0340844P.
XX
XX (PRIC-) PRICE FOUND LTD.
XX
XX Bergen AM, Yeager M;
XX WPI, 2003-268122/26.
XX
XX New nucleic acid molecule having polymorphisms in the serotonin receptor
PT 1D, delta-opioid receptor, or dopamine receptor D2, useful in diagnostic
PT and prognostic assays for eating disorders, such as anorexia and bulimia
PT nervosa.
XX
XX Example 3; Page 60; 149pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule
CC comprising a variant gene associated with an eating disorder and selected
CC from any of 119 polymorphisms with their corresponding genotyping in
CC database, alleles and HOBAS identification, given in the specification.
CC The novel nucleic acid molecule has polymorphisms in the serotonin
CC receptor 1D, delta-opioid receptor, or dopamine receptor D2, which is
CC useful in diagnostic and prognostic assays for eating disorders, in
CC particular anorexia nervosa and bulimia nervosa. This polynucleotide
CC sequence represents a opioid receptor 1D PCR primer of the invention
XX
XX Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 871 TTACAGCGCTGAGCCA 886
DB 16 TTACAGCGTGTGAGCCA 1
RESULT 2169
ADH70278/C
ID ADH70278 standard; DNA; 16 BP.
XX
XX ADH70278;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human Vbeta gene repeat sequence #68.
DE
XX
XX human, T-cell associated disease; Vbeta; autoimmune disease;
KM degenerative nervous system disease; graft versus host disease;
KM hypersensitivity disease; infectious disease; neoplastic disease;
KM Addison's disease; atrophic gastritis;
KM degenerative nervous system disease; multiple sclerosis;
KM Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KM allergy; type II hypersensitivity; Goodpasture's syndrome;
KM type IV hypersensitivity; leprosy; infectious disease; viral infection;
KM HIV; fungal infection; Candida; parasitic infection; schistosoma;
KM filaria; bacterial infection; Mycobacterium; neoplastic disease;
KM lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KM breast cancer; ds.
XX
XX Homo sapiens.
OS
XX
XX US2002150891-A1.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 05-MAR-1999; 99US-00263959.
PF
XX
XX 19-SEP-1994; 94US-00309335.
PR
XX 19-SEP-1995; 95US-00531241.
XX
XX (HOOD/) HOOD L E.
PA
XX (ROME/) ROMEN L.
XX

PI Hood LE, Rowen L;
XX
XX WPI, 2004-059052/06.
DR
XX
XX Kit for diagnosing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious disease, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
XX Disclosure; SEQ ID NO 472; 164pp; English.
PS
XX
XX The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC Vbetakna or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include type
CC I hypersensitivities such as contact with allergens that lead to
CC allergies, type II hypersensitivities such as those present in
CC Goodpasture's syndrome and type IV hypersensitivities such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
XX Sequence 16 BP; 13 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 430 TTATTTTATTTTATTTT 445
DB 16 TTATTTTATTTTATTTT 1
RESULT 2170
ADQ30362
ID ADQ30362 standard; DNA; 16 BP.
XX
XX ADQ30362;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human Vb1 exon 1d transcription factor binding fragment #81.
DE
XX
XX ds; Vb1 receptor; vanilloid receptor type 1; modulator;
KM pain transmission; primary sensory neuron; transcription factor;
KM detection; MZFI; NKapab; NFAT; GAVAI; sensitivity disorder; analgesia;
KM hyperalgesia; hyperalgesia; neuropathic; myalgia; human.
XX
XX Homo sapiens.
OS
XX
XX WO2004053120-A2.
PN
XX
XX 24-JUN-2004.
PD
XX
XX 01-DEC-2003; 2003WO-EP013522.
PF
XX
XX 09-DEC-2002; 2002DE-01057421.
PR
XX
XX (CHEF) GRUENENTHAL GMEH.
XX
XX Weihe E, Bieller A, Schaefer MKH;
PI
XX WPI, 2004-468868/44.
XX

XX New nucleic acid that modulates expression of the vanilloid receptor-1.
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.

XX Disclosure; Page 53; 68pp; German.

XX This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridizes to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-22344 of Genbank AL670399, 31673-36359 of AL661116, or
CC 44731-44231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbent assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MEFL, NFkappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating them,
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.

XX Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 GACTACAGGCGCCAC 753

Db 1 GACTACAGGTGCCAC 16

RESULT 2171

AA095863 standard; DNA; 17 BP.

XX AA095863;

XX 21-FEB-1996 (first entry)

XX Primer A (Group 11, set B) for marker D13S217, chromosome 13.

XX primer; polymerase chain reaction; PCR; linkage study; locus;

KM microsatellite marker sequence; automated genotyping; allele;

KM polymorphism; detection; Homo sapiens, ss.

XX Synthetic.

XX WO9515400-A1.

XX 08-JUN-1995.

XX 05-DEC-1994; 94WO-US013945.

XX 03-DEC-1993; 93US-00160837.

XX (UYJO) UNIT JOHNS HOPKINS.

XX Levitt RC;

XX MPI; 1995-215278/28.

XX Kit for automated genotyping concg. pairs of PCR primers - designed to
PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT with a characteristic fluorescence label, useful e.g. in detection of
PT disease related genetic rearrangement.

XX Disclosure; Fig 7K-2; 104pp; English.

XX The method aims to provide a collection of highly reproducible
CC microsatellite marker sequences (MMS) at approx. 10-50 cm intervals
CC throughout the human genome which can be detectably labelled. The MMS are
CC polymorphic, simple sequence repeats and can be used in automated
CC genotyping, esp. fluorescence-based. The primers correspond to the unique
CC DNA sequence surrounding each marker, and PCR is used to detect each
CC polymorphism. When the MMS show considerable polymorphism (ie. a
CC difference in the number of repeats) between individuals, the markers can
CC be particularly informative. The MMS can be ideal for linkage studies.
CC Kits comprise at least 4 groups, of at least 3 sets, each comprising
CC labelled primers for PCR amplification of the DNA. Group 11 primer pairs
CC are shown in AA095841-82. The published size range of the D13S217 allele
CC is 160-174 bp, and the degree of heterozygosity in the population is
CC about 67%

XX Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 393 TCGTGCGATTACAGGC 408

Db 2 TCGTGCGATCACAGGC 17

RESULT 2172

AAA22692 standard; RNA; 17 BP.

XX AAA22692;

XX 19-JUN-2000 (first entry)

XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5918.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KM Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KM dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KM tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX MPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.

XX (RIBO-) RIBOZYME PHARM INC.
XX
XX
XX Pavo PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA,
XX WPI, 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 240; 305pp; English.
XX
XX The present invention describes enzymatic cleave nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+03;
XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 797 CACCATGTCGCCAGG 812
DB 1 CACCAUGUGGCCAGG 16
RESULT 2175
ID AAA22691 standard; RNA; 17 BP.
AC AAA22691;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5917.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX OS
XX MO950403-A2.
XX
XX

PD 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavo PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI, 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 236; 305pp; English.
XX
XX The present invention describes enzymatic cleave nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 4 A; 0 C; 0 G; 0 T; 13 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 12.5%; Pred. No. 1.8e+03;
XX Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
OY 428 TTTTATTTTATTTT 443
DB 2 UUUUUAUUUUUUUUUU 17
RESULT 2176
ID AAA22960/c
XX AAA22960 standard; RNA; 17 BP.
AC AAA22960;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6186.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX

XX OS Homo sapiens.
 XX XX MO950403-A2.
 XX PD 07-OCT-1999.
 XX PF 24-MAR-1999; 99MO-US006507.
 XX PR 27-MAR-1998; 98US-0079678P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX DR WPI; 1999-591315/50.
 XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
 XX PT of an mRNA encoding an angiogenic factors.
 XX PS Claim 54; Page 253; 305pp; English.
 CC The present invention describes enzymatic cleave RNA molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ANNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23262 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT, Tie-2,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ANNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
 CC
 CC Query Match 1.5%; Score 14.4; DB 1; Length 17;
 CC Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 383 CCTCCCAAAAGTGTGG 398
 DB 16 CTTCCCAAAAGTGTGG 1
 XX
 AC AAA22965;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6191.
 KW Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytoskeletal; anti-diabetic;
 KW ophthalmologic; anti-inflammatory; anti-arthritis; anti-psoriatic; ARMD;

KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angioblastoma;
 KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX XX MO950403-A2.
 XX PD 07-OCT-1999.
 XX PF 24-MAR-1999; 99MO-US006507.
 XX PR 27-MAR-1998; 98US-0079678P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX DR WPI; 1999-591315/50.
 XX PT Novel ribozymes for modulating the synthesis, expression and/or stability
 XX PT of an mRNA encoding an angiogenic factors.
 XX PS Claim 54; Page 253; 305pp; English.
 CC The present invention describes enzymatic cleave RNA molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ANNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA22476 to AAA23262, AAA23343 to
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23262 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT, Tie-2,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ANNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
 CC
 CC Query Match 1.5%; Score 14.4; DB 1; Length 17;
 CC Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 212 TGGTCTGGAACCTCCG 227
 DB 17 TGGTCTGGAACCTCCG 2
 XX
 AC AAA22975;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6201.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
OS Homo sapiens.
XX MO9950403-A2.
XX 07-OCT-1999.
XX 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
XX (RIBO-) RIBOZYME PHARM INC.
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 254; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 14 A; 0 C; 0 G; 0 T; 3 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 603 TTTATTTTATTTT 618
DB 17 TTTTATTTTATTTT 2
RESULT 2179
AAA22835
ID AAA22835 standard; RNA; 17 BP.
XX

AC AAA22835;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6061.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX MO9950403-A2.
XX 07-OCT-1999.
XX 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
XX (RIBO-) RIBOZYME PHARM INC.
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 245; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 4 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1034 CTGGGATTACGGGCAC 1049
DB 1 CTGGGATUUCAGGCAC 16

```
RESULT 2180
AAA22833
ID AAA22833 standard; RNA; 17 BP.
XX
XX AAA22833;
XX
XX 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6059.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 245; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19086
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA21688 represent their corresponding target sequences;
XX CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1 5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+03;
XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 549 TCCCAAGTAGCTGGGA 564
Db :|||:|||||
1 UCCCGAGAGUCUGGGA 16

RESULT 2181
AAA22735
ID AAA22735 standard; RNA; 17 BP.
XX
XX AAA22735;
XX
XX 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5961.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX CC and AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
XX CC corresponding target sequences; AAA17685 to AAA18385 and AAA19086
XX CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX CC and AAA19155 to AAA19222 represent their corresponding target sequences;
XX CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX CC AAA21596 to AAA21688 represent their corresponding target sequences;
XX CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX CC AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
```


Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.8e+03;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

549 TCCCAAGTCTGGGA 564

1 UCCCGAGUAGUCGGA 16

RESULT 2182

AAA22818

AAA22818 strand; RNA; 17 BP.

AAA22818;

19-JUN-2000 (first entry)

Integrin subunit beta 3 substrate sequence SEQ ID NO:6044.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic; ophthalmologic; antiinflammatory; antiaerthetic; antiproliferative; ARMD; dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiodioma; tuberous sclerosis; pot-wine strain; Sturge Weber syndrome; Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99WO-US006507.

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.

Claim 54; Page 244; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a TIE-2 gene. AAA16775 to AAA19167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT, and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their corresponding target sequences. AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for TIE-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences. AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences. AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA24422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT. Integrin subunit beta-3, integrin subunit alpha-6, or TIE-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,

angiodioma of tuberous sclerosis, pot-wine strains, Sturge Weber syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, TIE-2, integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 81.2%; Pred. No. 1.8e+03;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

644 CCAGCTGAGTGCAG 659

2 CCAGGCUAGAGUCGAG 17

RESULT 2183

AAA25181

AAA25181 strand; DNA; 17 BP.

AAA25181;

19-JUN-2000 (first entry)

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1679.

Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Homo sapiens.

MO9954459-A2.

28-OCT-1999.

19-APR-1999; 99WO-US008547.

20-APR-1998; 98US-0082404P.

23-JUN-1998; 98US-00103636.

(RIBO-) RIBOZYME PHARM INC.

Thompson JD, Beigelman L, Mcswigen JA, Karpelky A, Bellon L,

Reynolds M, Zwick M, Jarvis T, Woolf T, Haebertl P,

Matulic-Adamic U;

WPI; 2000-013248/01.

New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.

Claim 77; Page 71; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A) that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and

CC antisense oligonucleotides used in the exemplification of the present
CC invention
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 596 TTTTATTTTATTTT 611
DB 1 TTTTGTATTTTATTTT 16
RESULT 2184
AAFO5508
ID AAFO5508 standard; DNA; 17 BP.
AC AAFO5508;
XX
XX
DT 16-FEB-2001 (first entry)
DE Hammerhead ribozyme substrate #2727.
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KM interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, Mcswigen J;
PI WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
XX
XX Claim 18; Page 118; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 1 A; 1 C; 2 G; 13 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 163 TTTTGTATTTTATTTT 178
DB 1 TTTTGTATTTTATTTT 16
RESULT 2185
AAFO6148
ID AAFO6148 standard; DNA; 17 BP.
XX

AC AAFO6148;
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Hammerhead ribozyme substrate #2945.
DE
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KM interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, Mcswigen J;
PI WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
XX
XX Claim 42; Page 123; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 2 A; 0 C; 2 G; 0 T; 13 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 1.8e+03;
Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 427 TTTTATTTTATTTT 442
DB 2 UUGUUAUUUUUUUU 17
RESULT 2186
AAFO6151
ID AAFO6151 standard; DNA; 17 BP.
XX
XX AAFO6151;
XX
XX 16-FEB-2001 (first entry)
XX
XX Hammerhead ribozyme substrate #2948.
DE
XX
XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KM interferon alpha; ss.
XX
XX Homo sapiens.
XX
XX WO200061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX

```
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Blatt L, Zwick M, Pavco P, Mowsiggen J,
PI
XX WPI, 2000-647423/62.
DR
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
XX Claim 42, Page 123, 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
CC
SQ Sequence 17 BP, 2 A, 1 C, 1 G, 0 T, 13 U, 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 1.8e+03;
Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
QY 429 TTTATTTTATTTT 444
DB 1 UGUUUUUUUUUUU 16
RESULT 2187
ID ABA91530 standard; DNA; 17 BP.
AC ABA91530;
XX
XX 23-APR-2002 (first entry)
DT
XX DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
DE
XX DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH misc_RNA 8
FT /*tag= a
FT /label= RNA
XX
XX WO200206531-A2.
XX
XX 24-JAN-2002.
PD
XX
XX 12-JUL-2001, 2001WO-US022166.
PF
XX
XX 14-JUL-2000, 2000US-00616761.
PR
XX 30-MAR-2001, 2001US-00823647.
PR
XX (GENE-) APPLIED GENE TECHNOLOGIES INC.
PA
XX
XX Datasupta N,
PI
XX
XX WPI, 2002-171819/22.
DR
XX
XX Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.
XX
XX Example 4; Page 49; 72pp; English.
PS
```

```
XX The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used
CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC the set had a different number of ribonucleotides, 1 in the present case.
CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC minutes. The results showed that 4 ribonucleotides were the minimum
CC number for RNA cleavage. The invention provides probes for nucleic acid
CC hybridisation. The probes form a hairpin structure comprising a double-
CC stranded stem and a single-stranded loop, and are capable of both
CC intramolecular and intermolecular hybridisation. The double-stranded stem
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC can be removed. Arrays and methods for nucleic acid hybridisation using
CC the probes are provided.
CC
SQ Sequence 17 BP, 1 A, 0 C, 0 G, 16 T, 0 U, 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 430 TTTATTTTATTTT 445
DB 1 TTTTATTTTATTTT 16
RESULT 2188
ID ABA91530 standard; DNA; 17 BP.
AC ABA91530;
XX
XX 16-AUG-2002 (first entry)
DT
XX Ataxia telangiectasia locus 56594896-WNeg-t capture probe.
DE
XX Ataxia telangiectasia; probe; biochip; array; capture; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200180155-A2.
XX
XX 25-OCT-2001.
PD
XX
XX 18-APR-2001, 2001WO-US012750.
PF
XX
XX 18-APR-2000, 2000US-0198045P.
PR
XX 22-NOV-2000, 2000US-0252880P.
PR
XX (COMB-) COMBINATRIX CORP.
PA
XX
XX Anderson BP, Quarles PA, Ghazvini S,
PI
XX
XX WPI, 2002-017664/02.
DR
XX
XX Automated process for custom-designed biochip design, comprises obtaining
PT desired target sequences from customer, creating sequence content motif
PT for an array and applying the motif to a surface suitable for later
PT detection.
XX
XX Example 5; Page 21; 47pp; English.
PS
XX The invention relates to a novel process for a manufacturer to obtain
CC customer orders for custom-designed biochips in an automated process. The
CC invention also includes an automated system and process for providing a
CC fully automated process for the design, manufacture and analysis of data
CC for biological array devices. The sequence represents a capture probe
CC designed in the invention for the "sample ataxia" set of targets, as an
CC example of an array that may be designed using the method of the
```

CC invention
XX
SQ Sequence 17 BP; 4 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 676 CACTGCACCTCTGCC 691
| | | | | | | | | | | | | | | | | | | | |
17 CACTGCATCTCTGCC 2
Db
RESULT 2189
ADG14612
ID ADG14612 standard; DNA; 17 BP.
AC ADG14612;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human IL-10 regulatory region PCR primer IL10-2763CR, SEQ ID NO:3.
XX
KW Therapeutic response; therapeutic outcome; interferon-alpha-2b;
KW ribavirin; hepatitis C virus; HCV infection; interleukin-10;
KW IL-10 regulatory region; single nucleotide polymorphism; SNP; haplotype;
KW genotype; cytotoxic T-lymphocyte antigen-4; CTLA-4 promoter;
KW CTLA-4 exon 1; bacterial infection; meningococcal infection;
KW rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
KW inflammatory bowel disease; multiple sclerosis; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN MO200268699-A1.
XX
PD 06-SEP-2002.
XX
PF 27-FEB-2002; 2002MO-US006207.
XX
PR 27-FEB-2001; 2001US-0271811P.
XX
PA (UABR-) UAB RES FOUNDED.
XX
PI Yee L, Tang J, Kaslow RA, Van Leeuwen DJ;
DR WPI; 2002-707021/76.
XX
PT Predicting a therapeutic response comprises comparing a first nucleic
PT acid allele in an interleukin-10 (IL-10) regulatory region with a second
PT nucleic acid allele in the IL-10 regulatory region associated with a
PT known outcome.
XX
PS Claim 12; SEQ ID NO 3; 34pp; English.
XX
CC The invention relates to a method for predicting an individual's
CC therapeutic response to the administration of interferon-alpha-2b and
CC ribavirin for the treatment of a pathological condition, especially
CC hepatitis C virus (HCV) infection. The method involves determining which
CC allelic form is present at positions -3575, -2763, -1082, -819 and -592
CC of the interleukin-10 (IL-10) regulatory region, and comparing these with
CC the allelic forms at these positions which are associated with a known
CC outcome of interferon-alpha-2b and ribavirin administration. Presence of
CC the single nucleotide polymorphisms -592A and -819T, the -592A/A or -
CC 819T/T genotypes, the combination of -592A/-819T as a haplotype,
CC homozygosity for -592A/-819T, -592A/-819T as a genotype, or possession of
CC the (108)TCATA haplotype (encompassing positions -3575, -2763, -1082, -
CC 819 and -592) is associated with a sustained response to interferon-alpha
CC or the (108)TCACC haplotype indicates that the patient will be non-
CC responsive to this therapy. The method optionally further comprises
CC detection of the allele at position -318 of the cytotoxic T-lymphocyte
CC antigen-4 (CTLA-4) promoter and the allele at position 49 of exon 1 of
CC the CTLA-4 gene. The invention also encompasses kits and oligonucleotide

CC primers for use in the methods of the invention. The method and primers
CC are useful for identifying and analysing genetic polymorphisms in the IL-
CC 10 regulatory region and/or cytotoxic T-lymphocyte antigen-4 which can be
CC used in predicting an individual's response to therapeutic intervention
CC with interferon-alpha-2b and ribavirin for HCV infection, and for
CC predicting the responsiveness of an individual to therapy for a
CC pathological condition, or for predicting the outcome of therapeutic
CC intervention in pathological conditions such as bacterial infection (e.g.
CC meningococcal infection), rheumatoid arthritis, systemic lupus
CC erythematosus, Sjogren's syndrome, inflammatory bowel disease or multiple
CC sclerosis. The present sequence is related to the invention.
XX
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 885 CACCACGCCCGGCTTA 900
| | | | | | | | | | | | | | | | | | | | |
1 CACCACGCCCGGCTTA 16
Db
RESULT 2190
ABT36747
ID ABT36747 standard; DNA; 17 BP.
XX
AC ABT36747;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 2384.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002MO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 311; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral

CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGCTGAGC 864
DB 1 GATCACAGCGCTGAGC 16
|||||

RESULT 2191
ABT39415/C
ID ABT39415 standard; DNA; 17 BP.
XX
XX AC ABT39415;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX DE Tumour suppression related human fukutin oligo SEQ ID No 5052.
XX
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX KW Homo sapiens.
XX
XX OS WO2003025175-A2.
XX
XX PN 27-MAR-2003.
XX
XX PD 17-SEP-2002; 2002WO-IB004208.
XX
XX PF 17-SEP-2001; 2001FR-00011978.
XX
XX PR 17-SEP-2001; 2001FR-00011978.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX DR WPI; 2003-313353/30.
XX
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; Page 624; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and

CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 386 CCCAAGTCTGGGAT 401
DB 17 CTCAAGTCTGGGAT 2
|||||

RESULT 2192
ABT36267/C
ID ABT36267 standard; DNA; 17 BP.
XX
XX AC ABT36267;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX DE Tumour suppression related human fukutin oligo SEQ ID No 1904.
XX
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX KW Homo sapiens.
XX
XX OS WO2003025175-A2.
XX
XX PN 27-MAR-2003.
XX
XX PD 17-SEP-2002; 2002WO-IB004208.
XX
XX PF 17-SEP-2001; 2001FR-00011978.
XX
XX PR 17-SEP-2001; 2001FR-00011978.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX DR WPI; 2003-313353/30.
XX
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; Page 255; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 480 GTGCAGTGTGTGATC 495

Db 16 GTGCAGTGTGTGATC 1

RESULT 2193

ABT38180
ID ABT38180 standard; DNA; 17 BP.

XX ABT38180;

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 3817.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PP 17-SEP-2002; 2002WO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PS Disclosure; Page 480; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 532 ATCTCTCTGCTCAGC 547

Db 2 ATCTCTCTGCTCAGC 17

RESULT 2194

ABT38796
ID ABT38796 standard; DNA; 17 BP.

XX ABT38796;

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 4433.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PP 17-SEP-2002; 2002WO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PS Disclosure; Page 552; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression

CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 532 ATCTCTGCTGCTGAG 547
DB 2 ATCTCTGCTGCTGAG 17
RESULT 2195
ABT36344
ID ABT36344 standard; DNA; 17 BP.
AC ABT36344;
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 1981.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 264; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX

SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 967 ATCTGCGCTCACTGCA 982
DB 2 ATCTGCGTCACTGCA 17
RESULT 2196
ABT39345/C
ID ABT39345 standard; DNA; 17 BP.
XX
AC ABT39345;
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4982.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 616; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 480 GTGACGTGGTGCATC 495
Db 16 GTGACGTGGTGCATC 1

RESULT 2197
ABT37365/C
ID ABT37365 standard; DNA; 17 BP.
XX
XX ABT37365;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3002.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX
XX Disclosure; Page 384; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 480 GTGACGTGGTGCATC 495
Db 16 GTGACGTGGTGCATC 1

RESULT 2198
ABT38008
ID ABT38008 standard; DNA; 17 BP.
XX
XX ABT38008;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3645.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX
XX Disclosure; Page 460; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

OY 532 ATCTCTGCTGCTCAGC 547
 DB 2 ATCTCTGCTGCTCAGC 17

RESULT 2199

ID ABT35457
 ABT35457 standard; DNA; 17 BP.

AC ABT35457;
 DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 1094.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002MO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR MPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

PS Disclosure; Page 161; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 667 ATTTGAGCTCAGTCA 682

|||||

DB 2 ATCATGCTCACTGCA 17

RESULT 2200
 ID ABT36801/C
 ABT36801 standard; DNA; 17 BP.

AC ABT36801;
 DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 2438.

KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002MO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR MPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumours and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

PS Disclosure; Page 318; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 4 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 225 CCGACTCAGATGATC 240

DB 16 CCGACTCAGATGATC 1

|||||

RESULT 2201

ABT36337/c
ID ABT36337 standard; DNA; 17 BP.

AC ABT36337/

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 1974.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrania; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PS Disclosure; Page 263; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterized by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrania. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention

SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 386 CCCAAGTGTGGAT 401

DB 17 CCCAAGTGTGGAT 2

RESULT 2202

ABT37220
ID ABT37220 standard; DNA; 17 BP.

AC ABT37220/

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 2857.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrania; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

PS Disclosure; Page 367; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterized by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrania. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention

SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 532 ATCTCTCTGCTGAGC 547

DB 2 ATCTCTCTGCTGAGC 17

RESULT 2203

ABT34597
ID ABT34597 standard; DNA; 17 BP.

```
XX ABT34597;
AC
XX
XX 12-JUN-2003 (first entry)
DT
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 234.
DE
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
OS
XX
XX WO2003025175-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004208.
PF
XX
XX 17-SEP-2001; 2001FR-00011978.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX
XX MPI; 2003-313353/30.
PT
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; Page 61; 720pp; French.
XX
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX
XX SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 532 ATCTCTCTGCTCAGC 547
XX |||||
XX 2 ATCTCTCTGCTCAGC 17
XX
XX RESULT 2204
XX ID ABT36198/c
XX AC ABT36198 standard; DNA; 17 BP.
XX
XX AC ABT36198;
```

```
XX
XX 12-JUN-2003 (first entry)
DT
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 1835.
DE
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
OS
XX
XX WO2003025175-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004208.
PF
XX
XX 17-SEP-2001; 2001FR-00011978.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX
XX MPI; 2003-313353/30.
PT
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; Page 247; 720pp; French.
XX
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX
XX SQ Sequence 17 BP; 5 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 480 GTGCAGTGTGTGATC 495
XX |||||
XX 16 GTGCAGTGTGTGATC 1
XX
XX RESULT 2205
XX ID ABT36270
XX AC ABT36270 standard; DNA; 17 BP.
XX
XX AC ABT36270;
XX
XX DT 12-JUN-2003 (first entry)
```

XX Tumour suppression related human fukutin oligo SEQ ID No 1907.
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophtenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX Homo sapiens.
XX WO2003025175-A2.
PN 27-MAR-2003.
PD 17-SEP-2002; 2002MO-IB004208.
PF 17-SEP-2001; 2001FR-00011978.
PR (MOLE-) MOLECULAR ENGINES LAB.
PA Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-313353/30.
DR New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX Disclosure; Page 256; 720pp; French.
PS The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophtenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 381 AGCTCTCCCAAGTGCT 396
Db 2 ATCTCTCCCAAGTGCT 17
RESULT 2206
ABT34566 standard; DNA; 17 BP.
XX
XX ABT34566;
XX 12-JUN-2003 (first entry)
DT Tumour suppression related human fukutin oligo SEQ ID No 203.
DE

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophtenia; protein chip; gene therapy; tumour suppression;
KM human fukutin; ds.
XX Homo sapiens.
XX WO2003025175-A2.
PN 27-MAR-2003.
PD 17-SEP-2002; 2002MO-IB004208.
PF 17-SEP-2001; 2001FR-00011978.
PR (MOLE-) MOLECULAR ENGINES LAB.
PA Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-313353/30.
DR New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX Disclosure; Page 57; 720pp; French.
PS The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, or a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophtenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 2 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 532 ATCTCTCTGCTCAGC 547
Db 2 ATCTCTCTGCTCAGC 17
RESULT 2207
ABT37351/C
ID ABT37351 standard; DNA; 17 BP.
XX
XX ABT37351;
XX 12-JUN-2003 (first entry)
DT Tumour suppression related human fukutin oligo SEQ ID No 2988.
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KM

KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumours and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 382; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acid of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 480 GTGCACTGTGTGATC 495
DB 16 GTGCACTGTGTGATC 1
RESULT 2208
ID ABT39059
AC ABT39059 standard; DNA; 17 BP.
XX
XX ABT39059;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 4696.
XX
XX Cytostatic; vinuclide; neuroprotective; noctropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
KW

KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumours and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 583; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acid of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 837 GATTCGCTGCTCGG 852
DB 1 GATTCGCTGCTCGG 16
RESULT 2209
ID ACA06514
AC ACA06514 standard; RNA; 17 BP.
XX
XX ACA06514;
XX
XX 03-JUN-2003 (first entry)
XX
XX NFKB sub-unit modulating inozyme substrate #333.
XX
XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW

lymphoma; glioma; multidrug resistant cancer; RBL-A-specific inhibitor;
chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischemia;
gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
transplant/graft rejection; reperfusion injury; glomerulonephritis;
allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX
OS Homo sapiens.
XX
PN US2002177568-A1.
XX
XX 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
XX 18-MAY-1994; 94US-00245466.
XX 15-AUG-1994; 94US-00291932.
XX 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINCOMB D T.
XX (MCSW/) MCSWIGEN J.
XX (DRAP/) DRAPER K G.
PI Stinchcomb DT, Mcswigen J, Draper KG;
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3, Page 32; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating RBL-A activity in a cell, for
CC treating a patient having a condition associated with the level of RBL-A.
CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
SQ Sequence 17 BP; 1 A; 9 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Beet Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 711 TCTGCCCCAGCCTCC 726
:|||||:|||||:|||||
DB 2 UCTGCCCCAGGCTCC 17

ACA06515
ID ACA06515 standard; RNA; 17 BP.
XX
XX ACA06515;
AC
XX
XX 03-JUN-2003 (first entry)
DT
XX
XX NFKB sub-unit modulating inozyme substrate #334.
DE
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
XX G-cleaver; amberzyme; cancer; RBL-A activity; breast cancer; human;
XX lung cancer; prostate cancer; colorectal cancer; brain cancer;
XX oesophageal cancer; stomach cancer; ovarian cancer; melanoma;
XX lymphoma; glioma; multidrug resistant cancer; RBL-A-specific inhibitor;
XX chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
XX cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
XX gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN US2002177568-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864785.
XX
XX 07-DEC-1992; 92US-00987132.
XX 18-MAY-1994; 94US-00245466.
XX 15-AUG-1994; 94US-00291932.
XX 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINCOMB D T.
XX (MCSW/) MCSWIGEN J.
XX (DRAP/) DRAPER K G.
PI Stinchcomb DT, Mcswigen J, Draper KG;
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3, Page 32; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating RBL-A activity in a cell, for
CC treating a patient having a condition associated with the level of RBL-A.
CC (I) is useful for cleaving RNA comprising a sequence of RBL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, RBL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic

CC nucleic acid molecule
XX
SQ Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other:
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 711 TCCTGCCCGACCTCC 726
DB 1 UCCUGCCCGAGCUC 16
RESULT 2211
ADB04319
ID ADB04319 standard; DNA; 17 BP.
AC ADB04319;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5305.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5305; 103pp; English.
PS
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other:
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 652 GAGTGCAGTGGCGCAA 667
DB 1 GAGTGCAGTGGCGCAA 16
RESULT 2212
ADB04448
ID ADB04448 standard; DNA; 17 BP.
AC ADB04448;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5434.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5434; 103pp; English.
PS
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX
SQ Sequence 17 BP; 4 A; 1 C; 8 G; 4 T; 0 U; 0 Other:
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 779 TTTAGTAGAGATGGG 794
DB 1 TTTAGTAGAGATGGG 16
RESULT 2213
ADB04436
ID ADB04436 standard; DNA; 17 BP.

```
XX ADB04436;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5422.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5422; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 4 A; 0 C; 2 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 768 TTTTGTGATTTTGG 783
XX | | | | | | | | | |
XX 2 TATTTGTATTTTGG 17
XX
XX RESULT 2214
XX ABZ60588
XX ID ABZ60588 standard; RNA; 17 BP.
XX
XX ABZ60588;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human K-Ras DNAzyme substrate #700.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
```

```
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer; modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 98; 185bp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HBR2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59898 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
XX ABZ6530 - ABZ6585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 4 A; 3 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+03;
XX Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 869 GATTACAGCGGTGAGC 884
XX | | | | | | | | | |
XX 1 GAUACAGCGGUGUC 16
XX
XX RESULT 2215
XX ABZ60580
XX ID ABZ60580 standard; RNA; 17 BP.
XX
XX ABZ60580;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human K-Ras DNAzyme substrate #692.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
```

PR 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswigen J;
 XX
 PS WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 98; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 1.8e+03;
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1000 TCAGCGATTCTCTG 1015
 :|||||:::|:
 2 UCACGCAUUCUCGUG 17
 DB
 RESULT 2216
 ABZ60570
 ID ABZ60570 standard; RNA; 17 BP.
 XX
 AC ABZ60570;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNAzyme substrate #691.
 XX
 KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016840.
 XX
 PR 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswigen J;
 XX
 PS WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 98; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524,
 CC ABZ6530 - ABZ6585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 1.8e+03;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 997 GGCTCAGCGATTCTC 1012
 :|||||:::|:
 2 GGUUCAGCAUUCUC 17
 DB
 RESULT 2217
 ABZ60570
 ID ABZ60570 standard; RNA; 17 BP.
 XX
 AC ABZ60570;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human K-Ras DNAzyme substrate #682.
 XX
 KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
 KM anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016840.
 XX
 PR 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswigen J;
 XX
 PS WPI; 2003-140484/13.
 XX
 PT Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 98; 185pp; English.
 XX
 CC The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 655 TGCAGTGGCGCAATCT 670
Db 2 UGCAGUGCGCCCAUCU 17
RESULT 2218
ID ABZ60600 standard; RNA; 17 BP.
XX
AC ABZ60600;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human K-Ras DNAzyme substrate #712.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 98; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1087 GAGCGCGGGTTTCACC 1102
Db 1 GAGACGGGCUUUCACC 16
RESULT 2219
ID ABZ60607 standard; RNA; 17 BP.
XX
AC ABZ60607;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human K-Ras DNAzyme substrate #719.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 98; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1124 AACTCTGACCTCAGG 1139
Db 1 AACCTCGACCTCAGG 16
RESULT 2220
ID ACC66396 standard; DNA; 17 BP.
XX

AC ACC66396;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 3643.
XX
XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; murine;
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
XX 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 456; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 1 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 837 GATCTGCTGCTCGG 852
DB 1 GATCTGCTGCTCTG 16
XX
RESULT 2221
ACC68207/C
ID ACC68207 standard; DNA; 17 BP.
XX
AC ACC68207;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5454.
XX
KM Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; murine;
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KM schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX

XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 668; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 6 A; 6 C; 3 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 480 GTGAGTGCTGTGATC 495
DB 16 GTGCAATGCTGTGATC 1
XX
RESULT 2222
ADB44023/C
ID ADB44023 standard; DNA; 17 BP.
XX
AC ADB44023;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #4346.
XX
KM Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX

PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 540; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 480 GTGCAGTGTGTGATC 495
Db 16 GTGCAGTGTGTGATC 1
RESULT 2223
ADB40272/c
ID ADB40272 standard; DNA; 17 BP.
XX
AC ADB40272;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #595.
XX
KW cytostratic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX
PS Disclosure; Page 101; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 7 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 480 GTGCAGTGTGTGATC 495
Db 16 GTGCAGTGTGTGATC 1
RESULT 2224
ADB43380
ID ADB43380 standard; DNA; 17 BP.
XX
AC ADB43380;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #3703.
XX
KW cytostratic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PS Disclosure; Page 464; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

CC SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCGCTGCTCGG 852

DB 1 GATCTGCGCTGCTCGG 16

RESULT 2225

ADB40001 ADB40001 standard; DNA; 17 BP.

AC ADB40001;

DT 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #324.

XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KW diagnosis.

OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

PF 17-SEP-2002; 2002WO-IB004219.

PR 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

PT New nucleic acid encoding human prostate membrane-specific antigen,

XX useful e.g. for treatment of tumors and viral infection, also related

PT polypeptide and antibodies.

XX Disclosure; Page 70; 771pp; French.

PS The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

CC SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 532 ATCTCTGCTGCTGAC 547

DB 2 ATCTCTGCTGCTGAC 17

RESULT 2226

ADB42612/C ADB42612 standard; DNA; 17 BP.

AC ADB42612;

DT 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #2935.

XX cytosstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KW diagnosis.

OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

PF 17-SEP-2002; 2002WO-IB004219.

PR 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

PT New nucleic acid encoding human prostate membrane-specific antigen,

XX useful e.g. for treatment of tumors and viral infection, also related

PT polypeptide and antibodies.

XX Disclosure; Page 375; 771pp; French.

PS The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 993 CCGGGCTCAAGCAT 1008
DB 17 CCGGGCTCAAGCAT 2

RESULT 2227
ADB42824
ID ADB42824 standard; DNA; 17 BP.
XX ADB42824;
AC
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #3147.
DE
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
XX Homo sapiens.
OS
XX
XX W02003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
XX Disclosure; Page 399; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
SQ

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 532 ATCTCTCTGCTCAGC 547
DB 2 ATCTCTCTGCTCAGC 17

RESULT 2228
ADB42925
ID ADB42925 standard; DNA; 17 BP.
XX ADB42925;
AC
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #3248.
DE
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
XX Homo sapiens.
OS
XX
XX W02003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
XX Disclosure; Page 411; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies

CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX

SQ Sequence 17 BP; 3 A; 4 C; 5 G; 0 U; 0 Other;
XX

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
YY

386 CCCAAGTGGCTGGAT 401
||| ||| ||| |||
Db 17 CCCAAGTGCTAGGAT 2
ZZ

RESULT 2230
ADB44164/C
ID ADB44164 standard; DNA; 17 BP.

AC ADB44164;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
DT

Tumour suppression/reversion associated nucleotide #4487.
DE
XX
XX cyrostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO2003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-441574/41.
DR
XX
XX

New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
PS Disclosure; Page 556; 771pp; French.
XX

The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and-to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules.
CC

CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 654 GTGAGTGGGCAATC 669
DB 16 GTGAGTGGGCAATC 1
RESULT 2231
ID ADB41301 standard; DNA; 17 BP.
XX
AC ADB41301;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #1624.
XX
KM cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN W02003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002MO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOL-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 221; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides; a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules.
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX

SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 667 ATCTGGCTCAGTCA 682
DB 2 ATCTGGCTCAGTCA 17
RESULT 2232
ID ADB40212 standard; DNA; 17 BP.
XX
AC ADB40212;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #535.
XX
KM cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN W02003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002MO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOL-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 94; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides; a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules.
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX

Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 967 ATCTGGCTCAGCA 982
Db 2 ATCTGGCTCAGCA 17

RESULT 2233
ADB44035
ADB44035 standard; DNA; 17 BP.

AC ADB44035;

DT 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #4358.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KM primer; probe; tumour suppression; tumour reversion; apoptosis;

KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KM diagnosis.

XX Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telexman A, Amson R, Tuijnder M;

DR WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,

PT useful e.g. for treatment of tumors and viral infection, also related

PS polypeptide and antibodies.

XX Disclosure; Page 541; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the

CC nucleotides; the nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour

CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as

CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors) are useful for prevention and/or treatment

CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours

CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,

CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.

XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

SO Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 532 ATCTCTGCTCAGC 547
Db 2 ATCTCTGCTCAGC 17

RESULT 2234
ADB45739/C
ADB45739 standard; DNA; 17 BP.

AC ADB45739;

DT 18-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #6062.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KM primer; probe; tumour suppression; tumour reversion; apoptosis;

KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

KM diagnosis.

XX Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telexman A, Amson R, Tuijnder M;

DR WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,

PT useful e.g. for treatment of tumors and viral infection, also related

PS polypeptide and antibodies.

XX Disclosure; Page 740; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC sequence having at least 80% identity, after optimal alignment, with the

CC nucleotides, a sequence that hybridizes under stringent conditions with

CC the nucleotides, or the complement, or corresponding RNA, of the

CC nucleotides; the nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro

CC sense and antisense sequences, of nucleotides involved in tumour

CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as

CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors) are useful for prevention and/or treatment

CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours

CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis

CC and/or prognosis of these diseases. The nucleotides and polypeptides can

CC also be used to screen for their specific interactive molecules,

CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.

XX Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

SO Query Match 1.5%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

RESULT 2235
ADB45601/c
ID ADB45601 standard; DNA; 17 BP.
XX
XX ADB45601;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Tumour suppression/reversion associated nucleotide #5924.
DE
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO2003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Tejerman A, Amson R, Tuijnder M;
PI
XX
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 724; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
CC
XX
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 480 GTGCAGTGGTGATC 495
OY |||||
DB 16 GTGCAGTGGTGATC 1
|||

```

```

XX
XX ADB45950;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Tumour suppression/reversion associated nucleotide #6273.
DE
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO2003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Tejerman A, Amson R, Tuijnder M;
PI
XX
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 765; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
CC
XX
XX Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 654 GTGCAGTGGCGCAATC 669
OY |||||
DB 16 GTGCAGTGGCGCAATC 1
|||

```

RESULT 2236
 ADB45950/c
 ID ADB45950 standard; DNA; 17 BP.

RESULT 2237
 ADE30865/c
 ID ADE30865 standard; DNA; 17 BP.
 AC ADE30865;
 XX
 XX 29-JAN-2004 (first entry)

```
XX XX Cholesterol homeostasis/adipogenesis related DNA seq id 252.
DE PF
XX XX expression vector; anorectic; antiarteriosclerotic; cardiant;
XX XX antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;
XX KW obesity; atherosclerosis; diabetes mellitus;
XX KW coronary artery heart disease; cholesterol homeostasis; ss;
XX KW differential expression.
XX OS
XX XX Homo sapiens.
XX PN
XX XX US2003180764-A1.
XX PD
XX XX 25-SEP-2003.
XX PF
XX XX 08-JAN-2003; 2003US-00339793.
XX PR
XX XX 09-JAN-2002; 2002US-0347286P.
XX PA
XX XX (LYNX-) LYNX THERAPEUTICS INC.
XX PI
XX XX Shang J, Bowen B;
XX DR
XX XX MPI; 2003-830986/77.
XX PT
XX XX Polynucleotides differentially regulated in response to cholesterol and
XX PT adipogenesis are useful to detect and treat associated conditions such as
XX PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
XX PT disease.
XX PS
XX XX Claim 8; SEQ ID NO 252; 59pp; English.
XX XX
XX CC The invention describes a composition comprising at least one expression
XX CC vector comprising a polynucleotide of the invention. The composition has
XX CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
XX CC The invention is used to detect and treat conditions associated with
XX CC elevated cholesterol and lipid or during adipogenesis, particularly
XX CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
XX CC disease. This sequence represents a polynucleotide differentially
XX CC expressed during cholesterol homeostasis and adipogenesis.
XX SQ
XX XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY
XX 480 GTGCAGTGTGTGATC 495
XX |||||
XX 16 GTGCAGTGTGTGATC 1
DB
XX
XX RESULT 2238
XX ADE30723/C
XX ID ADE30723 standard; DNA; 17 BP.
XX XX
XX AC ADE30723;
XX DT
XX XX 29-JAN-2004 (first entry)
XX DE
XX XX Cholesterol homeostasis/adipogenesis related DNA seq id 110.
XX XX
XX XX expression vector; anorectic; antiarteriosclerotic; cardiant;
XX KW antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;
XX KW obesity; atherosclerosis; diabetes mellitus;
XX KW coronary artery heart disease; cholesterol homeostasis; ss;
XX KW differential expression.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US2003180764-A1.
XX XX
XX PD 25-SEP-2003.
```

```
XX XX 08-JAN-2003; 2003US-00339793.
XX PF
XX XX 09-JAN-2002; 2002US-0347286P.
XX PR
XX XX (LYNX-) LYNX THERAPEUTICS INC.
XX PA
XX XX Shang J, Bowen B;
XX PI
XX XX MPI; 2003-830986/77.
XX DR
XX XX Polynucleotides differentially regulated in response to cholesterol and
XX PT adipogenesis are useful to detect and treat associated conditions such as
XX PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart
XX PT disease.
XX PS
XX XX Claim 8; SEQ ID NO 110; 59pp; English.
XX XX
XX CC The invention describes a composition comprising at least one expression
XX CC vector comprising a polynucleotide of the invention. The composition has
XX CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.
XX CC The invention is used to detect and treat conditions associated with
XX CC elevated cholesterol and lipid or during adipogenesis, particularly
XX CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart
XX CC disease. This sequence represents a polynucleotide differentially
XX CC expressed during cholesterol homeostasis and adipogenesis.
XX SQ
XX XX Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY
XX 993 CCCGGGCTCAAGCGAT 1008
XX |||||
XX 17 CCCGGGCTCAAGCGAT 2
DB
XX
XX RESULT 2239
XX ADH59597/C
XX ID ADH59597 standard; DNA; 17 BP.
XX XX
XX AC ADH59597;
XX XX
XX DT 25-MAR-2004 (first entry)
XX XX
XX XX Non-nucleotide probe of the invention #1.
XX DE
XX XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
XX KW probe.
XX KW
XX OS Synthetic.
XX XX
XX XX WO2003027328-A2.
XX PN
XX XX 03-APR-2003.
XX PD
XX XX 24-SEP-2002; 2002WO-US030573.
XX PF
XX XX 24-SEP-2001; 2001US-0324499P.
XX PR
XX XX (BOST-) BOSTON PROBES INC.
XX PA (DAKO-) DAKOCYTOMATION DENMARK AS.
XX XX
XX XX Kirszen NV, Hyldig-Nielsen JT, Williams BF;
XX XX
XX DR MPI; 2003-421160/39.
XX XX
XX XX Non-nucleotide probe for suppressing binding of detectable nucleic acid
XX PT probes to undesired sequences, has aggregate nucleobase sequence
XX PT homologous to randomly distributed repeat sequence of genomic nucleic
XX PT acid.
XX XX
```

PS Claim 10; SEQ ID NO 3; 103pp; English.

The present sequence represents a non-nucleotide probe. The probe is useful for suppressing the binding of one or more detectable nucleic acid probes, that are greater than 100 base pairs and that have been derived from genomic nucleic acid, to one or more undesired sequences in an assay for determining target genomic nucleic acid of a sample. The method comprises contacting the sample with the mixture of probes (preferably comprising 5-50 probes), contacting the sample with the one or more detectable nucleic acid probes, and determining the target genomic nucleic acid of the sample by determining the hybridization of the one or more detectable nucleic acid probes to the target genomic nucleic acid of the sample. The genomic nucleic acid is contained in a fixed tissue or a cell, and the sample is metaphase spreads, interphase nucleic or nucleic found in paraffin embedded tissue material or frozen tissue sections. The probe is also useful in comparing a sample of genomic nucleic acid with that of a control sample using a genomic nucleic acid reference array. The method comprises treating a sample of genomic nucleic acid and a control genomic nucleic acid, which are differentially labelled, the array or both the sample and control genomic nucleic acid and the array with the mixture of the probe under suitable hybridization conditions, contacting the array with treated mixture of sample and control genomic nucleic acid under suitable hybridization conditions, and comparing the intensities of the signals from the differential labels of the array to that caused by hybridization of the probes to genomic nucleic acid, thus determining one or more variations in copy numbers of sequences in the sample as compared with the relative copy numbers of substantially identical sequences in the control. The hybridization of the genomic array is determined using an intercalating dye or a detectable antibody, or its fragment, that is specific for a nucleic acid/nucleic acid hybrid. The sample of genomic nucleic acid to be tested and the reference of nucleic acid are labelled with detectable moiety such that hybridization of the genomic array is determined by determining the presence, absence, amount or location of the detectable label on the one or more genomic arrays. The genomic array comprises nucleic acid that is prepared from Bacterial Artificial Chromosome (BAC) clones. The present sequence represents a non-nucleotide probe of the invention.

sequence 17 BP; 0 A; 5 C; 10 G; 2 T; 0 U; 0 Other;

Query Match	1.5%	Score 14.4	DB 1	Length 17
Best Local Similarity	93.8%	Pred. No. 1.8e+03		
Matches 15	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	882	AGCCACCACGCCCGGC	897
Db	17	AGCCACCGCGCCCGGC	2

RESULT 2240

ADI49563
ID ADI49563 standard; DNA; 17 BP.

AC ADI49563;

DT 15-APR-2004 (first entry)

DE Human tumour suppression/reversion-related DNA sequence SegID2066.

KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytotoxic; virocidic; neuroprotective; neurotropic; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human

Homo sapiens.

PN W02003025177-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004523.

PR 17-SEP-2001; 2001FR-00011980.

XX
PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-313354/30.

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

PS Disclosure; SEQ ID NO 2066; 30pp; French

This invention relates to novel isolated nucleic acid sequences involved in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virocidic, neuroprotective, neurotropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishseqpc_sequences

Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match	1.5%	Score 14.4	DB 1	Length 17
Best Local Similarity	93.8%	Pred. No. 1.8e+03		
Matches 15, Conservative	0	Mismatches 1	Indels 0	Gaps 0

OY	667	ATCTGGCTCACTGCA	682
Db	2	ATCTTGGCTCACTGTA	17

RESULT 2241

ID ADI51563 standard; DNA; 17 BP.

AC ADI51563;

DT 15-APR-2004 (first entry)

Human tumour suppression/reversion-related DNA sequence SegID4066.

KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM cytostatic; vincristine; neuroprotective; nootropic; neuroleptic; probe;
 KM primer; PCR; gene chip; antisense; viral disease; tumour;
 KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human

Homo sapiens.

PN WO2003025177-A2.

27-MAR-2003 .
PD

17-SEP-2002; 2002WO-IB004523.

PR 17-SEP-2001; 2001FR-00011980.

PA (MOLE-) MOLECULAR ENGINES LAB

PI Telerman A, Amson R, Tuijnder M,

DR WPI; 2003-313354/30.

PT New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 4066; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, antiviral, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 480 GTGCACTGGTGCATC 495
DB 16 GTGCACTGGTGCATC 1
RESULT 2242
AD147683/C
ID AD147683 standard; DNA; 17 BP.
XX
XX AC AD147683;
XX
XX 15-APR-2004 (first entry)
XX
XX Human tumour suppression/reversion-related DNA sequence SeqID186.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; probe;
XX primer; PCR; gene chip; antisense; viral disease; tumour;
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO2003025177-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-IB004523.
XX
XX PR 17-SEP-2001; 2001FR-00011980.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313354/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumours and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; SEQ ID NO 186; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytostatic, antiviral, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 654 GTGCACTGGCGCATC 669
DB 16 GTGCACTGGCGCATC 1
RESULT 2243
AD148354/C
ID AD148354 standard; DNA; 17 BP.
XX
XX AC AD148354;
XX
XX 15-APR-2004 (first entry)
XX
XX Human tumour suppression/reversion-related DNA sequence SeqID857.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; probe;
XX primer; PCR; gene chip; antisense; viral disease; tumour;
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO2003025177-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-IB004523.
XX
XX PR 17-SEP-2001; 2001FR-00011980.
XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313354/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumours and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX PS Disclosure; SEQ ID NO 857; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, antiviral, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.

CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 480 GTGCAGTGTGTGATC 495
|||
16 GTGCAGTGTGTGATC 1

RESULT 2244
ADIS2733/c
ID ADIS2733 standard; DNA; 17 BP.

XX ADIS2733;

DT 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SegID5236.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytosolic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX Homo sapiens.

XX WO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

XX Disclosure; SEQ ID NO 5236; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 654 GTGCAGTGTGTGATC 669
|||
16 GTGCAGTGTGTGATC 1

RESULT 2245
ADIS2722
ID ADIS2722 standard; DNA; 17 BP.

XX ADIS2722;

DT 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SegID5225.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytosolic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX Homo sapiens.

XX WO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.

XX Disclosure; SEQ ID NO 5225; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 667 ATCTTGCTCACTGCA 682
|||
2 ATCTAGGCTCACTGCA 17

```
RESULT 2246
ADIS2147/c
ID ADIS2147 standard; DNA; 17 BP.
XX
XX
AC ADIS2147;
XX
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID4650.
XX
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025177-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
XX
PR 17-SEP-2001; 2001PR-00011980.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313354/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 4650; 30pp; French.
XX
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
XX
SQ Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 480 GTGCAGTGTGTGATC 495
DB 16 GTGCAGTGTGTGATC 1
XX
XX
RESULT 2247
ADIS2737/c
ID ADIS2737 standard; DNA; 17 BP.
XX
XX
AC ADIS2737;
XX
XX
DT 15-APR-2004 (first entry).
```

```
XX
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID5240.
XX
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025177-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
XX
PR 17-SEP-2001; 2001PR-00011980.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313354/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 5240; 30pp; French.
XX
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 480 GTGCAGTGTGTGATC 495
DB 16 GTGCAGTGTGTGATC 1
XX
XX
RESULT 2248
AD149735
ID AD149735 standard; DNA; 17 BP.
XX
XX
AC AD149735;
XX
XX
DT 15-APR-2004 (first entry)
XX
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2238.
XX
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX
```


PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 4593; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC Specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 993 CCCGGCTCAGCGCAT 1008
DB 17 CCCAGGCTCAGCGCAT 2
XX
RESULT 2251
AD149985
ID AD149985 standard; DNA; 17 BP.
XX
AC AD149985;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SegID2488.
XX
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 2488; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC Specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 533 ATCCTCCTGCTCAGC 547
DB 2 ATCCTCCTGCTCAGC 17
XX
RESULT 2252
AD152788/c
ID AD152788 standard; DNA; 17 BP.
XX
AC AD152788;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SegID5291.
XX
KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 5291; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 654 GTGCAGTGGCGCATC 669
|||
Db 16 GTGCAGTGGCGCATC 1

RESULT 2253
AD147513/C
ID AD147513 standard; DNA; 17 BP.

XX AD147513;

DT 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID16.

KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytoskeletal; virucide; neuroprotective; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

XX Homo sapiens.

PN WO2003025177-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004523.

PR 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

PS Disclosure; SEQ ID NO 16; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, neuroleptic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 993 CCGGCTCAAGCAT 1008
|||
Db 17 CCGGCTCAAGCAT 2

RESULT 2254
AD150287/C
ID AD150287 standard; DNA; 17 BP.

XX AD150287;

DT 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID2790.

KM tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytoskeletal; virucide; neuroprotective; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

XX Homo sapiens.

PN WO2003025177-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004523.

PR 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

PT New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

PS Disclosure; SEQ ID NO 2790; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, neuroleptic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant polypeptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 945 CAGGCTGAGTGCAT 960
|||
Db 17 CAGGCTGAGTGCAT 2

```
RESULT 2255
AD120628
ID AD120628 standard; DNA; 17 BP.
XX
XX
AC AD120628;
XX
XX
DT 15-APR-2004 (first entry)
XX
DE Putative eRNA sequence #37.
XX
XX
KM ds; eRNA.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2003025229-A1.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-AU001286.
XX
PR 19-SEP-2001; 2001US-0324127P.
XX
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Mattick J, Gagen M, Stanley S;
XX
XX
DR WPI; 2003-371830/35.
XX
XX
PT Identifying an eRNA or a DNA sequence comprising an eRNA-encoding
PT sequence in the nucleome of a eukaryotic cell, comprising identifying non
PT -protein-encoding nucleotide sequences within an mRNA transcript or a DNA
PT sequence.
XX
XX
PS Example 14; SEQ ID NO 118; 137bp; English.
XX
XX
CC The present invention relates to identifying an eRNA or a DNA sequence
CC comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell
CC comprising identifying non-protein-encoding nucleotide sequences within an
CC mRNA transcript or a DNA sequence encoding same in the nucleome. The
CC methods are useful for identifying an eRNA or DNA for modifying a genetic
CC network in cell to alter the cells phenotype. The present sequence
CC represents a putative eRNA sequence of the invention.
XX
XX
SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 163 TTTTGATTTTTTTTTT 178
DB 2 TTTTGATTTTTTTTTT 17
XX
XX
RESULT 2256
ACCS3368/C
ID ACCS3368 standard; DNA; 17 BP.
XX
XX
AC ACCS3368;
XX
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #2135.
XX
XX
KM ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
```

```
XX
XX
PD 27-DEC-2002.
XX
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
XX
DR WPI; 2003-250498/25.
XX
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX
PS Claim 1; Page 533; 798pp; French.
XX
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 993 CCCGGGCTCAACGAT 1008
DB 17 CCCAGGCTCAACGAT 2
XX
XX
RESULT 2257
ACCS4015
ID ACCS4015 standard; DNA; 17 BP.
XX
XX
AC ACCS4015;
XX
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #2782.
XX
XX
KM ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
XX
OS Homo sapiens.
XX
XX
PN FR2826373-A1.
XX
XX
PD 27-DEC-2002.
XX
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
XX
DR WPI; 2003-250498/25.
XX
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX
PS Claim 1; Page 682; 798pp; French.
XX
```

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 837 GATCTGCTGCTCGG 852
DB 1 GATCTGCTGCTCAG 16

RESULT 2258

ACCS2025
ID ACC52025 standard; DNA; 17 BP.

XX ACC52025;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #792.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;

KW cellular degeneration.

XX Homo sapiens.

OS FR2826373-A1.

XX PD 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX WP1; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumour cells and cell degeneration.

XX Claim 1; Page 223; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 667 ATCTTGCTCACTGCA 682
DB 2 ATCATGCTCACTGCA 17.

RESULT 2259

ACCS1578/c
ID ACC51578 standard; DNA; 17 BP.

XX ACC51578;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #345.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;

KW cellular degeneration.

XX Homo sapiens.

OS FR2826373-A1.

XX PD 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX WP1; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 120; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX

Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 480 GTGCGTGTGTGATC 495
DB 16 GTGCGTGTGCTGATC 1

RESULT 2260

ACCS3015
ID ACC53015 standard; DNA; 17 BP.

XX ACC53015;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #1782.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.

OS Homo sapiens.

PN FR2826373-A1.
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 452; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumor suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumor cells or cellular degeneration
XX
XX Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 532 ATCCTCTGCTCAGC 547
DB 2 ATCCTCCGCTCAGC 17
XX
XX RESULT 2261
XX ID ACC53596 standard; DNA; 17 BP.
XX
XX AC ACC53596;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #2363.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
XX Homo sapiens.
OS
XX FR2826373-A1.
PN
XX
XX 27-DEC-2002.
PD
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX

PS Claim 1; Page 586; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumor suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumor cells or cellular degeneration
XX
XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 667 ATCTTGCTCACTGCA 682
DB 2 ATCTAGGCTCACTGCA 17
XX
XX RESULT 2262
XX ID ACC54007 standard; DNA; 17 BP.
XX
XX AC ACC54007;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #2774.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
XX Homo sapiens.
OS
XX FR2826373-A1.
PN
XX
XX 27-DEC-2002.
PD
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijinder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 680; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumor suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumor cells or cellular degeneration
XX
XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.8e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 837 GATCTGCTGCTCGG 852
XX

Db 1 GATCTGCCGCTCGG 16
RESULT 2263
ACCS2967/c
ID ACCS2967 standard, DNA, 17 BP.
XX
XX
AC ACCS2967;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #1734.
XX
KM s8; tumour suppressor; antitumour; cytostatic; tumour suppression;
KM tumour regression; apoptosis; virus resistance; diagnosis;
KM cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijinder M, Teleman A, Amson R;
PI WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 440; 798pp; French.
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 386 CCCAAGTGTGGGAT 401
Db 17 CCCAAGTGTGGGAT 2
RESULT 2264
ADL50195
ID ADL50195 standard; RNA, 17 BP.
XX
AC ADL50195;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1309.
XX
KM antisense oligonucleotide; neurite growth inhibitor; NOGO;
KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KM protein kinase PKR; cerebrovascular accident;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KM restenosis; asthma; Crohn's disease; diabetes; obesity;
KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KM substrate; ds.
XX
OS unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
XX
PR 29-MAY-2001; 2001US-0294412P.
XX
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
PI WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3728; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 948 GCTGAGTGCAGATGC 963
Db 1 GCTGAGTGCAGATGC 16
RESULT 2265
ADL50217
ID ADL50217 standard; RNA, 17 BP.
XX
AC ADL50217;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1331.
XX
KM antisense oligonucleotide; neurite growth inhibitor; NOGO;
KM prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KM protein kinase PKR; cerebrovascular accident;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX
OS unidentified.
XX
XX
PN MO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002MO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
XX
DR WPI; 2003-058513/05.
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 3750; 317pp; English.
XX
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
XX
SQ Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 369 TCACCTGCTCTCAGCC 384
Db 2 UCCACGCGCCGCGCC 17
RESULT 2266
ADL50746
ID ADL49442 standard; RNA; 17 BP.
XX
XX
AC ADL49442;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #556.
XX
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
XX
OS unidentified.
XX
XX
PN MO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002MO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX
XX
DR WPI; 2003-058513/05.
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 2975; 317pp; English.
XX
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
XX
SQ Sequence 17 BP; 2 A; 1 C; 2 G; 0 T; 12 U; 0 Other;
XX
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
QY 1066 CTAATTTTGTATTT 1081
Db 1 CUAAUUUUUGUUUU 16
RESULT 2267
ADL50746
ID ADL50746 standard; RNA; 17 BP.
XX
XX
AC ADL50746;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #1860.
XX
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
OS Unidentified.
XX WO200281628-A2.
XX 17-OCT-2002.
PD 03-APR-2002; 2002WO-US010512.
PF 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX (RIBO-) RIBOZYME PHARM INC.
PA Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
PI WPI; 2003-058513/05.
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 4279; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC reterososis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 197 CCAATGTCGACGCT 212
DB 2 CCAUGUGGCCAGCGCU 17
RESULT 2268
ADL49424
ID ADL49424 standard; RNA; 17 BP.
XX
AC ADL49424;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #538.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
OS Unidentified.
XX WO200281628-A2.
XX 17-OCT-2002.
PD 03-APR-2002; 2002WO-US010512.
PF 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX (RIBO-) RIBOZYME PHARM INC.
PA Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
PI WPI; 2003-058513/05.
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2957; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC reterososis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 2 G; 0 T; 6 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.8e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 678 CTGCACTCTGCTC 693
DB 1 CUGCACTUCGCTC 16
RESULT 2269
ADL49431
ID ADL49431 standard; RNA; 17 BP.
XX
AC ADL49431;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #545.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
XX 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2964; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 702 AAGTATTCCTGCGCC 717
|||:|:|:|:|:|:|
Db 1 AAGGAGUUCUCGCGCC 16
|||:|:|:|:|:|:|
RESULT 2270
ADL49441
ID ADL49441 standard; RNA; 17 BP.
XX
AC ADL49441;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human PKR substrate sequence #555.
XX
DE antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
XX 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2974; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 1 C; 2 G; 0 T; 11 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
QY 1066 CTAATTTTGTGATTT 1081
|:|:|:|:|:|:|:|:|:|:|:|:|
Db 2 CUAAUUUUUGUUUU 17
|:|:|:|:|:|:|:|:|:|:|:|:|
RESULT 2271
ADL49952
ID ADL49952 standard; RNA; 17 BP.
XX
AC ADL49952;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human PKR substrate sequence #1066.
XX
DE antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3485; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX retemosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection,
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 0 T; 3 U; 0 Other;
XX
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+03;
XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1109 GTCAGGCTGCTCTCAA 1124
DB 2 GCCAGGCTGCTCTCAA 17
XX
XX
XX RESULT 2272
XX ADL50425
XX ID ADL50425 standard; RNA; 17 BP.
XX
XX AC ADL50425;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human PKR substrate sequence #1539.
XX
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3958; 317bp; English.
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX invention are useful for treating: cerebrovascular accident, central
XX nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX retemosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX disease, lupus, multiple sclerosis, transplant/graft rejection,
XX ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX nucleic acids of the invention are also useful for down-regulating the
XX expression of a target gene and as a diagnostic tool to examine genetic
XX drifts and mutations within diseased cells or to detect the presence of a
XX target RNA in a cell. The present RNA sequence represents a human PKR
XX substrate sequence.
XX
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;
XX
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+03;
XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 1124 AACTCTGACCTCAGG 1139
DB 1 AACCTCGACCTCAGG 16
XX
XX
XX RESULT 2273
XX ADL49452
XX ID ADL49452 standard; RNA; 17 BP.
XX
XX AC ADL49452;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human PKR substrate sequence #566.
XX
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
XX protein kinase PKR; cerebrovascular accident;
XX central nervous system injury; CNS injury; spinal cord injury; cancer;
XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW	reletemosis; asthma; Crohn's disease; diabetes; obesity;
KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW	substrate; de.
OS	Unidentified.
XX	
XX	WO200281628-A2.
XX	
PD	17-OCT-2002.
XX	
PE	03-APR-2002; 2002MO-US010512.
XX	
XX	05-APR-2001; 2001US-00827395.
PR	29-MAY-2001; 2001US-0294412P.
PR	28-AUG-2001; 2001US-0315315P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
XX	
PI	Blaet L, Chowwria B, Haeblerl P, Mcswigen J, Poanugh K;
XX	
XX	WPI; 2003-058513/05.
DR	
PT	Novel enzymatic nucleic acid that down-regulates expression of neurite
PT	growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT	protein kinase PKR genes, for treating cancer and inflammatory disease.
PS	
PS	Claim 59; SEQ ID NO 2985; 317pp; English.
CC	
CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC	that down regulate the expression or inhibit the function of a receptor
CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC	Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC	invention are useful for treating: cerebrovascular accident, central
CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC	resenensis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC	disease, lupus, multiple sclerosis, transplant/graft rejection,
CC	ischaeimia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC	nucleic acids of the invention are also useful for down-regulating the
CC	expression of a target gene and as a diagnostic tool to examine genetic
CC	drifts and mutations within diseased cells or to detect the presence of a
CC	taget RNA in a cell. The present RNA sequence represents a human PKR
CC	substrate sequence.
CC	
SQ	Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
DY	
Query Match	1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity	75.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
DY	797 CACCATGTTCGCCAGG 812
:::	
1 CACCAGUUGGCCAGG 16	
RESULT 2274	
ADL49925	
ID ADL49925 standard; RNA; 17 BP.	
AC ADL49925;	
DT 20-MAY-2004 (first entry)	
XX Human PKR substrate sequence #1039.	
XX	
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;	
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;	
KW protein kinase PKR; cerebrovascular accident;	
KW central nervous system injury; CNS injury; spinal cord injury; cancer;	
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;	

KW		restenosis; asthma; Crohn's disease; diabetes; obesity;
KM		autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM		graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KV		allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XK		substrate; dg.
XX		Unidentified.
XX		
PN		WO200281628-A2.
PD		17-OCT-2002.
PP		03-APR-2002; 2002WO-US010512.
PR		05-APR-2001; 2001US-00827395.
PR		29-MAY-2001; 2001US-0294412P.
PR		28-AUG-2001; 2001US-0315315P.
PA	(RIBO-)	RIBOZYME PHARM INC.
PI	Blaet L,	Chowrira B, Haeberli P, Mcswigen J, Fonaugh K;
DR	WPJ;	2003-058513/05.
PT		Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D ₂ receptor, Ikappab kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.
PS	Claim 59;	SEQ ID NO 3458; 317bp; English.
CC	The invention comprises	nucleic acids (e.g., antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D ₂ receptor (PTGDR), Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g., melanoma, lymphoma or glioma), inflammatory disease (e.g., rheumatoid arthritis, osteoarthritis or asthma), Crohn's disease, diabetes, obesity, autoimmune diseases, lupus, multiple sclerosis, transplant/graft rejection, ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g., asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.
SQ	Sequence 17 BP;	2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;
Query Match	1.5%;	Score 14.4; DB 1; Length 17;
Best Local Similarity	62.5%;	Pred. No. 1.8e+03;
Matches	10; Conservative	5; Mismatches 1; Indels 0; Gaps 0.
DY	1006 GATTCCTCGTGCAG	1021 ::: :: :
Db	2 GAUUCUCGCCUCAG	17
RESULT 2275		
IDL50192		
ID	ADLS0192 standard; RNA;	17 BP.
AC	ADLS0192;	
DT	20-MAY-2004	(first entry)
DE	Human PKR substrate sequence #1306.	
KX		
KM	antisense oligonucleotide; neurite growth inhibitor; NOGO;	
KM	prostaglandin D ₂ receptor; PTGDR; ikappab kinase; IKK;	
KM	protein kinase PKR; cerebrovascular accident;	
KM	central nervous system injury; CNS injury; spinal cord injury; cancer;	
KM	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;	

restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 3725; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 6 C; 5 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 935 CTCTGTACCCAGGCT 950
||:|||||:
||:|||||:
Db 2 CUCUGUGCCACAGGCU 17
RESULT 2276
ADL50735
ID ADL50735 standard; RNA, 17 BP.
XX
AC ADL50735;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #1849.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
PN MO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002MO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
DR Novel enzymatic nucleic acid that down-regulates expression of neurite
XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
XX protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 4268; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 665 CAATCTTGCTCACTG 680
||:|||||:
||:|||||:
Db 2 CAGUCUUGGCUACUG 17
RESULT 2277
ADH17665/c
ID ADH17665 standard; DNA, 17 BP.
XX
AC ADH17665;
XX
DT 11-MAR-2004 (first entry)
XX
DE Forward PCR primer Ag6837 used to analyse human NOV expression.
XX
XX NOV; antidiabetic; anorectic; cardiant; hypotensive;
KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;
KW protozoacide; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;
KW dermatological; antiasthmatic; antilipemic; metabolic; diabetes;

KM obesity; infection; anorexia; cancer; cardiovascular; hypertension;
 KM atherosclerosis; neurodegenerative; Alzheimer's disease; Parkinson's;
 KM epilepsy; immune; osteoarthritis; haemopoietic;
 KM inflammatory skin disorder; asthma; dyslipidaemia; neurogenesis;
 KM cell differentiation; proliferation; haemopoiesis; wound healing;
 KM angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KM pharmacogenomic; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003093432-A2.
 XX
 PD 13-NOV-2003.
 XX
 PF 02-MAY-2003; 2003WO-US013690.
 XX
 PR 02-MAY-2002; 2002US-0377321P.
 PR 08-MAY-2002; 2002US-0378730P.
 PR 24-MAY-2002; 2002US-0383075P.
 PR 29-MAY-2002; 2002US-0384044P.
 PR 30-MAY-2002; 2002US-0384215P.
 PR 30-MAY-2002; 2002US-0384296P.
 PR 30-MAY-2002; 2002US-0384297P.
 PR 30-MAY-2002; 2002US-0384327P.
 PR 31-MAY-2002; 2002US-0385211P.
 PR 02-JUL-2002; 2002US-0393333P.
 PR 09-AUG-2002; 2002US-0402154P.
 PR 09-AUG-2002; 2002US-0402171P.
 PR 09-AUG-2002; 2002US-0402204P.
 PR 22-AUG-2002; 2002US-0402055P.
 PR 22-AUG-2002; 2002US-0405175P.
 PR 27-AUG-2002; 2002US-0406129P.
 PR 23-SEP-2002; 2002US-0412854P.
 PR 30-SEP-2002; 2002US-0414975P.
 PR 07-OCT-2002; 2002US-0416611P.
 PR 24-OCT-2002; 2002US-0420851P.
 PR 31-OCT-2002; 2002US-0422547P.
 PR 01-MAY-2003; 2003US-00428275.
 XX
 PA (CUBA-) CUBAGEN CORP.
 XX
 PI Alvarez E, Anderson DW, Boldog FL, Catterton E, Edinger SR,
 PI Fernandes ER, Gerlach VL, Gorman L, Grosse WM, Guo X, Ji W,
 PI Kekuda R, Li L, Macdougall JR, Padigaru M, Patunajan M,
 PI Peterson JD, Rastelli L, Shinkets RA, Spytek KA, Stone DJ,
 PI Vernet CM, Voss EZ, Zhong M;
 XX
 DR WPI; 2004-053040/05.
 XX
 PT New isolated NOVX polypeptide, useful for preventing, diagnosing or
 PT creating NOVX-associated disorders, e.g. osteoarthritis, obesity,
 PT atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
 XX
 PS Example C; SEQ ID NO 355; 478pp; English.
 XX
 CC The invention relates to a novel isolated NOVX polypeptide. The
 CC polypeptide of the invention demonstrates antidiabetic, anorectic,
 CC cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide,
 CC antibacterial, fungicide, protozoacide, nootropic, neuroprotective,
 CC antiparkinsonian, anticonvulsant, osteopathic, antiarthritic,
 CC antiinflammatory, dermatological, antiasmatic and antipneumic
 CC activities. The polypeptides, nucleic acid molecules and antibodies may
 CC be useful in the manufacture of a medicament for treating metabolic
 CC disorders, diabetes, obesity, infectious diseases (viral, bacterial,
 CC fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular
 CC diseases including hypertension and atherosclerosis, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune
 CC disorders such as osteoarthritis, haemopoietic disorders, inflammatory
 CC skin disorders, asthma and various types of dyslipidaemia. The nucleic
 CC acids and polypeptides may also be used as targets for the identification
 CC of small molecules that modulate or inhibit neurogenesis, cell
 CC differentiation, cell proliferation, haemopoiesis, wound healing and

CC angiogenesis, in gene therapy and the in generation of antibodies that
 CC bind immunospecifically to NOVX substances for use in therapeutic or
 CC diagnostic methods. The nucleic acids may be further used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine and pharmacogenomics. The current sequence is that of the human
 CC NOVX-related PCR primer which was used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 369 TCCACCTGCTCAGCC 384
 Db 16 TCCACCTGCTCAGCC 1
 XX
 RESULT 2278
 ADI35123/C
 ID ADI35123 standard; DNA; 17 BP.
 XX
 AC ADI35123;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human PLA2G1B gene polymorphism genotyping second PCR primer.
 XX
 KW PLA2G1B; fat deposition; leanness; single nucleotide polymorphism;
 KW non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
 KW hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
 KW microalbuminuria; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO2004002295-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020830.
 XX
 PR 27-JUN-2002; 2002US-0392361P.
 XX
 PA (SEOU-) SEQUENOM INC.
 XX
 PI Adam GR, Langdown ML;
 XX
 DR WPI; 2004-082843/08.
 XX
 PT Diagnosing a predisposition to fat deposition or leanness, useful for
 PT diagnosing a predisposition to e.g. diabetes or hypertension, comprises
 PT detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
 PT the subject.
 XX
 PS Example 2; Page 47; 91pp; English.
 XX
 CC The invention relates to diagnosing a predisposition to fat deposition or
 CC leanness in a subject comprising detecting the presence or absence of a
 CC polymorphic variation associated with fat deposition at a polymorphic
 CC site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a
 CC subject, where the presence of the polymorphic variation indicates a
 CC predisposition to fat deposition in the subject. The polymorphic
 CC variation is a guanine at position 7328 or thymine at position 9182 of
 CC the present sequence. The method is useful for diagnosing a
 CC predisposition to fat deposition or leanness in a subject, and
 CC consequently for diagnosing a predisposition to non-insulin dependent
 CC diabetes mellitus (NIDDM) in a subject and conditions such as
 CC hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,
 CC hypercoagulability, or microalbuminuria, which can lead to early
 CC prescription of preventive measures. Sequences ADI3514-ADI35123
 CC represent PCR primers used for genotyping polymorphisms in a human

CC PIA2G1B nucleotide sequence.
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 634 ACTCTGTGACCCAGGC 649
 16 ACTCTGTGACCCAGGC 1
 Db 16 ACTCTGTGACCCAGGC 1
 RESULT 2279
 ADK96811
 ID ADK96811 standard; DNA; 17 BP.
 AC ADK96811;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Primer of the invention #2531.
 XX
 KW human; single nucleotide polymorphism; SNP; ss; primer.
 KM
 OS Synthetic.
 OS
 PN JP2003259875-A.
 XX
 PD 16-SEP-2003.
 XX
 PF 08-MAR-2002; 2002JP-00064373.
 XX
 PR 08-MAR-2002; 2002JP-00064373.
 XX
 PA (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2004-093977/10.
 XX
 PT Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.
 XX
 PS Claim 2; SEQ ID NO 5840; 2627bp; Japanese.
 XX
 CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.
 XX
 SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 281 CCACCATGCCCGGCTC 296
 2 CCACCATGCCCGGCTC 17
 Db 2 CCACCATGCCCGGCTC 17
 RESULT 2280
 ADK13208/C
 ID ADK13208 standard; DNA; 17 BP.
 AC ADK13208;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human glioma endothelial marker (GEM) long tag SEQ ID NO:386.
 XX
 KW glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;

KW anticancer; antiglioma; immune response; cytostatic;
 KW multi-drug sensitive glioma; human; long tag; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO2004016758-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 15-AUG-2003; 2003WO-US025614.
 XX
 PR 15-AUG-2002; 2002US-0403390P.
 PR 01-APR-2003; 2003US-0458978P.
 XX
 PA (GEN2) GENZYME CORP.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Madden ST, Wang CJ, Cook BP, Lattera J, Walter K,
 XX
 DR WPI; 2004-247973/23.
 XX
 PT Diagnosing glioma by detecting expression product of any one of 255
 PT genes, glioma endothelial markers, in brain tissue sample suspected of
 PT being neoplastic, and comparing the expression with expression in normal
 PT brain tissue sample.
 XX
 PS Example 2; SEQ ID NO 386; 114bp; English.
 XX
 CC The present invention describes a method (M1) for aiding in the diagnosis
 CC of glioma. (M1) involves detecting an expression product of at least one
 CC gene (I) in a first brain tissue sample (T) suspected of being
 CC neoplastic, where (I) is chosen from any one of 255 genes (glioma
 CC endothelial markers (GEMs)) as given in specification, and comparing the
 CC expression of (I) in (T) with expression of (I) in a second normal brain
 CC tissue sample (R), where increased expression of (I) in (T) relative to
 CC (R), identifies (T) as likely to be neoplastic. Also described: (1)
 CC treating (M2) glioma involves contacting cells of the glioma with an
 CC antibody that specifically binds to a extracellular epitope; (2)
 CC identifying (M3) a test compound as potential anticancer or antiglioma
 CC drug involves contacting a test compound with the cell which expresses
 CC (1), monitoring an expression product of the at least one gene and
 CC identifying test compound as a potential anticancer drug if it decreases
 CC the expression of at least one gene; (3) identifying (M4) a test compound
 CC as potential anticancer or antiglioma drug involves contacting a test
 CC compound with the cell which expresses mRNA of at least one gene
 CC identified by a tag as described above, monitoring mRNA of the gene, and
 CC identifying the expression of at least one gene; and (4) inducing (M5) an
 CC immune response to glioma involves administering to a mammal, a protein
 CC or (I). (I) have cytostatic activities, and can be used to trigger immune
 CC destruction of glioma cells, and as immune response inducers. (M1) is
 CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi-
 CC drug sensitive glioma in a human. (M5) is useful for inducing an immune
 CC response to a glioma in a mammal having glioma or in a mammal who has had
 CC a glioma surgically removed. The present sequence represents a human GEM
 CC long tag oligonucleotide, which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 732 AGCTGGAGCTACAGGC 747
 17 AGCTGGAGCTACAGGC 2
 Db 17 AGCTGGAGCTACAGGC 2
 RESULT 2281
 ADJ10024/C
 ID ADJ10024 standard; DNA; 17 BP.

XX AC ADJ10024;
XX 17-JUN-2004 (first entry)
XX DT
XX DE PCR primer 30 to genotype SNPs of human phospholipase A2 (PLA2G1B) DNA.
XX human; PCR; ss; fat reduction; fat deposition; phospholipase A2; PLA2G1B;
XX appetite suppressant; lipase inhibitor; exercise regimen; obesity;
XX non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
XX hyperinsulin; antidiabetic; primer.
XX Homo sapiens.
XX OS
XX PN WO2004002236-A2.
XX PD 08-JUN-2004.
XX PF 27-JUN-2003; 2003WO-US020831.
XX PR 27-JUN-2002; 2002US-0392362P.
XX PA (SEQU-) SEQUENOM INC.
XX PI Adam GIR, Langdown ML, Denissenko MP, Dennis E, Cantor C;
XX PI Rubin B;
XX DR MPI; 2004-071944/07.
XX PT Identifying a candidate therapeutic for fat reduction, useful for
XX PT treating diabetes, by introducing a test molecule to a system comprising
XX PT PLA2G1B protein or nucleic acid, and determining the presence of
XX PT interaction between the compounds.
XX PS Example 2; Page 72; 116pp; English.
XX CC This invention relates to a novel candidate therapeutic agent useful for
XX CC fat reduction and disorders related to fat depositions. Specifically, it
XX CC refers to polymorphic variations in the phospholipase A2 (PLA2G1B) DNA,
XX CC which is located on chromosome 12q24 and has been associated with central
XX CC fat deposition. The present invention describes methods to detect the
XX CC presence or absence of these single nucleotide polymorphisms of PLA2G1B,
XX CC in particular G7328A and T9182G, and subsequently provide treatment that
XX CC reduces fat deposition. This treatment may consist of an appetite
XX CC suppressant, a lipase inhibitor, a phospholipase inhibitor, an exercise
XX CC regimen, a dietary regimen, psychological counseling, psychotherapy or a
XX CC psychotherapeutic. Accordingly, PLA2G1B is a target for reducing fat
XX CC deposition and it can be used to treat both obesity and non-insulin
XX CC dependent diabetes mellitus (NIDDM), as well as cardiovascular disorders
XX CC such as hypertension. As such, it exhibits antidiabetic activity. This
XX CC oligonucleotide sequence is a PCR primer used to amplify a region of
XX CC interest (i.e. genotype SNPs) in human PLA2G1B DNA of the invention.
XX SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
SQ Query Match 1.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 634 ACTCTGTACCCAGGC 649
DB 16 ACTCTGTACCCAGGC 1
RESULT 2282
ADN06450
ID ADN06450 standard; DNA; 17 BP.
XX
AC ADN06450;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human FLAP related microsatellite marker SEQ ID NO:98.

XX KW leukotriene synthase inhibitor; myocardial infarction;
XX KW acute coronary syndrome; antiatherosclerotic; cardiac; antianginal;
XX KW leukotriene biosynthesis inhibitor; leukotriene receptor antagonist;
XX KW 5-lipoxygenase activating protein; FLAP; human; chromosome 13;
XX KW chromosome 13q12; polymorphism; 5-lipoxygenase gene promoter;
XX KW 5-LO gene promoter; diabetes; hypertension; hypercholesterolaemia;
XX KW obesity; inflammatory marker; low density lipoprotein; cholesterol;
XX KW high density lipoprotein; angina; atherosclerosis; microsatellite marker;
XX KW ss.
XX Homo sapiens.
XX OS
XX PN WO2004035741-A2.
XX PD 29-APR-2004.
XX PF 16-OCT-2003; 2003WO-US032556.
XX PR 17-OCT-2002; 2002US-0419433P.
XX PR 21-FEB-2003; 2003US-0449331P.
XX PA (DECO-) DECODE GENETICS EHF.
XX PI Helgadottir A, Gurney ME, Gulcher JR;
XX PI
XX DR MPI; 2004-357211/33.
XX PT Use of leukotriene synthase inhibitor for manufacture of a medicament
XX PT for treatment for myocardial infarction or susceptibility to myocardial
XX PT infarction in individual.
XX PS Disclosure; SEQ ID NO 98; 306pp; English.
XX CC The present invention describes using a leukotriene synthase inhibitor
XX CC (I) for the manufacture of a medicament for the treatment of myocardial
XX CC infarction or susceptibility to myocardial infarction in an individual.
XX CC Also described is a method (MI) for the treatment of acute coronary
XX CC syndrome (ACS) in an individual comprising administering (I). (I) has
XX CC antiatherosclerotic, cardiac and antianginal activities, and can be used
XX CC as a leukotriene biosynthesis inhibitor, and a leukotriene receptor
XX CC antagonist. (I) can be used for the manufacture of a medicament for the
XX CC treatment of myocardial infarction or susceptibility to myocardial
XX CC infarction in an individual who has at least one risk factor chosen from
XX CC an at-risk haplotype for myocardial infarction, an at-risk haplotype in
XX CC the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a
XX CC FLAP nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-
XX CC LO) gene promoter; in an individual who has at least one risk factor
XX CC chosen from diabetes, hypertension, hypercholesterolaemia, elevated
XX CC lip(a), obesity, past or current smoker; in an individual having elevated
XX CC inflammatory marker chosen from C-reactive protein (CRP), serum amyloid
XX CC A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue
XX CC necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
XX CC soluble intervascular adhesion molecule (sICAM), E-selectin, matrix
XX CC metalloproteinase type-1, matrix metalloproteinase type-2, matrix
XX CC metalloproteinase type-3 and matrix metalloproteinase type-9; in an
XX CC individual having increased low density lipoprotein (LDL) cholesterol
XX CC and/or decreased high density lipoprotein (HDL) cholesterol; in an
XX CC individual having increased leukotriene synthase; in an individual
XX CC having previous myocardial infarction or acute coronary syndrome (ACS)
XX CC event, stable angina; or in an individual who has atherosclerosis or who
XX CC requires treatment to restore blood flow in arteries. (MI) is useful for
XX CC treating an individual suffering from acute coronary syndrome chosen from
XX CC unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-
XX CC elevation myocardial infarction (STEMI). The human FLAP gene is located
XX CC on chromosome 13, more specifically to 13q12. The present sequence
XX CC represents a microsatellite marker used in the exemplification of the
XX CC present invention.
SQ Query Match 1.5%; Score 14.4; DB 1; Length 17;
Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

PR 25-NOV-2002; 2002US-0429136P.
 PR 24-JUL-2003; 2003US-0490234P.
 XX (SEQU-) SEQUENCOW INC.
 PA
 PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
 DR WPI; 2004-441082/41.
 XX
 PT Identifying a subject at risk of breast cancer by detecting the presence
 PT or absence of one or more nucleotide polymorphic variations, useful for
 PT diagnosing, preventing and/or treating breast cancer.
 XX
 PS Example 3; Page 82; 286pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject at risk
 CC of breast cancer which comprises detecting the presence or absence of one
 CC or more polymorphic variations associated with breast cancer in a nucleic
 CC acid sample from a subject. The method of the invention has cytostatic
 CC applications and may be useful for identifying a risk of breast cancer,
 CC as well as therapeutic and prophylactic treatments that specifically
 CC target breast cancer, such as gene therapy. The current sequence is that
 CC of an extend primer of the invention which was used to genotype single
 CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;
 CC GPIV:GPIV) DNA which is located at chromosomal position 19q13.4.
 CC
 SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 OY
 Query Match 1.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.8e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 17 GGATTACAGCTGTCA 413
 17 GGATTACAGCTGTCA 2
 RESULT 2286
 AAQ95849/c
 ID AAQ95849 standard; DNA; 18 BP.
 XX
 AC AAQ95849;
 XX
 DT 21-FEB-1996 (first entry)
 XX
 DE Primer A (Group 11, set A) for marker D6S344, chromosome 6.
 XX
 KW primer; polymerase chain reaction; PCR; linkage study; locus;
 KW microsatellite marker sequence; automated genotyping; allele;
 KW polymorphism; detection; Homo sapiens; ss.
 XX
 OS Synthetic.
 XX
 PN WO9515400-A1.
 XX
 PD 08-JUN-1995.
 XX
 PF 05-DEC-1994; 94WO-US013945.
 XX
 PR 03-DEC-1993; 93US-00160837.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Levitt RC;
 DR WPI; 1995-215278/28.
 XX
 PT Kit for automated genotyping contg. pairs of PCR primers - designed to
 PT amplify polymorphic nucleotide repeat sequences, arranged in sets each
 PT with a characteristic fluorescence label, useful e.g. in detection of
 PT disease related genetic rearrangement.
 XX
 PS Disclosure; Fig 7K-2; 104pp; English.

XX
 CC The method aims to provide a collection of highly reproducible
 CC microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
 CC throughout the human genome which can be detectably labelled. The MMS are
 CC polymorphic, simple sequence repeats and can be used in automated
 CC genotyping, esp. fluorescence-based. The primers correspond to the unique
 CC DNA sequence surrounding each marker, and PCR is used to detect each
 CC polymorphism. When the MMS show considerable polymorphism (ie. a
 CC difference in the number of repeats) between individuals, the markers can
 CC be particularly informative. The MMS can be ideal for linkage studies.
 CC Kits comprise at least 4 groups, of at least 3 sets, each comprising
 CC labelled primers for PCR amplification of the DNA. Group 11 primer pairs
 CC are shown in AAQ95841-82. The published size range of the D6S344 allele
 CC is 139-159 bp, and the degree of heterozygosity in the population is
 CC about 72%
 XX
 SQ Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 OY
 Query Match 1.5%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 16 GTGACCCAGGCTGGAG 654
 16 GTGACCCAGGCTGGAG 1
 RESULT 2287
 AAX36673/c
 ID AAX36673 standard; DNA; 18 BP.
 XX
 AC AAX36673;
 XX
 DT 13-JUL-1999 (first entry)
 XX
 DE PCR primer for marker D6S344.
 XX
 KW PCR primer; detection; glaucoma allele; haplotype analysis; human; GLC1B;
 KW chromosome 2; chromosome 6; GLC6p25; haplotype profile;
 KW presymptomatic glaucoma; symptomatic glaucoma; ss.
 XX
 OS Synthetic.
 XX
 OS Homo sapiens.
 XX
 PN WO9916899-A2.
 XX
 PD 08-APR-1999.
 XX
 PF 29-SEP-1998; 98WO-CA000924.
 XX
 PR 30-SEP-1997; 97CA-02217097.
 XX
 PA (UYLA-) UNIV LAVAL.
 XX
 PI Raymond V, Morissette J, Falardeau P, Cote G, Anctil J;
 DR WPI; 1999-263704/22.
 XX
 PT Haplotype analyses for indirect detection of glaucoma.
 XX
 PS Claim 18; Page 28; 41pp; English.
 XX
 CC This sequence represents a PCR primer used in the method of the
 CC invention. The method is for detecting the presence of alleles for
 CC glaucoma comprising haplotype analysis of human chromosome 2 and 6
 CC respectively, where the haplotypes are associated with loci GLC1B and
 CC GLC6p25 respectively. The primers are used to amplify gene sequences to
 CC generate information necessary to compile haplotype profiles. The
 CC haplotype profiles can be used to detect presymptomatic and symptomatic
 CC glaucoma. They can also be used to localise, isolate and identify the
 CC GLC1B and GLC6p25 loci so that detection of individuals with glaucoma is
 CC enhanced. The haplotype analyses also provide means for identification
 CC and following of mutant alleles in pedigrees or populations.

CC Identification of presymptomatic individuals using the methods allows
 CC intervention in the disease process and obviates the impact of inheriting
 CC a mutant allele causing disease, by medically disrupting the initiation
 CC or progression of the disease
 XX
 SQ Sequence 18 BP, 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 639 GTGACCCAGGCTGGAG 654
 |||||
 16 GTGACCCAGGCTGGAG 1

RESULT 2288
 AAA09767/c
 ID AAA09767 standard; DNA; 18 BP.

AC AAA09767;

DT 23-JUN-2000 (first entry)

DE Primer #17.

KM Primer; cytochrome P450; drug metabolism; omeprazole; pentaprazole;
 KM phenytoin; verapamil; propofol; tolbutamide; S-warfarin; imipramin;
 KM anti-malarial prodrug; proganil; tricyclic anti-depressant; ss.

OS Homo sapiens.

PN MO200012757-A1.

PD 09-MAR-2000.

PF 25-AUG-1999; 99MO-SE001449.

PR 28-AUG-1998; 98SE-00002897.

PA (SANG-) SANGTEC MEDICAL AB.

PI Hauzenberger D;

DR WPI; 2000-282939/24.

PT Determining the ability of cells to metabolize a drug using a primer
 PT complementary to a target sequence immediately adjacent and 5' in
 PT relation to a defined point mutation of single-stranded DNA encoding a
 PT cytochrome P450 isoform.

PS Disclosure; Page 23; 28pp; English.

XX The invention relates to a method for determining the ability of a cell
 CC to metabolise a drug. The method comprises using a detection primer
 CC complementary to a sequence 5' in relation to a point mutation of single-
 CC stranded DNA encoding a cytochrome P450 isoform, and detecting the
 CC hybridisation. Cytochrome P450 is a group of enzymes located in the
 CC endoplasmic reticulum primarily in the liver. Cytochrome P450 (CYP) is
 CC involved in the major route of phase I drug metabolism. The polymorphism
 CC of these enzymes results in the appearance of different phenotypes with
 CC differential capacities to metabolise drugs. The method allows for the
 CC detection of a mutation in a CYP nucleotide sequence, where the mutation
 CC is known to affect the isoform's ability to metabolise a drug. The method
 CC is useful for measuring a patient's ability to metabolise a drug, as
 CC specifically drugs which are metabolised by cytochrome P450 such as
 CC omeprazole, pentaprazole, phenytoin, verapamil, propofol, tolbutamide,
 CC S-warfarin, tricyclic antidepressants such as imipramin and anti-malarial
 CC prodrugs such as proganil

SQ Sequence 18 BP, 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 822 ATCTCTGACCTGTG 837
 |||||
 16 ATCTCTGACCTGTG 1

RESULT 2289
 AAF24965
 ID AAF24965 standard; DNA; 18 BP.

AC AAF24965;

DT 30-APR-2001 (first entry)

DE PCR primer used to amplify the human krt1 gene exon 12.

KM Human; krt1 gene; Ras gene; cavernoma; gene therapy; angiogenesis;
 KM vascular malformation; dysplasia; angioma; tumour; PCR primer; ss.

OS Homo sapiens.

PN FR2795732-A1.

PD 05-JAN-2001.

PF 01-JUL-1999; 99FR-00008504.

PR 01-JUL-1999; 99FR-00008504.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Tournier LE, Laberge Le Couteux S, Labauge P;

DR WPI; 2001-149774/16.

PT New primers for amplifying regions of the krt1 gene, useful for
 PT diagnosis, particularly by detecting mutations, cavernomas, and gene
 PT therapy with this gene.

PS Claim 1; Page 16; 39pp; French.

XX PCR primers AAF24962-65 were used to amplify exon 12 of the human krt1
 CC gene. Krt1 is a member of the Ras gene family. Mutations in the krt1
 CC gene are responsible for certain vascular abnormalities. The primers are
 CC used to detect mutations in the krt1 gene, specifically those mutations
 CC that are associated with presence of cavernomas, for diagnosis. The krt1
 CC gene, or its derivatives, are useful in gene therapy for controlling or
 CC inhibiting angiogenesis, e.g. in cases of vascular malformation or
 CC dysplasia, or angioma, and the krt1 protein, optionally modified, may be
 CC used similarly, particularly for treatment of tumours

SQ Sequence 18 BP, 2 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 209 GGCTGCTCTGAACTC 224
 |||||
 1 GGCTGCTCTGAACTC 16

RESULT 2290
 ABA82331/c
 ID ABA82331 standard; DNA; 18 BP.

AC ABA82331;

DT 25-JAN-2002 (first entry)

DE Zmax1 gene region physical map preparation STS marker #290.

XX Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200177327-A1.
XX
PD 18-OCT-2001.
XX
XX 21-JUN-2000; 2000WO-US016951.
XX
PF 05-APR-2000; 2000US-00543771.
XX
PR 05-APR-2000; 2000US-00544398.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2001-657171/75.
XX
DR New high bone mass (HBM) and Zmax1 genes and proteins useful for
XX modulating bone mass for the treatment of e.g. osteoporosis.
XX
PT Disclosure; Page 35; 443pp; English.
XX
PS The present invention describes the human Zmax1 gene and the high bone
XX mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
XX genes have osteopathic activities. The genes can be used in gene therapy,
XX anti-sense therapy and in the production of vaccines. They can be used in
XX the diagnosis and treatment of bone disorders including osteoporosis,
XX Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
XX
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
XX the exemplification of the present invention
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 359 GCTCAGCAGTCCACC 374
XX |||||
DB 17 GCTCAGCAGTCCCTCC 2
XX
RESULT 2291
XX AAL49482/c
XX ID AAL49482 standard; DNA; 18 BP.
XX
AC AAL49482;
XX
DT 22-NOV-2002 (first entry)
XX
XX Trisomy 21 diagnosis kit PCR primer PRR21S1412F.
XX
XX Trisomy 21; PCR; primer; prenatal diagnosis; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN DE10059776-A1.
XX
XX 18-JUL-2002.
XX
PD 01-DEC-2000; 2000DE-01059776.
XX
XX 01-DEC-2000; 2000DE-01059776.
XX
PR 01-DEC-2000; 2000DE-01059776.
XX
XX (ADNA-) ADNAGEN AG.
XX

PI Waschuetza S, Tamak C, Wehmeier L;
XX
XX WPI; 2002-644765/70.
XX
DR Diagnostic kit for prenatal detection of trisomy 21, comprises primer
XX pairs specific for amplification of short tandem repeat regions in
XX chromosome 21.
XX
XX Claim 12; Page 6; 10pp; German.
XX
XX The present invention relates to a diagnostic kit for detecting trisomy
XX 21 in a human foetus, which comprises at least two pairs of
XX oligonucleotide primers suitable for amplification, by polymerase chain
XX reaction (PCR), of both strands of a target DNA sequence, i.e. a short
XX tandem repeat region of human chromosome 21. The kit is used for
XX prenatal, non-invasive diagnosis of trisomy 21. The present sequence is
XX an oligonucleotide suitable for use in the kit of the invention
XX
SQ Sequence 18 BP; 3 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 674 CTCACGCACTCTG 689
XX |||||
DB 16 CTCACGCACTCTCG 1
XX
RESULT 2292
XX ABK23128/c
XX ID ABK23128 standard; DNA; 18 BP.
XX
XX ABK23128;
XX
AC 09-APR-2002 (first entry)
XX
DT Human Zmax1 cDNA reverse PCR primer #145.
XX
XX Human Zmax1 cDNA reverse PCR primer #145.
XX
DE Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
XX lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
XX osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
XX neurovascular condition; wound healing; gene therapy; PCR primer; probe;
XX bone development disorder; antiarteriosclerotic; cardiovascular;
XX osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
XX WO200192891-A2.
XX
PN 06-DEC-2001.
XX
PD 25-MAY-2001; 2001WO-US016946.
XX
PF 26-MAY-2000; 2000US-00578900.
XX
PR (GENO-) GENOME THERAPEUTICS CORP.
XX (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
XX Carulli JP, Little RD, Recker RR, Johnson ML;
XX
PI WPI; 2002-097784/13.
XX
XX Identifying molecules involved in lipid regulation, useful for
XX diagnosing, treating or preventing e.g., arteriosclerosis, comprises
XX identifying a molecule that binds to high bone mass gene or its
XX corresponding wild type gene.
XX
PS Disclosure; Page 40; 409pp; English.
XX
XX The invention relates to a method for identifying a molecule involved in
XX lipid regulation comprising identifying a molecule that binds to or
XX inhibits binding of a molecule to high bone mass (HBM) or its wild type
XX

CC gene, Zmaxi. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmaxi and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmaxi and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
CC
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 359 GCTCAGCAGTCCACC 374
Db 17 GCTCAGCAGTCCCTCC 2
RESULT 2293
AB210657/c
ID AB210657 standard; DNA; 18 BP.
AC AB210657;
XX
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #797.
XX
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO20027272-A2;
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwoppe I, Ziebarth H;
XX
XX WPI; 2003-018942/01.
XX
XX
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
XX Claim 15; Page 55; 117pp; English.
XX
XX The present invention describes a method for detecting and
XX differentiating between haematopoietic cell proliferative disorders
XX associated with at least 1 gene and/or their regulatory regions in a
XX subject. The method comprises contacting a target nucleic acid in a
XX biological sample obtained from the subject with at least 1 reagent,
XX which distinguishes between methylated and non-methylated CpG
XX dinucleotides within the target nucleic acid. AB209861 to AB211118

CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclases, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferation disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
XX
SQ Sequence 18 BP; 3 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 220 AACTCCGACCTCAGA 235
Db 16 AACTCCGACCTCAAA 1
RESULT 2294
ACC45711/c
ID ACC45711 standard; DNA; 18 BP.
XX
XX ACC45711;
XX
XX
DT 02-JUN-2003 (first entry)
XX
XX
DE Human HBM SRS marker reverse primer #145.
XX
XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
XX
XX
OS Homo sapiens.
OS
XX
PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX (AMHP) WYETH.
XX
XX
XX Babi J P, Bex FJ, Yaworsky FJ, Bodine PV;
XX
XX WPI; 2003-129278/12.
XX
XX
XX New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
XX
XX Disclosure; Page 56; 603pp; English.
XX
XX The invention relates to novel transgenic animals expressing the high
XX bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
XX comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
XX an LRP5 that is modulated by an altered gene control sequence introduced

CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention

SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 359 GCTCAAGCAGTCCACC 374
|||||
17 GCTCAAGCAGTCCCTCC 2

Db

RESULT 2295
ADA26921/c
ID ADA26921 standard; cDNA; 18 BP.

AC ADA26921;
XX

DT 20-NOV-2003 (first entry)

DE Human PGC-1 alpha promoter CRE sequence SEQ ID NO:15.

XX

XX type I muscle formation; PGC-1 alpha; cardiant; antidiabetic; anorectic;
XX immunomodulator; antidepressant; gene therapy;
XX aberrant type I muscle formation disorder; heart failure; disuse atrophy;
XX mitochondrial myopathy; systemic metabolic disorder; diabetes; obesity;
XX cachexia; anorexia; human; promoter; ds.

OS Homo sapiens.

XX

PN WO2003068944-A2.

XX

PD 21-AUG-2003.

XX

PF 13-FEB-2003; 2003WO-US004792.

XX

PR 13-FEB-2002; 2002US-0357069P.

XX

PA (DAND) DANA FARBER CANCER INST INC.

XX

PI Spiegelman BM, Lin U;

XX

PT WPI; 2003-689670/65.

XX

PT Use of agents that modulate PGC-1alpha expression or activity, for
PT modulating type I muscle formation or treating a disorder associated with
PT aberrant type I muscle formation e.g. heart failure, diabetes or a
PT mitochondrial myopathy.

XX

PS Disclosure; Fig 1B; 114P; English.

XX

XX The present invention describes a method of modulating type I muscle
XX formation comprising contacting a cell with an agent that modulates PGC-1
XX alpha expression or activity, so that type I muscle formation is
XX modulated. Also described: (1) a method for identifying a compound
XX capable of modulating type I muscle formation comprising contacting a
XX cell with a compound, and determining whether PGC-1 alpha expression or

CC activity is modulated; (2) a method for identifying a compound capable of
CC treating a disorder associated with aberrant type I muscle formation
CC comprising assaying the ability of the compound to modulate the
CC expression or activity of PGC-1 alpha; (3) compounds identified by the
CC method of (1) or (2); (4) a method for treating a subject having a
CC disorder associated with aberrant type I muscle formation comprising
CC administering to the subject an agent capable of modulating PGC-1 alpha
CC expression or activity; (5) a method for increasing type I muscle
CC formation in a subject comprising administering to the subject an agent
CC capable of increasing PGC-1 alpha expression or activity; and (6) a non-
CC human transgenic animal comprising an exogenous PGC-1 alpha nucleic acid
CC molecule, where the exogenous PGC-1 alpha nucleic acid molecule is
CC expressed in the skeletal muscle of the animal. Expression vectors and
CC host cells comprising the PGC-1 alpha nucleic acids, and antibodies that
CC specifically bind PGC-1 alpha polypeptides, are also described. PGC-1
CC alpha has cardiant, antidiabetic, anorectic, immunomodulator and
CC antidepressant activities, and can be used in gene therapy. The agents
CC that modulate PGC-1 alpha expression or activity are useful for
CC modulating type I muscle formation or treating a disorder associated with
CC aberrant type I muscle formation, e.g. heart failure, disuse atrophy, a
CC mitochondrial myopathy, or a systemic metabolic disorder such as
CC diabetes, obesity, cachexia or anorexia. The PGC-1 alpha nucleic acid
CC molecules, polypeptides, antibodies and modulators are useful in drug
CC screening assays or in gene therapy. The transgenic animals are useful in
CC screening assays designed to identify agents or compounds that are
CC involved with type I muscle formation. The present sequence represents a
CC human PGC-1 alpha promoter CRE nucleotide sequence, which is used in the
CC exemplification of the present invention.

SQ Sequence 18 BP; 4 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. NO. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1122 CAACTCTGACTTCA 1137
|||||
18 CAACTCTGACTTCA 3

Db

RESULT 2296
ADA26920/c
ID ADA26920 standard; cDNA; 18 BP.

AC ADA26920;
XX

DT 20-NOV-2003 (first entry)

DE Mouse PGC-1 alpha promoter CRE sequence SEQ ID NO:14.

XX

XX type I muscle formation; PGC-1 alpha; cardiant; antidiabetic; anorectic;
XX immunomodulator; antidepressant; gene therapy;
XX aberrant type I muscle formation disorder; heart failure; disuse atrophy;
XX mitochondrial myopathy; systemic metabolic disorder; diabetes; obesity;
XX cachexia; anorexia; mouse; promoter; ds.

OS Mus musculus.

XX

PN WO2003068944-A2.

XX

PD 21-AUG-2003.

XX

PF 13-FEB-2003; 2003WO-US004792.

XX

PR 13-FEB-2002; 2002US-0357069P.

XX

PA (DAND) DANA FARBER CANCER INST INC.

XX

PI Spiegelman BM, Lin U;

XX

PT WPI; 2003-689670/65.

XX

PT Use of agents that modulate PGC-1alpha expression or activity, for

PT modulating type I muscle formation or treating a disorder associated with
PT aberrant type I muscle formation e.g. heart failure, diabetes or a
XX mitochondrial myopathy.
PS Disclosure; Fig 1B; 114pp; English.
XX
XX The present invention describes a method of modulating type I muscle
CC formation comprising contacting a cell with an agent that modulates PGC-1
CC alpha expression or activity, so that type I muscle formation is
CC modulated. Also described: (1) a method for identifying a compound
CC capable of modulating type I muscle formation comprising contacting a
CC cell with a compound, and determining whether PGC-1 alpha expression or
CC activity is modulated; (2) a method for identifying a compound capable of
CC treating a disorder associated with aberrant type I muscle formation
CC comprising assaying the ability of the compound to modulate the
CC expression or activity of PGC-1 alpha; (3) compounds identified by the
CC method of (1) or (2); (4) a method for treating a subject having a
CC disorder associated with aberrant type I muscle formation comprising
CC administering to the subject an agent capable of modulating PGC-1 alpha
CC expression or activity; (5) a method for increasing type I muscle
CC formation in a subject comprising administering to the subject an agent
CC capable of increasing PGC-1 alpha expression or activity; and (6) a non-
CC human transgenic animal comprising an exogenous PGC-1 alpha nucleic acid
CC molecule, where the exogenous PGC-1 alpha nucleic acid molecule is
CC expressed in the skeletal muscle of the animal. Expression vectors and
CC host cells comprising the PGC-1 alpha nucleic acids, and antibodies that
CC specifically bind PGC-1 alpha polypeptides, are also described. PGC-1
CC alpha has cardiac, antidiabetic, anorectic, immunomodulator and
CC antidepressant activities, and can be used in gene therapy. The agents
CC that modulate PGC-1 alpha expression or activity are useful for
CC modulating type I muscle formation or treating a disorder associated with
CC aberrant type I muscle formation, e.g. heart failure, disuse atrophy, a
CC mitochondrial myopathy, or a systemic metabolic disorder such as
CC diabetes, obesity, cachexia or anorexia. The PGC-1 alpha nucleic acid
CC molecules, polypeptides, antibodies and modulators are useful in drug
CC screening assays or in gene therapy. The transgenic animals are useful in
CC screening assays designed to identify agents or compounds that are
CC involved with type I muscle formation. The present sequence represents a
CC mouse PGC-1 alpha promoter CRE nucleotide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 18 BP; 4 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1122 CAAACTCCTGACCTCA 1137
DB 18 CAAACTCCTGACCTCA 3
RESULT 2297
ADB98409/c
ID ADB98409 standard; DNA; 18 BP.
XX
AC ADB98409;
XX
DT 04-DEC-2003 (first entry)
XX
DE Sequence tagged site #390 used to prepare Zmax1 (LRP5) gene region map.
XX
XX Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
XX
XX Homo sapiens.
OS
XX MO200292000-A2.
PN
XX 21-NOV-2002.
PD
XX 13-MAY-2002; 2002WO-US014877.
PF
XX

PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
XX Allen K, Antosiewicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
PI WPI; 2003-129214/12.
XX
XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
XX Example 2; Page 63; 629pp; English.
PS
XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)
CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
CC region.
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 359 GCTCAGCAGTCCAC 374
DB 17 GCTCAGCAGTCCAC 2
RESULT 2298
ACA58053/c
ID ACA58053 standard; DNA; 18 BP.
XX
AC ACA58053;
XX
DT 09-JUN-2003 (first entry)
XX
XX Human familial bipolar affective disorder chromosome marker #1.
DE
XX Human; genotype determination; familial bipolar affective disorder;
KW chromosomal region linked; locus associated with resistance; D4S402;
KW D4S424; D4S431; D4S404; D1S394; D1S29; chromosome marker; primer; ss.
XX
XX Homo sapiens.
OS
XX US2002192655-A1.
PN
XX 19-DEC-2002.
PD
XX 13-JUN-2001; 2001US-00881012.
PF
XX 29-MAR-1996; 96US-0014334P.
PR 20-OCT-1997; 97US-0062924P.
PR 19-OCT-1998; 98US-00175158.
XX
XX (GINN/) GINN F I.
PA (EGL/) EGLAND J A.
PA (PAUL/) PAUL S M.
XX
XX Ginn EI, Egeland JA, Paul SM;
PI WPI; 2003-352706/33.
XX
XX

XX Determining a genotype associated with increased or decreased resistance
PT to familial bipolar affective disorder in a family comprises determining
PT the genotype of e.g., chromosomal regions D4S402 and D4S424.
XX
XX Disclosure; Page 8; 79pp; English.
XX
XX The present invention relates to a method of determining a genotype
CC associated with increased or decreased resistance to familial bipolar
CC affective disorder. The method comprises determining the genotype with at
CC least one marker of at least one chromosomal region linked to a locus
CC associated with resistance to bipolar affective disorder, where the
CC chromosomal regions are included of and localised between D4S402 and
CC D4S424, D4S431 and D4S404, or D11S394 and D11S29. The invention also
CC discloses a kit for determining a genotype associated with increased or
CC decreased resistance to familial bipolar affective disorder, where the
CC kit comprises markers for two or more of the chromosomal regions cited.
CC The method and kit are useful for determining a genotype associated with
CC increased or decreased resistance to familial bipolar affective disorder
CC in a family affected by bipolar affective disorder, for determining the
CC contribution of these chromosomal regions to bipolar affective disorder
CC in an affected family member, and for assessing an increased or
CC decreased risk of developing bipolar illness for a tested individual from
CC an affected family. ACA58053-ACA58292 represent primers used in the
CC present invention
XX
XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SO
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. NO. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 639 GTGACCCAGGCTGGAG 654
DB 16 GTGACCCAGGCTGGAG 1
XX
XX RESULT 2299
ADN92832
ID ADN92832 standard; DNA; 18 BP.
XX
XX ADN92832;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX SNP-containing cardiovascular associated gene primer #162.
DE
XX
XX SNP; single nucleotide polymorphism; cardiovascular associated gene;
KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;
KW ss.
XX
XX Homo sapiens.
OS
XX
XX WO2003057911-A2.
PN
XX
XX 17-JUL-2003.
PD
XX
XX 07-JAN-2003; 2003WO-EP000060.
PF
XX
XX 08-JAN-2002; 2002EP-00000153.
PR
XX
XX (PARB) BAYER AG.
PA
XX
XX Stropp U, Schwens S, Kallabis H;
PI
XX
XX WPI; 2003-577532/54.
DR
XX
XX New isolated polynucleotides comprising single nucleotide polymorphisms
PT of the cardiovascular gene, useful for assessing predisposition or
PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,
PT restenosis or stroke.
XX

PS Disclosure; Page 72; 187pp; English.
XX
XX The invention relates an isolated polynucleotide (I) encoded by a
CC cardiovascular associated (CA) gene, having allelic variation contained
CC in a functional surrounding like full length cDNA for CA gene
CC polypeptide, and with or without the CA gene promoter sequence. (I) is a
CC polynucleotide comprising single nucleotide polymorphisms predicting
CC cardiovascular disease. The polynucleotides are useful for assessing
CC predisposition or susceptibility to a cardiovascular disease, e.g.
CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
CC inflammation, myocardial infarction, and stroke. These may also be used
CC to predict personal medication schemes omitting adverse drug reactions,
CC or as probes for detecting genetic polymorphisms and as templates for the
CC recombinant production of normal or variant peptides/polypeptides encoded
CC by the genes. This sequence corresponds to a PCR primer to amplify one of
CC the genes of the invention.
XX
XX Sequence 18 BP; 4 A; 2 C; 6 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. NO. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 387 CCAAGTGCTGGATT 402
DB 2 CTAAGTGCTGGATT 17
XX
XX RESULT 2300
ADN06584
ID ADN06584 standard; DNA; 18 BP.
XX
XX ADN06584;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Human FLAP related microsatellite marker SEQ ID NO:234.
DE
XX
XX leukotriene synthase inhibitor; myocardial infarction;
KW acute coronary syndrome; antiatherosclerotic; cardiant; antilanginal;
KW leukotriene biosynthesis inhibitor; leukotriene receptor antagonist;
KW 5-lipoxygenase activating protein; FLAP; human; chromosome 13;
KW chromosome 13q12; polymorphism; 5-lipoxygenase gene promoter;
KW 5-lO gene promoter; diabetes; hypertension; hypercholesterolaemia;
KW obesity; inflammatory marker; low density lipoprotein; cholesterol;
KW high density lipoprotein; angina; atherosclerosis; microsatellite marker;
KW ss.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO2004035741-A2.
PN
XX
XX 29-APR-2004.
PD
XX
XX 16-OCT-2003; 2003WO-US032556.
PF
XX
XX 17-OCT-2002; 2002US-0419433P.
PR
XX
XX 21-FEB-2003; 2003US-0449331P.
PR
XX
XX (DECO-) DECODE GENETICS EHF.
PA
XX
XX Helgadottir A, Gurney ME, Gulcher JR;
PI
XX
XX WPI; 2004-357211/33.
DR
XX
XX Use of leukotriene synthase inhibitor for manufacture of a medicament
PT for treatment for myocardial infarction or susceptibility to myocardial
PT infarction in individual.
XX
XX Disclosure; SEQ ID NO 234; 306pp; English.
PS
XX
XX The present invention describes using a leukotriene synthase inhibitor
CC

CC (1) for the manufacture of a medicament for the treatment of myocardial
CC infarction or susceptibility to myocardial infarction in an individual.
CC Also described is a method (M1) for the treatment of acute coronary
CC syndrome (ACS) in an individual comprising administering (1). (1) has
CC antithrombotic, cardiant and antineoplastic activities, and can be used
CC as a leukotriene biosynthesis inhibitor, and a leukotriene receptor
CC antagonist. (1) can be used for the manufacture of a medicament for the
CC treatment of myocardial infarction or susceptibility to myocardial
CC infarction in an individual who has at least one risk factor chosen from
CC an at-risk haplotype for myocardial infarction, an at-risk haplotype in
CC the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a
CC FLAP nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-
CC LO) gene promoter; in an individual who has at least one risk factor
CC chosen from diabetes, hypertension, hypercholesterolaemia, elevated
CC lip(a), obesity, past or current smoker; in an individual having elevated
CC inflammatory marker chosen from C-reactive protein (CRP), serum amyloid
CC A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue
CC necrosis factor- α , soluble vascular cell adhesion molecule (sVCAM),
CC soluble intervascular adhesion molecule (sICAM), E-selectin, matrix
CC metalloproteinase type-1, matrix metalloproteinase type-2, matrix
CC metalloproteinase type-3 and matrix metalloproteinase type-9; in an
CC individual having increased low density lipoprotein (LDL) cholesterol
CC and/or decreased high density lipoprotein (HDL) cholesterol; in an
CC individual having increased leukotriene synthesis; in an individual
CC having previous myocardial infarction or acute coronary syndrome (ACS)
CC event, stable angina; or in an individual who has atherosclerosis or who
CC requires treatment to restore blood flow in arteries. (M1) is useful for
CC treating an individual suffering from acute coronary syndrome chosen from
CC unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-
CC elevation myocardial infarction (STEMI). The human FLAP gene is located
CC on chromosome 13, more specifically to 13q12. The present sequence
CC represents a microsatellite marker used in the exemplification of the
CC present invention.

XX XX Sequence 18 BP; 2 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 282 CACCATGCCGCTCT 297
Db 1 CACCATGCCGCTCT 16

RESULT 2301
AD056531/c
ID AD056531 standard; DNA; 18 BP.

XX XX AD056531;

DT 12-AUG-2004 (first entry)

XX XX Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #56.

DE gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;
KM single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.

XX OS Homo sapiens.

XX WO2004044164-A2.

XX PD 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035879.

XX 06-NOV-2002; 2002US-0424475P.

XX 23-JUL-2003; 2003US-0489703P.

XX (SEQU-) SEQUENOM INC.
XX Roth RB, Nelson MR, Braun A, Kammerer SM;
PI

XX WPI, 2004-411721/38.
DR Identifying a subject at risk of melanoma, useful for treating melanoma.
XX Identifying a subject at risk of melanoma, useful for treating melanoma.
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.

XX Example 5; Page 84; 295pp; English.

XX The invention relates to a method of identifying a subject at risk of
CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.

XX XX Sequence 18 BP; 6 A; 6 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 1.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1092 GGGGTTCCACCATTT 1107
Db 17 GGGGTTCCACCATTT 2

RESULT 2302
AD056506/c
ID AD056506 standard; DNA; 18 BP.

XX XX AD056506;

DT 12-AUG-2004 (first entry)

XX XX Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #31.

DE gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;
KM single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.

XX OS Homo sapiens.

XX WO2004044164-A2.

XX PD 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035879.

XX 06-NOV-2002; 2002US-0424475P.

XX 23-JUL-2003; 2003US-0489703P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM;
PI

XX WPI, 2004-411721/38.

XX Identifying a subject at risk of melanoma, useful for treating melanoma,
PT comprises detecting the presence or absence of one or more polymorphic
PT variations associated with melanoma in a nucleic acid sample from a
PT subject.

XX Example 5; Page 84; 295pp; English.

XX The invention relates to a method of identifying a subject at risk of

CC melanoma comprising detecting the presence or absence of one or more
CC polymorphic variations associated with melanoma in a nucleic acid sample
CC from a subject. Preventing melanoma in a subject comprises detecting the
CC presence or absence of one or more polymorphic variations associated with
CC melanoma in a nucleic acid sample from a subject; and administering a
CC melanoma preventative to a subject in need thereof based upon the
CC presence or absence of the one or more polymorphic variations in the
CC nucleic acid sample. The preventative reduces ultraviolet (UV) light
CC exposure to the subject. The methods, nucleic acids, proteins, and
CC compositions are useful for treating melanoma. The present sequence
CC represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.
XX
SQ Sequence 18 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 1 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 492 GATCAGCTGCTACTGC 507
DB 16 GATCCAGCTCAGCTGC 1
XX
RESULT 2303
AD056556
ID AD056556 standard; DNA; 18 BP.
XX
AC AD056556;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP probe #81.
XX
XX Gene therapy; human; ss; melanoma;
XX melanoma associated polymorphic variation; SNP;
XX single nucleotide polymorphism; cyclin-dependent kinase 10; CDK10; probe.
XX
XX Homo sapiens.
XX
XX WO200404164-A2.
XX
XX 27-MAY-2004.
XX
XX 06-NOV-2003; 2003WO-US035879.
XX
XX 06-NOV-2002; 2002US-0424475P.
XX
XX 23-JUL-2003; 2003US-0489703P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
XX WPI; 2004-411721/38.
XX
XX Identifying a subject at risk of melanoma, useful for treating melanoma,
XX comprises detecting the presence or absence of one or more polymorphic
XX variations associated with melanoma in a nucleic acid sample from a
XX subject.
XX
XX Example 5; Page 85; 295pp; English.
XX
XX The invention relates to a method of identifying a subject at risk of
XX melanoma comprising detecting the presence or absence of one or more
XX polymorphic variations associated with melanoma in a nucleic acid sample
XX from a subject. Preventing melanoma in a subject comprises detecting the
XX presence or absence of one or more polymorphic variations associated with
XX melanoma in a nucleic acid sample from a subject; and administering a
XX melanoma preventative to a subject in need thereof based upon the
XX presence or absence of the one or more polymorphic variations in the
XX nucleic acid sample. The preventative reduces ultraviolet (UV) light
XX exposure to the subject. The methods, nucleic acids, proteins, and
XX compositions are useful for treating melanoma. The present sequence
XX represents a human cyclin-dependent kinase 10, CDK10, proximal SNP probe.

XX
SQ Sequence 18 BP; 5 A; 2 C; 6 G; 4 T; 0 U; 1 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 869 GATTACAGCTGTGAGC 884
DB 1 GATTACAGCTGTGAGC 16
XX
RESULT 2304
ADP45830
ID ADP45830 standard; DNA; 18 BP.
XX
AC ADP45830;
XX
DT 26-AUG-2004 (first entry)
XX
DE Extend primer 22 used to genotype human ICAM-1/ICAM-4/ICAM-5 SNP.
XX
XX breast cancer; cytostatic; gene therapy; human;
XX intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;
XX CD54; cell surface glycoprotein P3.58; ICAM-4;
XX Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;
XX ss; primer; PCR; SNP; single nucleotide polymorphism; probe.
XX
XX Homo sapiens.
XX
XX WO2004047623-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037948.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
XX WPI; 2004-441051/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the ICAM, MAPK10, KIAA0861, NIMA1 or GALE
XX regions which are associated with breast cancer in a nucleic acid sample
XX from a subject.
XX
XX Example 4; Page 83; 289pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of one or
XX more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a subject at risk of
XX breast cancer, for early diagnosis, prevention and treatment of breast
XX cancer, possibly via gene therapy, as well as to analyse and predict a
XX response to a breast cancer treatment and in clinical drug trials. The
XX current sequence is that of an Extend primer (also described as probe) of
XX the invention which was used to genotype human intercellular adhesion
XX molecule ICAM-1/ICAM-4/ICAM-5 gDNA. ICAM-1 (human rhinovirus receptor/BB2
XX CD54; cell surface glycoprotein P3.58) has been mapped to chromosome
XX position 19p13.3-p13.2, ICAM-4 (Landsteiner-Wiener blood group, LW) has
XX been mapped to chromosomal position 19p13.2-cen and ICAM-5
XX (telencephalin) has been mapped to chromosomal position 19p13.2.
XX
SQ Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.5%; Score 14.4; DB 1; Length 18;
XX Best Local Similarity 93.8%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
OY      732 AGCTGGACTACAGGC 747
      |||||
      2 AGCTGGACCAACAGGC 17

RESULT 2305
AAH91142
ID      AAH91142 standard; DNA; 36 BP.
XX
XX      AAH91142:
XX
XX      09-OCT-2001 (first entry)
XX
XX      Human inflammatory bowel disease associated polymorphic site #217.
XX
XX      Human inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX      single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX      chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      misc_feature      19
XX      /tag= a
XX      /note= "SNP, optionally G or T at this position"
XX
XX      WO200142511-A2.
XX
XX      14-JUN-2001.
XX
XX      11-DEC-2000; 2000MO-US033632.
XX
XX      10-DEC-1999; 99US-0170257P.
XX      10-APR-2000; 2000US-0196046P.
XX
XX      (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (ELLIPIS ) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX      Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K.
XX
XX      WPI; 2001-367874/38.
XX
XX      Testing for the presence of polymorphisms associated with inflammatory
XX      bowel disease, using a hybridization assay.
XX
XX      Claim 1; Page 48; 463pp; English.
XX
XX      The present invention describes a method for detecting the presence of
XX      polymorphisms associated with inflammatory bowel diseases such as
XX      ulcerative colitis and Crohn's disease. The methods can be used to detect
XX      the presence of genetic polymorphisms associated with inflammatory bowel
XX      disease and correlating their occurrence with disease states. They may be
XX      used in this way for phenotypic correlations, forensics, paternity
XX      testing, medicine and genetic analysis. The present sequence is a
XX      polymorphic site described in the exemplification of the invention
XX
XX      Sequence 36 BP; 5 A; 10 C; 13 G; 7 T; 0 U; 1 Other:
XX
XX      Query Match      1.4%; Score 14.2; DB 1; Length 36;
XX      Best Local Similarity 61.1%; Pred. No. 2.3e+03;
XX      Matches 22; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY      1032 AGCTGGATTACGGCAGCTCCACACAGCCCGCT 1067
      |||||
      1 AGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36

RESULT 2306
AAV39596/C
ID      AAV39596 standard; CDNA; 14 BP.
XX
XX      AAV39596;
```

```
XX
XX      28-SEP-1998 (first entry)
XX
XX      Microsatellite analysis detection primer SEQ ID NO:39.
XX
XX      Mass spectrometry; diagnosis; detection; biological sample; infection;
XX      genetic disease; chromosomal abnormality; identification; heredity;
XX      pathogenic organism; telomerase activity; oncogene mutation;
XX      cancer-specific sequence; primer; ss.
XX
XX      Synthetic.
XX
XX      WO9820166-A2.
XX
XX      14-MAY-1998.
XX
XX      06-NOV-1997; 97MO-US020444.
XX
XX      06-NOV-1996; 96US-00744481.
XX      06-NOV-1996; 96US-00744590.
XX      06-NOV-1996; 96US-00746036.
XX      06-NOV-1996; 96US-00746055.
XX      23-JAN-1997; 97US-00786988.
XX      23-JAN-1997; 97US-00787639.
XX      19-SEP-1997; 97US-00933792.
XX      08-OCT-1997; 97US-00947801.
XX
XX      (SEQU-) SEQUENOM INC.
XX
XX      Koster H, Tang K, Fu D, Siebert CW, Little DP, Higgins GS;
XX      Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
XX      Lough DM;
XX
XX      WPI; 1998-286975/25.
XX
XX      Sequencing nucleic acid by mass spectrometric analysis - for detecting
XX      nucleic acids, telomerase activity, oncogene mutations, or cancer-
XX      specific sequences, for diagnosis of disease.
XX
XX      Example 11; Page 130; 478pp; English.
XX
XX      A process has been developed for determining the sequence of a target
XX      nucleic acid. The process comprises: (i) generating at least two
XX      fragments (F) from the target nucleic acid; and (ii) analysing F by mass
XX      spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically
XX      claimed primers for use in the mass spectrometric analysis of the above
XX      process. The process is used to detect genetic diseases (e.g.
XX      haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's
XX      disease, cystic fibrosis and many others) or chromosomal abnormalities
XX      (or predisposition); infections and cancers; also for establishing
XX      identity and heredity. Particular applications are diagnosis of
XX      neuroblastoma, detecting telomerase, determining family relationships and
XX      HLA compatibility, and in genetic fingerprinting. Compared with known
XX      methods using MS, this process requires fewer specific reagents and is
XX      better suited to automation. Extended primers are shorter; primer
XX      annealing is more efficient and the process allows detection of many
XX      sequences simultaneously. The present sequence represents an
XX      oligonucleotide used in an example from the present invention
XX
XX      Sequence 14 BP; 2 A; 4 C; 3 G; 5 T; 0 U; 0 Other:
XX
XX      Query Match      1.4%; Score 14; DB 1; Length 14;
XX      Best Local Similarity 100.0%; Pred. No. 1.7e+03;
XX      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      620 GAGACAGAGTCTCA 633
      |||||
      14 GAGACAGAGTCTCA 1

RESULT 2307
AAA23392
ID      AAA23392 standard; RNA; 14 BP.
```

```
XX AC AAA23392;
XX DT 19-JUN-2000 (first entry)
XX DE Integrin subunit beta 3 target site SEQ ID NO:6618.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; halpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 276; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiodiroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 14 BP; 1 A; 8 C; 2 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 1.4%; Score 14; DB 1; Length 14;
XX Best Local Similarity 78.6%; Pred. No. 1.7e+03;
XX Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 2308
AAA23382
ID AAA23382 standard; RNA; 14 BP.
XX
XX AAA23382;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 target site SEQ ID NO:6608.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX Integrin alpha 6 subunit; integrin subunit beta 3; halpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 275; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiodiroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 14 BP; 1 A; 6 C; 3 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 1.4%; Score 14; DB 1; Length 14;
XX Best Local Similarity 71.4%; Pred. No. 1.7e+03;
```

Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 968 TCTCGGCTCACTGC 981
 :||:||||:||||:
 Db 1 UTCGGCTCUCACGCC 14

RESULT 2309
 AAA23406/c
 ID AAA23406 standard; RNA; 14 BP.

AC AAA23406;
 DT 19-JUN-2000 (first entry)
 XX

Integrin subunit beta 3 target site SEQ ID NO:6632.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99MO-US006507.

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC.

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.

Claim 54; Page 277; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
 AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 and AA17168 to AA17560 and AA17623 to AA17684 represent their
 corresponding target sequences; AA17685 to AA18385 and AA19087 to
 AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 and AA19155 to AA19222 represent their corresponding target sequences;
 AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 AA21596 to AA21688 represent their corresponding target sequences;
 AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
 for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 AA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT,
 integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
 syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 and other syndromes and diseases related to the levels of ARNT, Tie-2,
 integrin subunit alpha-6, or integrin subunit beta-3.

XX Sequence 14 BP; 3 A; 4 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TGCCCAAGCTGGTC 352
 |||||
 Db 14 TGCCCAAGCTGGTC 1

RESULT 2310
 AAA23388
 ID AAA23388 standard; RNA; 14 BP.

AC AAA23388;
 DT 19-JUN-2000 (first entry)
 XX

Integrin subunit beta 3 target site SEQ ID NO:6614.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

24-MAR-1999; 99MO-US006507.

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC.

Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JH;

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.

Claim 54; Page 275; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
 AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 and AA17168 to AA17560 and AA17623 to AA17684 represent their
 corresponding target sequences; AA17685 to AA18385 and AA19087 to
 AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 and AA19155 to AA19222 represent their corresponding target sequences;
 AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 AA21596 to AA21688 represent their corresponding target sequences;
 AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
 for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 AA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT,
 integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as

CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angioidema of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kipkel-Trennaway-Weber syndrome, Oeler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX

SQ Sequence 14 BP; 3 A; 8 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCTCAGCCTCCGCA 390
 |||:|||||:
 1 CCTCAGCCTCCGCA 14

Db

RESULT 2311
 ACA62884
 ID ACA62884 standard; DNA; 14 BP.

XX ACA62884;

XX 21-AUG-2003 (first entry)

XX Repeated nucleic acid detection method, human probe Alu125.

XX Repeated nucleic acid detection, human; alu; probe; ss.

OS Homo sapiens.

PN US2003022163-A1.

XX 30-JAN-2003.

XX 15-DEC-2000; 2000US-00739909.

XX 21-JUL-1999; 99US-00358972.

XX 25-AUG-1999; 99US-00383316.

XX (MAND/) MANDREKAR M. N.

XX (TERE/) TEREBA A.

XX (SHULTZ) SHULTZ J W.

PI Mandrekar MN, Tereba A, Shultz JW;

XX MPI; 2003-479484/45.

XX Determining presence or absence of desired nucleic acids that contain

XX multiple repeats of predetermined nucleic acid target sequences in a

XX sample, by using nucleic acid hybridization methods.

PS Claim 1, Page 27, 31pp; English.

XX The invention describes a method of determining presence or absence of a

XX desired nucleic acid (NA) that contains multiple repeats of a

XX predetermined NA target sequence in a NA sample. The method involves

XX providing a treated sample that may contain the desired NA in which

XX several predetermined repeating NA target sequences are hybridized with a

XX NA probe, analysing for presence or absence of the desired NA. The method

XX is useful for determining the presence or absence of desired nucleic

XX acids that contain multiple repeats of a predetermined NA target

XX sequence, in a NA sample obtained from a biological sample, where the

XX repeated sequence includes several predetermined repeated sequence that

XX differ in length and/or sequence. The methods can be efficiently used for

XX distinguishing human and bacterial NA. The method is highly sensitive,

XX and enables detection and quantification of the presence of a NA without

XX the need to undergo a NA target sequence enrichment step prior to a NA

XX hybrid detection step. The method enables rapid and accurate detection of

XX a desired NA that contains multiple repeats of a NA target sequence. This

XX sequence represents a probe used to detect the human Alu repeat sequences

SQ Sequence 14 BP; 2 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 CTGAGTCGAGTGG 662
 |||:|||||:
 1 CTGAGTCGAGTGG 14

Db

RESULT 2312
 ADH70473
 ID ADH70473 standard; DNA; 14 BP.

XX ADH70473;

XX 25-MAR-2004 (first entry)

XX Human Vbeta gene repeat sequence #263.

XX human; T-cell associated disease; Vbeta; autoimmune disease;

XX degenerative nervous system disease; graft versus host disease;

XX hypersensitivity disease; infectious disease; neoplastic disease;

XX Addison's disease; atrophic gastritis;

XX degenerative nervous system disease; multiple sclerosis;

XX Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;

XX allergy; type-II hypersensitivity; Goodpasture's syndrome;

XX type IV hypersensitivity; leprosy; infectious disease; viral infection;

XX HIV; fungal infection; Candida; parasitic infection; schistosom;

XX filaria; bacterial infection; Mycobacterium; neoplastic disease;

XX lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;

XX breast cancer; ds.

XX Homo sapiens.

XX US2002150891-A1.

XX 17-OCT-2002.

XX 05-MAR-1999; 99US-00263959.

XX 19-SEP-1994; 94US-00309335.

XX 19-SEP-1995; 95US-00531241.

XX (HOOD/) HOOD L. E.

XX (ROME/) ROMEN L.

XX Hood LE, Rowen L;

XX MPI; 2004-059052/06.

XX Kit for diagnosing and treating T-cell associated diseases e.g.

XX autoimmune, degenerative nervous system and infectious disease, comprises

XX nucleic acid primers specifically priming and allowing amplification of a

XX Vbeta gene.

XX Disclosure; SEQ ID NO 667; 164pp; English.

XX The invention relates to a kit for diagnosing and treating T-cell

XX associated diseases which comprises a panel of nucleic acid primers

XX specifically priming and allowing amplification of each Vbeta gene,

XX VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant

XX rejection and diagnosing and treating T-cell associated diseases

XX including autoimmune diseases, degenerative nervous system diseases,

XX graft versus host disease, hypersensitivity diseases, infectious diseases

XX and neoplastic diseases. Autoimmune diseases include Addison's disease,

XX atrophic gastritis. Degenerative nervous system diseases include multiple

XX sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type

XX I hypersensitivities such as contact with allergens that lead to

XX allergies, Type II hypersensitivities such as those present in

XX Goodpasture's syndrome and Type IV hypersensitivities such as those

XX manifested in leprosy. Infectious diseases include viral infections

CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus *Candida*, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC *Mycobacterium*. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a *Vbeta* gene repeat sequence.

XX Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 428 TTTTATTTATTTT 441
 Db 1 TTTTATTTATTTT 14

RESULT 2313

ID AAT52086
 AAT52086 standard; RNA; 15 BP.

XX AAT52086;

AC 25-MAR-2003 (revised)
 DT 24-MAR-1997 (first entry)

DE Human ICM hammerhead ribozyme target sequence (nt. position 2769).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW 89.

XX Homo sapiens.
 OS
 XX
 XX MO9523225-A2.
 PN
 XX
 XX 31-AUG-1995.
 PD
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 PF
 XX

XX 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245726.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314337.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.

PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.

PI Stinchcomb DT, Chowitra B, Dizenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpislsky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Belgelman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 DR WPI; 1995-351090/45.

PT Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.

PS Claim 2; Page 175; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICM-1 target sequences and thereby
 CC inhibit ICM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)

XX Sequence 15 BP; 2 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 15;
 Best Local Similarity 78.6%; Pred. No. 1.8e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 635 CTCTGTACCCAGG 648
 Db 2 CTCUGCACCCAGG 15

RESULT 2314
 AAT52112
 ID AAT52112 standard; RNA; 15 BP.

XX AAT52112;

AC 25-MAR-2003 (revised)
 DT 25-MAR-1997 (first entry)

DE Human ICM hammerhead ribozyme target sequence (nt. position 2853).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW 89.

XX Homo sapiens.
 OS
 XX
 XX MO9523225-A2.
 PN
 XX
 XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB000156.
 PR 23-FEB-1994; 94US-00201109.
 PR 23-FEB-1994; 94US-00201109.

PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245735.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291933.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00316397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowitra B, Drenzo A, Draper KG, Dudycz LM;
 PI Grimm S, Karpitsky A, Kisch K, Matulic-Adamic J, Mcswigen JA;
 PI Modak A, Pavco P, Belgien L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Mincott FB, Wolff T;
 XX
 DR WPI; 1995-351090/45.
 PT Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX
 PS Claim 2; Page 175; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesized with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICM-1 target sequences and thereby
 CC inhibit ICM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
 XX
 QY
 DB 719 CAGCCTCTGAGTA 732
 |||||:|:|:|:|:
 2 CAGCCUCCUGAGA 15
 Query Match 1.4%; Score 14; DB 1; Length 15;
 Best Local Similarity 78.6%; Pred. No. 1.8e+03;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2315
 ADH70501
 ID ADH70501 standard; DNA; 15 BP.
 XX
 AC ADH70501;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human Vbeta gene repeat sequence #291.

XX human; T-cell associated disease; Vbeta; autoimmune disease;
 KW degenerative nervous system disease; graft versus host disease;
 KW hypersensitivity disease; infectious disease; neoplastic disease;
 KW Addison's disease; atrophic gastritis;
 KW degenerative nervous system disease; multiple sclerosis;
 KW Alzheimer's disease; hypersensitivity; Goodpasture's syndrome;
 KW allergy; type II hypersensitivity; leprosy; infectious disease; viral infection;
 KW type IV hypersensitivity; candida; parasitic infection; schistosoma;
 KW HIV; fungal infection; candida; parasitic infection; schistosoma;
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
 KW breast cancer; de.
 XX
 OS Homo sapiens.
 XX
 PN US2002150891-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 05-MAR-1999; 99US-00263959.
 XX
 PR 19-SEP-1994; 94US-00309335.
 PR 19-SEP-1995; 95US-00351241.
 XX
 PA (HOOD/) HOOD L E.
 PA (ROWE/) ROWEN L.
 XX
 PI Hood LE, Rowen L;
 XX
 DR WPI; 2004-059052/06.
 PT
 PT kit for diagnosing and treating T-cell associated diseases e.g.
 PT autoimmune, degenerative nervous system and infectious disease, comprises
 PT nucleic acid primers specifically priming and allowing amplification of a
 PT Vbeta gene.
 XX
 PS Disclosure; SEQ ID NO 695; 164pp; English.
 XX
 CC The invention relates to a kit for diagnosing and treating T-cell
 CC associated diseases which comprises a panel of nucleic acid primers
 CC specifically priming and allowing amplification of each Vbeta gene,
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
 CC rejection and diagnosing and treating T-cell associated diseases
 CC including autoimmune diseases, degenerative nervous system diseases,
 CC graft versus host disease, hypersensitivity diseases, infectious diseases
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
 CC atrophic gastritis. Degenerative nervous system diseases include multiple
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include type
 CC I hypersensitivity diseases such as contact with allergens that lead to
 CC allergies. Type II hypersensitivity diseases such as those present in
 CC Goodpasture's syndrome and type IV hypersensitivity diseases such as those
 CC manifested in leprosy. Infectious diseases include viral infections
 CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus Candida, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a Vbeta gene repeat sequence.
 CC
 SQ Sequence 15 BP; 3 A; 0 C; 0 G; 12 T; 0 U; 0 Other;
 XX
 QY
 DB 428 TTTATTTTATTTT 441
 |||||:|:|:|:|:
 1 TTTATTTTATTTT 14
 Query Match 1.4%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2316
 ADQ30131

ID	ADQ030131 standard; DNA; 15 BP.	
AC	ADQ030131;	
XX		
DT	09-SEP-2004 (first entry)	
XX		
DE	Murine VRI exon 1d transcription factor binding fragment #23.	
XX		
OS	def; VRI receptor; vanilloid receptor type 1; modulator;	
XX	pain transmission; primary sensory neuron; transcription factor;	
KW	detection; MZFI, NKkappa; NRAT; GATRA1; sensitivity disorder; analgesia;	
KM	hyperalgesia; hyperalgesia; neuralgia; myalgia; murine.	
XX		
MS	mus sp.	
XX		
PN	WO2004053120-A2.	
PD	24-JUN-2004.	
XX		
PF	01-DEC-2003; 2003WO-EP013522.	
XX		
PR	09-DEC-2002; 2002DE-01057421.	
XX	(CHEF) GRUENENTHAL GMBH.	
PA		
PT	Weine E, Bieller A, Schaefer MKH;	
XX		
DR	WPI: 2004-468868/44.	
XX		
PT	New nucleic acid that modulates expression of the vanilloid receptor-1,	
PT	useful for control of pain or sensitivity disorders, comprises sequences	
PT	from control regions of the receptor gene.	
PS		
XX	Disclosure; Page 49; 68pp; German.	
XX		
CC	This invention describes a novel nucleic acid containing a specific	
CC	segment having at least one region that modulates expression of the VRI	
CC	(vanilloid receptor type 1) receptor, or a functional derivative, allele	
CC	or fragment of this region, or a sequence that hybridizes to it under	
CC	standard conditions. The VRI modulator is derived from one or more of	
CC	positions 221931-223344 of GenBank AF670399, 31673-36359 of AF663116, or	
CC	44731-43231 or 36616-33151 of AF168787 and is involved in transmission of	
CC	pain, particularly in primary sensory neurons. The invention also	
CC	describes a vector that contains the VRI modulator, host cells containing	
CC	this vector (other than human germ or embryonal stem cells) and a method	
CC	for modulating expression of the VRI receptor by introducing the	
CC	modulator or the vector into a cell that contains the VRI gene. The	
CC	products of the invention are used for detecting a transcription factor	
CC	from its binding to a regulatory sequence (or a double-stranded	
CC	oligonucleotide fragment of it), e.g. by Western blotting or enzyme-	
CC	linked immunosorbent assay, particularly for diagnosis of diseases	
CC	associated with overexpression or underexpression of the transcription	
CC	factor. The region that modulates VRI receptor expression includes a	
CC	binding site for a transcription factor, e.g. MZFI, NKkappa, NRAT or	
CC	GATRA1. The nucleic acids of the invention, or vectors containing them,	
CC	are used for prevention or treatment of pain, also for treating	
CC	sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also	
CC	neuralgia and myalgia, that are associated with activity of the VRI	
CC	receptor. This sequence represents a fragment of murine VRI exon 1d DNA	
CC	which is capable of binding to a transcription factor.	
XX		
SQ	Sequence 15 BP; 0 A; 0 C; 3 G; 12 T; 0 U; 0 Other;	
	Query Match 1.4%; Score 14; DB 1; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 1.8e+03;	
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	908 TTTTGTGTTGTTG 921	
DB	2 TTTTGTGTTGTTG 15	

RESULT 2317

ID	ADEI4023	standard; DNA; 16 BP.
XX	ADEI4023;	
AC		
XX	29-JAN-2004	(first entry)
DT		
XX		
DE	Optineurin promoter motif, repeat element or regulatory region #132.	
XX		
KW	Human, optineurin; ds, ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder.	
KV	glaucoma related disorder; motif; repeat element; regulatory region.	
OS	Homo sapiens.	
XX		
FN	US2003190617-A1.	
XX		
PD	09-OCT-2003.	
XX		
PF	06-MAR-2002; 2002US-00091281.	
PR		
XX	06-MAR-2002; 2002US-00091281.	
PA	(STEE/) SI E.	
XX	(RAYM/) RAYMOND V.	
PA	(MORI/) MORISSETTE J.	
XX		
P1	Raymond V, Morissette J, Si E,	
DR	MPJ, 2003-864168/80.	
XX		
PT	New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognosis and treat glaucoma and related disorders.	
PT		
PS	Claim 11; SEQ ID NO 134; 159pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid (NI) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter appearing as ADEI3890. Also included are the optineurin promoter operably linked to a heterologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample obtained from a cell or bodily fluid (comprising detecting a polymorphism in a promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence of an optineurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive disorder resulting in loss of visual field in a patient (or the severity or progression of glaucoma in a patient, comprising providing amplification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optineurin promoter and amplifying the DNA) and detecting a polymorphism (comprising obtaining a sample containing human genomic DNA, providing a nucleic acid capable of detecting a SNP located within an optineurin promoter, and detecting the polymorphism). The invention is used to diagnose and prognosis glaucoma and also to treat glaucoma related disorders. The present sequence is an optineurin promoter motif, repeat element or putative regulatory region.	
CC		
XX		
SEQ	Sequence 16 BP; 4 A; 6 C; 2 G; 4 T; 0 U; 0 Other;	
Query Match	1.4%; Score 14; DB 1; Length 16;	
Best Local Similarity	100.0%; Pred. No. 1.8e+03;	
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1124 AACCTCGAGCCTCA 1137 	
DB	3 AACCTCGAGCCTCA 16	

RESULT 2318
ADH70756
ID ADH70756 standard; DNA; 16 BP.
XX
XX ADH70756;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human Vbeta gene repeat sequence #546.
DE
XX human; T-cell associated disease; Vbeta; autoimmune disease;
KW degenerative nervous system disease; graft versus host disease;
KW hypersensitivity disease; infectious disease; neoplastic disease;
KW Addison's disease; atrophic gastritis;
KW degenerative nervous system disease; multiple sclerosis;
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;
KW allergy; type II hypersensitivity; Goodpasture's syndrome;
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;
KW HIV; fungal infection; Candida; parasitic infection; schistosoma;
KW filarial bacterial infection; Mycobacterium; neoplastic disease;
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
KW breast cancer; ds.
XX
XX Homo sapiens.
OS
XX
XX US2002150891-A1.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 05-MAR-1999; 99US-00263959.
PF
XX
XX 19-SEP-1994; 94US-00309335.
PR
XX
XX 19-SEP-1995; 95US-00531241.
PA
XX
XX (HOOD/) HOOD L E.
PA (ROME/) ROWEN L.
PI
XX
XX Hood LE; Rowen L;
XX
XX WPI; 2004-059052/06.
DR
XX
XX kit for diagnosing and treating T-cell associated diseases e.g.
PT autoimmune, degenerative nervous system and infectious diseases, comprises
PT nucleic acid primers specifically priming and allowing amplification of a
PT Vbeta gene.
XX
XX
XX disclosure; SEQ ID NO 950; 164pp; English.
PS
XX
XX The invention relates to a kit for diagnosing and treating T-cell
CC associated diseases which comprises a panel of nucleic acid primers
CC specifically priming and allowing amplification of each Vbeta gene,
CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
CC rejection and diagnosing and treating T-cell associated diseases
CC including autoimmune diseases, degenerative nervous system diseases,
CC graft versus host disease, hypersensitivity diseases, infectious diseases
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
CC atrophic gastritis. Degenerative nervous system diseases include multiple
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include type
CC I hypersensitivity diseases such as contact with allergens that lead to
CC allergies, type II hypersensitivity diseases such as those present in
CC Goodpasture's syndrome and type IV hypersensitivity diseases such as those
CC manifested in leprosy. Infectious diseases include viral infections
CC caused by viruses such as HIV, fungal infections such as those caused by
CC the yeast genus Candida, parasitic infections such as those caused by
CC schistosomes, filaria and bacterial infections such as those caused by
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC breast. The present sequence represents a Vbeta gene repeat sequence.
XX
XX
XX Sequence 16 BP; 2 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
SQ

Query Match 1.4%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 433 TTTATTTTTTTTA 446
1 TTTATTTTTTTTA 14
Db

RESULT 2319
AAT93362
ID AAT93362 standard; DNA; 17 BP.
XX
XX AAT93362;
XX
XX 06-MAR-1998 (first entry)
DT
XX
DE Primer #2 for D10S1765 microsatellite marker.
XX
XX IMAGE clone 264611; gene fragment; human; chromosome 10; D10S541 marker;
KW D10S215 marker; tumour suppressor gene; prostatic cancer; cancer therapy;
KW melanoma; glioma; non-Hodgkin's lymphoma; cancer susceptibility;
KW diagnosis; prognosis; mutation detection; suppressor gene; neoplasia;
KW hyperplasia; 10q loss tumour; PCR primer; amplify; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO9715666-A1.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 22-OCT-1996; 96WO-GB002588.
PF
XX
XX 23-OCT-1995; 95US-0005840P.
PR
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Spurr N, Gray IC;
PI
XX
XX WPI; 1997-259037/23.
DR
XX
XX Nucleic acid hybridising to chromosome 10 tumour suppressor gene - useful
PT for diagnosis, prognosis and treatment of prostatic cancer and for
PT assessing susceptibility to cancer.
XX
XX
XX Example 7; Page 68; 127pp; English.
PS
XX
XX AAT93357-T93362 represent amplification primers for microsatellite
CC markers. Mutations in the amplified sequences can be detected using the
CC nucleic acid sequences of the invention (see AAT93326-T93354). The
CC nucleic acid of the invention (I) is able to hybridise selectively to the
CC region of human chromosome 10 bounded by the markers D10S541 and D10S215.
CC (I) is a tumour suppressor gene, particularly involved in prostatic
CC cancer but also in melanoma, glioma and non-Hodgkin's lymphoma. Any
CC nucleic acid that hybridises selectively to the specified chromosomal
CC region can be used to determine susceptibility of a patient to cancer and
CC for diagnosis/prognosis, especially of prostatic cancer, i.e. by
CC detecting mutations. The wild-type suppressor gene can also be used to
CC treat cancer, especially when included in a viral vector. Similar
CC detection methods can be based on the amount of protein encoded by (I),
CC or its truncation or loss, in a sample, particularly using labelled
CC molecules capable of hybridising to the protein, particularly antibodies.
CC The labelled molecules when coupled to a cytotoxin can be used for cancer
CC treatment. The encoded protein can be used to raise antibodies and these
CC used to screen DNA expression libraries or for polypeptide isolation. (I)
CC allows differential diagnosis between neoplasia and hyperplasia of the
CC prostate (all tumours with a 10q loss have lost this region) and
CC determination of micro-metastases in the blood
XX
XX
XX Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
CC
SQ Sequence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 21.4%; Pred. No. 1.9e+03;
Matches 3; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
OY 908 TTTTGTGTGTG 921
Db 2 UUUUGUUUUUG 15
RESULT 2322
AAA22967/c
ID AAA22967 standard; RNA; 17 BP.
XX
AC AAA22967;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6193.
XX
Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
KW Homo sapiens.
OS
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI, 1999-591315/50.
DR
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 253; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of

CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
CC
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 339 TGCCCAAGCTGCTC 352
Db 14 TGCCCAAGCTGCTC 1
RESULT 2323
AAA22807
ID AAA22807 standard; RNA; 17 BP.
XX
AC AAA22807;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6033.
XX
Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
KW Homo sapiens.
OS
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI, 1999-591315/50.
DR
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 243; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme

CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, psoriasis, verruca vulgaris,
CC neovascular glaucoma, myopic degeneration, Sturge Weber
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

SO Sequence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 21.4%; Pred. No. 1.9e+03;
Matches 3; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 908 TTTTGTGTTGTTG 921
Db 1 UUUUUUUUUUUU 14

RESULT 2324
AAA22973/C
ID AAA22973 standard; RNA; 17 BP.

AC AAA22973;
XX
DT 19-JUN-2000 (first entry)
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6199.

XX Human; aryl hydriocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; AMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.
OS
XX
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
DR
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS
XX Claim 54; Page 254; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydriocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,

CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, psoriasis, verruca vulgaris,
CC neovascular glaucoma, myopic degeneration, Sturge Weber
CC angiobroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

SO Sequence 17 BP; 8 A; 3 C; 0 G; 0 T; 6 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 ATTTTGTAGAGA 789
Db 14 ATTTTGTAGAGA 1

RESULT 2325
AAA22846
ID AAA22846 standard; RNA; 17 BP.

AC AAA22846;
XX
DT 19-JUN-2000 (first entry)
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6072.

XX Human; aryl hydriocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; AMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiobroma;
KM tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.
OS
XX
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
DR
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS
XX Claim 54; Page 246; 305pp; English.

CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to CC
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3

SO Sequence 17 BP; 5 A; 1 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 776 ATTTTACTAGACGA 789

DB 3 AUUUUAGUAGAGA 16

RESULT 2326
 AAF06152
 ID AAF06152 standard; DNA; 17 BP.
 AC AAF06152;
 XX
 XX
 DT 16-FEB-2001 (first entry)
 XX
 XX Hammerhead ribozyme substrate #2949.
 DE
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blact L, Zwick M, Pavco P, Mcswiggen J;
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 123; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid

CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha

SO Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 14.3%; Pred. No. 1.9e+03;
 Matches 2; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 431 TATTTATTTT 444

DB 1 UUUUUUUUUUUU 14

RESULT 2327
 AAF05507
 ID AAF05507 standard; DNA; 17 BP.

AC AAF05507;
 XX
 XX

DT 16-FEB-2001 (first entry)
 XX
 XX

DE Hammerhead ribozyme substrate #2726.

KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Blact L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.

PS Claim 18; Page 118; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid

CC molecules that act as inhibitors of the expression of repressor genes

CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription

CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).

CC Inhibition of the repressors removes prevents inhibition (and

CC consequently increases expression of) genes involved in the production of

CC erythropoietin, granulocyte colony stimulating factor protein and

CC interferon alpha

SO Sequence 17 BP; 1 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 TTTTGATTTT 176

DB 3 TTTTGATTTT 16

RESULT 2328

ABT36209

ID ABT36209 standard; DNA; 17 BP.

AC ABT36209;

DT 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 1846.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX anti-sense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrania; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

OS Homo sapiens.

PN WO2003025175-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004208.

PR 17-SEP-2001; 2001FR-00011978.

PA (MOLE-) MOLECULAR ENGINES LAB.

PI Telemann A, Amson R, Tuijnder M;

DR WPI; 2003-313353/30.

PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfect cells.

PS Disclosure; Page 248; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optional
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrania. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention

SQ Sequence 17 BP; 5 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;

QY 492 GATCAGAGCTCACT 505

DB 1 GATCAGAGCTCACT 14

RESULT 2329

ADB04202

ID ADB04202 standard; DNA; 17 BP.

AC ADB04202;

DT 20-NOV-2003 (first entry)

DE Human MDZ7 scanning oligonucleotide SEQ ID 5188.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.

OS Homo sapiens.

PN EP1281758-A2.

PD 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

DR WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

PS Example 8; SEQ ID NO 5188; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.

SQ Sequence 17 BP; 2 A; 0 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0;

QY 162 ATTTGGATTTT 175

DB 3 ATTTGGATTTT 16

RESULT 2330

ADB04201

ID ADB04201 standard; DNA; 17 BP.

AC ADB04201;

DT 20-NOV-2003 (first entry)

DE Human MDZ7 scanning oligonucleotide SEQ ID 5187.

```
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PI WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5187; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 0 C; 3 G; 12 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 162 ATTTGTATTTT 175
DB 4 ATTTGTATTTT 17
XX
RESULT 2331
ADB04204
ID ADB04204 standard; DNA; 17 BP.
XX
AC ADB04204;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5190.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
```

```
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PI WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5190; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 0 C; 2 G; 12 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 162 ATTTGTATTTT 175
DB 1 ATTTGTATTTT 14
XX
RESULT 2332
ADB04203
ID ADB04203 standard; DNA; 17 BP.
XX
AC ADB04203;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5189.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
```

PA (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX
 DR WPI, 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 5189; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 3 G; 11 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No.1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 162 ATTTTGATTTT 175
 |||||
 Db 2 ATTTTGATTTT 15
 |||||
 RESULT 2333
 ID ADB04279 standard; DNA; 17 BP.
 XX
 AC ADB04279;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD27 scanning oligonucleotide SEQ ID 5265.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI, 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 5265; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 4 A; 1 C; 3 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred.No.1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 614 TTTTTCAGACAGA 627
 |||||
 Db 4 TTTTTCAGACAGA 17
 |||||
 RESULT 2334
 ID ADB04286 standard; DNA; 17 BP.
 XX
 AC ADB04286;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD27 scanning oligonucleotide SEQ ID 5272.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI, 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 5272; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 4 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 TTGAGACAGAGTCT 631

Db 1 TTGAGACAGAGTCT 14

RESULT 2335

ADB04311 ID ADB04311 standard; DNA; 17 BP.

XX ADB04311,

XX 20-NOV-2003 (first entry)

XX Human MDZ7 scanning oligonucleotide SEQ ID 5297.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 5297; 103bp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences; MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is

XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,

XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome

XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross

CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 GGCTGAGTGCAGT 660

Db 4 GGCTGAGTGCAGT 17

RESULT 2336

ACC64260 ID ACC64260 standard; DNA; 17 BP.

XX ACC64260;

XX 01-JUL-2003 (first entry)

XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1507.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;

XX tumour suppression; tumour reversal; apoptosis; virus resistance;

XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrenia; ss.

XX Mus musculus.

XX WO2003025176-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.

XX Disclosure; Page 207; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC68806), which are associated with tumour suppression, tumour

XX reversal, apoptosis and virus resistance. The oligonucleotides are

XX useful as (1) as probes and primers for detecting, identifying,

XX quantifying and/or amplifying nucleic acid, e.g. as one component of a

XX gene chip, in vitro as (anti)sense reagents; and (2) for production of a

XX recombinant polypeptides. The oligonucleotides are useful for preparation

XX of pharmaceuticals for prevention and/or treatment of viral diseases that

XX are characterised by development of tumours or cell degeneration,
XX specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 837 GATTCGCTGCTC 850

Db 1 GATTCGCTGCTC 14

RESULT 2337
ACC67292
ID ACC67292 standard; DNA; 17 BP.
XX
AC ACC67292;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4539.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
tumor suppression; tumor reversal; apoptosis; virus resistance;
KW viral disease; tumor; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 561; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
ACC68806), which are associated with tumour suppression, tumour
CC reversal, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 3 A; 1 C; 1 G; 12 T; 0 U; 0 Other;
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 426 CTTTATTATTAT 439
DB 4 CTTTATTATTAT 17
RESULT 2338
ACC68567
ID ACC68567 standard; DNA; 17 BP.
XX
AC ACC68567;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5814.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
tumor suppression; tumor reversal; apoptosis; virus resistance;
KW tumor suppression; tumor reversal; apoptosis; virus resistance;

KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 710; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
ACC68806), which are associated with tumour suppression, tumour
CC reversal, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 837 GATCTGCTGCTCC 850
DB 1 GATCTGCTGCTCC 14
RESULT 2339
ADB40764
ID ADB40764 standard; DNA; 17 BP.
XX
AC ADB40764;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #1087.
XX
KW Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumor suppression; tumor reversal; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.

PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 276; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virostatic, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 837 GATCTGCTGCTC 850
DB 1 GATCTGCTGCTC 14
XX
RESULT 2342
AD148718
ID AD148718 standard; DNA; 17 BP.
XX
XX AD148718;
AC
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID1221.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KM cytostatic; virostatic; neuroprotective; neurotropic; neuroleptic; probe;
KM primer; PCR; gene chip; antisense; viral disease; tumour;
KM cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
OS
XX
XX WO2003025177-A2.
PN
XX
PD 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004523.
PF
XX 17-SEP-2001; 2001FR-00011980.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M,
PI
XX
XX WPI; 2003-313354/30.
DR
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX
PS Disclosure; SEQ ID NO 1221; 30pp; French.
XX
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytostatic, virostatic, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 717 CCCAGCCTCCTGAG 730
DB 4 CCCAGCCTCCTGAG 17
XX
RESULT 2343
AD149435
ID AD149435 standard; RNA; 17 BP.
XX
XX AD149435;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX
DE Human PKR substrate sequence #549.
XX
XX
KM antisense oligonucleotide; neurite growth inhibitor; NOGO;
KM prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KM protein kinase PKR; cerebrovascular accident;
KM central nervous system injury; CNS injury; spinal cord injury; cancer;
KM melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KM restenosis; asthma; Crohn's disease; diabetes; obesity;
KM autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KM graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KM allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KM substrate; ds.
XX
XX
OS Unidentified.
XX
XX
XX WO200281628-A2.
FN
XX
XX 17-OCT-2002.
PD
XX
XX 03-APR-2002; 2002WO-US010512.
PF
XX
XX 05-APR-2001; 2001US-00827395.
PR
XX 29-MAY-2001; 2001US-0294412P.
PR
XX 28-AUG-2001; 2001US-0315315P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Blatt L, Chowrira B, Haeblerli P, McGawigen J, Fossnaugh K;
PI
XX
XX WPI; 2003-058513/05.
DR
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 2968; 317pp; English.
XX
XX
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX that down regulate the expression or inhibit the function of a receptor
XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.

XX SQ Sequence 17 BP; 3 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 724 TCCTAGTAGCTGG 737
||:||||:|||||

Db 1 UCCUGAGUAGCUUG 14

RESULT 2344

ADL49461

ID ADL49461 standard; RNA; 17 BP.

AC ADL49461;

DT 20-MAY-2004 (first entry)

XX Human PKR substrate sequence #575.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

KW protein kinase PKR; cerebrovascular accident;

KW central nervous system injury; CNS injury; spinal cord injury; cancer;

KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;

KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;

KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;

KW substrate; ds.

XX Unidentified.

OS WO200281628-A2.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blact J, Chowrira B, Haeblerli P, Mcswigen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

XX growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

XX protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2994; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

XX that down regulate the expression or inhibit the function of a receptor

XX for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.

XX SQ Sequence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 1.4%; Score 14; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 1.9e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 394 GCTGGATTACAGG 407
||:||||:|||||

Db 1 GCUGGAGUACAGG 14

RESULT 2345

ACC85669

ID ACC85669 standard; DNA; 17 BP.

AC ACC85669;

DT 22-APR-2004 (first entry)

XX RNA ligand aptamer marker/probe Anti-BBSII.

XX RNA aptamer; ligand; heat shock factor protein; PKR; primer; ss.

XX Synthetic.

XX WO2004001065-A2.

XX 31-DEC-2003.

XX 24-JUN-2003; 2003WO-US019966.

XX 24-JUN-2002; 2002US-0391255P.

XX (CORR) CORNELL RES FOUND INC.

XX Shi H, Lie JT;

XX WPI; 2004-071741/07.

XX Identifying RNA ligands that bind to a target molecule comprises treating

XX a first pool of RNA ligands that collectively bind more than one target

XX to reduce the concentration or eliminate the presence of target-binding

XX RNA ligands.

XX Disclosure; Page 65; Opp; English.

XX The present invention relates to a method of identifying RNA ligands that

XX bind to a target molecule, comprising treating a first pool of RNA

XX ligands that collectively bind more than one target under conditions

XX effective to reduce the concentration or eliminate the presence of one or

XX more predominate target-binding RNA ligands from the first pool of RNA

XX ligands. In particular, the method can be used to identify RNA aptamers

XX capable of binding to heat shock factor protein. The present sequence is

XX a DNA sequence shown in the exemplification of the invention

XX SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 14; DB 1; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 805 TCGCCAGGTGATC 818
 |||||
 DB 4 TCGCCAGGTGATC 17

RESULT 2346
 ADP08721
 ID ADP08721 standard; DNA; 17 BP.

AC ADP08721;

DT 26-AUG-2004 (first entry)

XX Extend primer 58 used to genotype human glycoprotein VI polymorphism.

XX breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;

KM GP6; GPVI; chromosome 19q13.4; ss; PCR; primer; SNP;

XX single nucleotide polymorphism.

OS Homo sapiens.

PN WO2004047767-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037966.

XX 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441082/41.

XX Identifying a subject at risk of breast cancer by detecting the presence

PT of absence of one or more nucleotide polymorphic variations, useful for

PT diagnosing, preventing and/or treating breast cancer.

XX Example 3; Page 83; 286pp; English.

XX The invention relates to a novel method for identifying a subject at risk

CC of breast cancer which comprises detecting the presence or absence of one

CC or more polymorphic variations associated with breast cancer in a nucleic

CC acid sample from a subject. The method of the invention has cytostatic

CC applications and may be useful for identifying a risk of breast cancer,

CC as well as therapeutic and prophylactic treatments that specifically

CC target breast cancer, such as gene therapy. The current sequence is that

CC of an extend primer of the invention which was used to genotype single

CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GP6;

CC GPVI; GPVI) DNA which is located at chromosomal position 19q13.4.

XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

SO Query Match 1.4%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;

XX CENPC1 extend primer #72.

XX Cytostatic; Gene therapy; breast cancer; human; DLG1; KIA0783; DPF3;

KM CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;

XX Centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.

OS Homo sapiens.

PN WO2004047514-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037943.

XX 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441037/41.

XX Identifying a subject at risk of breast cancer by detecting the presence

PT of polymorphic variations in the DLG1, KIA0783, DPF3 or CENPC1 regions

PT which are associated with breast cancer in a nucleic acid sample from a

PT subject.

XX Example 6; Page 91; 227pp; English.

XX The present invention relates to a method for identifying a subject at

CC risk of breast cancer. The method comprising detecting the presence or

CC absence of one or more polymorphic variations associated with breast

CC cancer in a nucleic acid sample from a subject. The nucleic acid sample

CC comprises the DLG1 region (AD079402), KIA0783 region (AD079403), DPF3

CC region (AD079404) or CENPC1 region (AD079405). The gene DLG1 (discs,

CC large homolog 1 (Drosophila)) is also known as synapse-associated protein

CC 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The

CC gene KIA0783 is also known as PHF14 and PHD finger protein 14. KIA0783

CC has been mapped to chromosomal position 7p21.3. The KIA0783 protein is a

CC novel gene with unknown function, however, being a zinc finger protein,

CC it likely to be a transcription factor. The gene DPF3 (D4, zinc and

CC double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079

CC and 2810403B03R1k. DPF3 is a Rho family guanine-nucleotide exchange

CC factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The

CC gene CENPC1 (centromere protein C1) is also known as Centromere

CC autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-

CC q13.3. CENPC1 is a centromere autoantigen and a component of the inner

CC kinetochore plate. The CENPC1 protein is required for maintaining proper

CC useful for identifying a subject at risk of breast cancer, to analyse and

CC diagnosis, prevention and treatment of breast cancer, to analyse and

CC predict a response to a breast cancer treatment, and in clinical drug

CC trials. The present sequence was used in an example from the invention.

XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

SO Query Match 1.4%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 691 CTCGCCGGGTTCAAG 704
 |||||
 DB 17 CTCGCCGGGTTCAAG 4

RESULT 2348

ACC84459/C

ID ACC84459 standard; DNA; 42 BP.

XX ACC84459;

AC ACC84459;

XX 26-AUG-2004 (first entry)

DT	28-AUG-2003	(first entry)	
XX			
DE	NTP peptide encoding sequence #6.		
XX			
KW	Cycostatic; Antibacterial; Immunosuppressive; Antiinflammatory;		
KW	neural thread protein; NTP; tumour; ds.		
XX			
OS	Unidentified.		
XX			
PN	WO2003008443-A2.		
XX			
PD	30-JAN-2003.		
XX			
PF	19-JUL-2002; 2002WO-CA001105.		
XX			
PR	19-JUL-2001; 2001US-0306150P.		
PR	19-JUL-2001; 2001US-0306161P.		
PR	16-NOV-2001; 2001US-0331477P.		
XX			
PA	(NTMO-) NTMOX CORP.		
XX			
PI	Averback PA;		
XX			
DR	WPI; 2003-247999/24.		
DR	P-P8DB; ABR63254.		
XX			
PS	Disclosure; Page 17; 77pp; English.		
XX			
CC	The present invention relates to a neural thread protein (NTP) peptide		
CC	referred to as cell death peptide. Thought to be cytostatic,		
CC	antibacterial, immunosuppressive and antiinflammatory. It is useful for		
CC	treating a condition in a patient requiring removal or destruction of		
CC	cells, for treating a condition such as benign or malignant tumor,		
CC	inflammatory disease, autoimmune disease and infectious disease. The		
CC	peptide useful for treatment is derived from the amino acid sequence for		
CC	a pancreatic thread protein. The peptide is conjugated, linked or bound		
CC	to a molecule chosen from antibody or its fragment, antibody-like binding		
CC	molecule, where the molecule has a higher affinity for binding to a tumor		
CC	or other target than binding to other cells. Treatment using NTP peptides		
CC	can remove benign tumors with less risk and fewer of the undesirable side		
CC	effects of surgery. The present sequence is an NTP encoding sequence		
XX			
SO	Sequence 42 BP; 6 A; 16 C; 11 G; 9 T; 0 U; 0 Other;		
	Query Match	1.4%;	Score 14; DB 1; Length 42;
	Best Local Similarity	60.5%;	Pred. No. 2.3e+03;
	Matches 23; Conservative	0;	Mismatches 15; Indels 0; Gaps 0;
QY	534 CCTCGTGCCTGAGCTCCCAAGTAGCTGGAGACANA 571		
DB	39 CCTGTATGCCAGCTACTCAGAGGCTGGGGCAGAGA 2		
	RESULT 2349		
	ACC84454/C		
ID	ACC84454 standard; DNA; 60 BP.		
XX			
AC	ACC84454;		
XX			
DT	28-AUG-2003 (first entry)		
XX			
DE	NTP peptide encoding sequence #1.		
XX			
KW	Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;		
KW	neural thread protein; NTP; tumour; ds.		
XX			
OS	Unidentified.		
XX			
PN	WO2003008443-A2.		

```

XX
PI scinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
XX
XX WPI; 1996-010927/01.
XX
PT New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
PT for treating restenosis or cancer.
XX
XX Claim 1; Page 68; 128pp; English.
XX
CC The present sequence represents the preferred target sequence for an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the human c-myb sequence at the base position indicated in the descriptor
CC line. The c-myb sequence was screened for optimal ribozyme target sites
CC using a computer folding algorithm, and regions of the mRNA which did not
CC form secondary folding structures and contained potential ribozyme
CC cleavage sites were identified. Ribozymes were synthesised and their
CC activities optimised by either varying the length of the binding arms or
CC by modification to prevent degradation by nucleases. The ribozymes cleave
CC the c-myb sequence and can be used to prevent smooth muscle cell
CC hyperproliferation in restenosis, especially after coronary angioplasty,
CC and in cancers
XX
SQ Sequence 17 BP, 5 A; 9 C; 0 G; 0 T; 3 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 475 ATGAAGTGCAGTGTGT 491
DB 17 ATGAGATGAGAGTGTGT 1
XX
RESULT 2351
AAT43035/c
ID AAT43035 standard; DNA; 17 BP.
XX
XX AAT43035;
XX
DT 25-JUN-1997 (first entry)
XX
XX Juvenile glaucoma marker afm278ye5 upstream amplification primer.
XX
XX Microsatellite; genetic marker; screening; detection; PCR primer;
XX polymerase chain reaction; juvenile glaucoma; predisposition; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX /note= "linked to JOE fluorochrome label"
XX
XX WO9633287-A1.
XX
XX 24-OCT-1996.
XX
XX 18-APR-1996; 96WO-FR000592.
XX
XX 18-APR-1995; 95FR-00004590.
XX
XX (INRM ) INSEEM INST NAT SANTE & RECH MEDICALE.
XX
XX Garchon H, Bach J;
XX
XX WPI; 1996-485791/48.
XX
XX Detecting pre-disposition to juvenile glaucoma - from presence of
XX specific microsatellite markers on chromosome 1q21q31, also DNA from the
XX region defined by these markers.
XX
XX Example; Page 7; 25pp; French.

```

```

XX
CC Predisposition to juvenile glaucoma is detected by characterising the
CC following microsatellite markers on chromosome 1q21q31 associated with
CC occurrence of juvenile glaucoma: afm350yh1; afm122x3; ngal; afm1;
CC afm248w5; afm278ye5; afm212xb10; afm157xe7 and NG45. An oligonucleotide
CC primer of the present sequence was used with a primer having the sequence
CC given in AAT43035 to amplify the afm278ye5 marker. Apart from detecting
CC predisposition to disease, the microsatellites should allow localisation,
CC and thus isolation, of the gene involved in juvenile glaucoma
XX
SQ Sequence 17 BP, 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 961 GGCCAAATCTCGGCTCA 977
DB 17 GGCTCAATCTCGGCTCA 1
XX
RESULT 2352
AAT85611
ID AAT85611 standard; DNA; 17 BP.
XX
XX AAT85611;
XX
DT 24-FEB-1998 (first entry)
XX
XX CADASIL mutation detection marker D19S841 flanking nucleotide sequence.
XX
XX CADASIL; marker; mutation; detection; genotypic diagnosis; chromosome 19;
XX microsatellite; genotyping; subcortical infarct;
XX cerebral autosomal dominant arteriopathy; leukoencephalopathy; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX EP780478-A1.
XX
XX 25-JUN-1997.
XX
XX 21-DEC-1995; 95EP-00402910.
XX
XX 21-DEC-1995; 95EP-00402910.
XX
XX 21-DEC-1995; 95EP-00402910.
XX
XX (INRM ) INSEEM INST NAT SANTE & RECH MEDICALE.
XX (AST-) ASSISTANCE PUBLIQUE.
XX
XX Tournier-Lasserre E, Joutel A, Bousser M, Bach J;
XX
XX WPI; 1997-322151/30.
XX
XX Indirect genotypic diagnosis of CADASIL - uses markers genetically linked
XX (within a 2 cM interval) to the mutated gene.
XX
XX Disclosure; Page 5; 13pp; English.
XX
XX A novel method has been developed for indirect genotypic diagnosis of
XX CADASIL (cerebral autosomal dominant arteriopathy with subcortical
XX infarcts and leukoencephalopathy) for symptomatic or at risk individuals
XX or foetuses belonging to a family suspected or known to be affected by
XX CADASIL. The method involves the use of markers genetically linked to the
XX mutated gene responsible for CADASIL in order to detect whether or not
XX the tested individual is carrying the chromosome 19 marker alleles that
XX have been linked to the disease gene in this given family and to estimate
XX his carrier risk, characterised in that the method is based on the
XX localisation of the gene in the interval of 2 cM spanned by the flanking
XX markers D19S226 and D19S19 and in that one uses at least 2 markers
XX located each on one side of the gene. The present sequence represents a
XX flanking nucleotide sequence of a new D19S841 marker. The method is used
XX for diagnosis of CADASIL and to estimate carrier risk in a given family.
XX Two new microsatellites D19S841 and 11547 have been identified and mapped

```

CC within the 2 cm interval. These very highly polymorphic markers are
 CC located very close to the gene within this interval. Their use in the
 CC diagnostic method according to the invention will further increase its
 CC accuracy and safety

CC Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match: 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 353 TCCTGAGCTCAGCAGT 369
 DB 1 TCCTGAGCTCAGCAGT 17

RESULT 2353
 AAX69800
 ID AAX69800 standard; RNA; 17 BP.

AC AAX69800;

XX 28-JUL-1999 (first entry)

DE Human flt1 VEGF receptor hammethead ribozyme substrate #1095.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

KW KDR; hammethead ribozyme; hairpin ribozyme; cleavage; ocular disease;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

KW foetal liver kinase 1; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO9715662-A2.

PD 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

PF 26-OCT-1995; 95US-0005974P.

PR 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

PA (CHIR) CHIRON CORP.

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX MPI; 1997-259017/23.

DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the

XX synthesis, expression and/or stability of a mRNA encoding 1 or more

XX receptors of vascular endothelial growth factor (VEGF). A patient

XX (preferably human) having a condition associated with the level of the

XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX treated by administering the nucleic acid molecule or the expression

XX vector to the patient. AAX67275 to AAX75752 represent specific examples

XX of nucleic acid molecules from the present invention

XX Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

XX Query Match: 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 5.9%; Pred. No. 1.9e+03;

XX Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

QY 426 CTTTATTATTATT 442
 DB 1 CUUUUUUUUUUUUU 17

RESULT 2354
 AAX70075
 ID AAX70075 standard; RNA; 17 BP.

AC AAX70075;

XX 28-JUL-1999 (first entry)

DE Human flt1 VEGF receptor hammethead ribozyme substrate #1370.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

KW KDR; hammethead ribozyme; hairpin ribozyme; cleavage; ocular disease;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

KW foetal liver kinase 1; ss.

XX Homo sapiens.

OS Homo sapiens.

PN WO9715662-A2.

PD 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

PF 26-OCT-1995; 95US-0005974P.

PR 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

PA (CHIR) CHIRON CORP.

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX MPI; 1997-259017/23.

DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 88; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the

XX synthesis, expression and/or stability of a mRNA encoding 1 or more

XX receptors of vascular endothelial growth factor (VEGF). A patient

XX (preferably human) having a condition associated with the level of the

XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX treated by administering the nucleic acid molecule or the expression

XX vector to the patient. AAX67275 to AAX75752 represent specific examples

XX of nucleic acid molecules from the present invention

XX Sequence 17 BP; 1 A; 2 C; 2 G; 0 T; 12 U; 0 Other;

XX Query Match: 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 17.6%; Pred. No. 1.9e+03;

XX Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

XX QY 904 TTAATTTTGTGTTT 920

DB 1 UCACUUUUUUUUUU 17

RESULT 2355
 AAX70073
 ID AAX70073 standard; RNA; 17 BP.

XX AAX70073;

XX

DT 28-JUL-1999 (first entry)
 XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1368.
 DE
 XX
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 88; 218pp; English.
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 CC
 CC
 SQ Sequence 17 BP; 1 A; 2 C; 2 G; 0 T; 12 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 17.6%; Pred. No. 1.9e+03;
 Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
 QY 902 TTTAATTTTGTGTGT 918
 DB 1 UUCACUUUUUUUUUU 17
 RESULT 2356
 AAX70074
 ID AAX70074 standard; RNA; 17 BP.
 XX
 XX AAX70074;
 AC
 XX
 XX 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1369.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX

XX
 EN MO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 88; 218pp; English.
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 CC
 CC
 SQ Sequence 17 BP; 1 A; 2 C; 2 G; 0 T; 12 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 17.6%; Pred. No. 1.9e+03;
 Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;
 QY 903 TTTAATTTTGTGTGT 919
 DB 1 UUCACUUUUUUUUUU 17
 RESULT 2357
 AAX63009
 ID AAX63009 standard; RNA; 17 BP.
 XX
 AC AAX63009;
 XX
 XX 16-JUL-1999 (first entry)
 XX
 DE Delta-9 desaturase hammerhead ribozyme target SEQ ID NO:884.
 XX
 KW Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;
 KW caffeine synthesis; coffee plant; nicotine production; tobacco;
 KW fruit ripening; flower pigmentation; lignin production; ss.
 XX
 OS Zea mays.
 XX
 PN MO9710328-A2.
 XX
 PD 20-MAR-1997.
 XX
 PF 12-JUL-1996; 96WO-US011689.
 PR 13-JUL-1995; 95US-0001135P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (DOMC) DOMELANCO.

XX Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;
 SQ Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 730 GTAGCTGGAGCTACAGG 746
 17 GCAGCTGGAGCTACAGG 1
 Db
 RESULT 2360
 AAV97762/c
 ID AAV97762 standard; RNA; 17 BP.
 AC AAV97762;
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DB Human EGF-R target sequence nucleotide position 4295.
 XX
 KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9833893-A2.
 XX
 PD 06-AUG-1998.
 XX
 PF 14-JAN-1998; 98MO-US000730.
 XX
 PR 31-JAN-1997; 97US-0036476P.
 PR 04-DEC-1997; 97US-00985162.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (UYAS-) UNIV ASTON.
 PI Akhtar S, Fell P, Mcswiggen JA;
 XX
 DR WPI; 1998-437449/37.
 XX
 PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 PT
 PS Claim 5; Page 79; 109pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules (NAs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGF-R
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 CC
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 520 CTGAGATCAAGCATCCT 536
 17 CTGAGATCAAGCATCCT 1
 Db

RESULT 2361
 AAV48871/c
 ID AAV48871 standard; DNA; 17 BP.
 XX
 AC AAV48871;
 XX
 DT 15-OCT-1998 (first entry)
 XX
 DE ErbB-2 gene antisense oligonucleotide ErbB-2-N-80.
 XX
 KW ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN EP856579-A1.
 XX
 PD 05-AUG-1998.
 XX
 PF 31-JAN-1997; 97EP-00101531.
 XX
 PR 31-JAN-1997; 97EP-00101531.
 XX
 PA (BIOG-) BIOLOGIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA Schlingensiepen K, Brysch W;
 PI
 DR WPI; 1998-400910/35.
 XX
 PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
 PT consecutive guanosine or inosine - and have specific ratio of residues
 PT able to form two or three hydrogen bonds, have greater activity and
 PT reduced toxicity, used therapeutically or to modulate growth of cells in
 PT culture.
 PT
 PS Example 4; Fig 6d; 286pp; English.
 XX
 CC AAV48709-886 represent antisense oligonucleotides directed against the
 CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in
 CC significant reduction in ErbB-2 protein expression, while
 CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
 CC exemplify the invention. The specification describes oligonucleotides
 CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
 CC can each form three hydrogen bonds to cytosine; do not contain four
 CC consecutive nucleotides able to form three H-bonds each to four
 CC consecutive cytosines; do not contain two sequences of three consecutive
 CC nucleotides each able to form three H-bonds to three consecutive
 CC cytosines, and the ratio between residues able to form two H-bonds each
 CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
 CC oligonucleotides are used to modulate expression of genes, particularly
 CC the genes for p53, Erb-2, JunB, JunD, TGF-beta 1 or beta 2 to control
 CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
 CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
 CC oligonucleotides can also be used to analyse function of proteins (by
 CC altering their expression or activity) and therapeutically, e.g. in cases
 CC of cancer or (targeting TGF) for stimulating the immune system
 CC
 SQ Sequence 17 BP; 10 A; 2 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 434 TTTATTTTTTTTAAAGAC 450
 17 TTTCTTTTTTTTAAAGAC 1
 Db
 RESULT 2362
 AAV95124/c
 ID AAV95124 standard; RNA; 17 BP.
 XX
 AC AAV95124;
 XX

```
XX 24-FEB-1999 (first entry)
DT
XX Canine IL-2 receptor g-chain substrate position 374.
DE
XX Human, IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX
OS Synthetic.
OS Canis sp.
XX
PN WO9824913-A2.
XX
PD 11-JUN-1998.
XX
PF 02-DEC-1997; 97WO-US021748.
XX
PR 03-DEC-1996; 96US-00758306.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Mcswigen JA;
XX
DR WPI; 1998-33332/29.
XX
PT Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
XX
PS Claim 4; Page 46; 61pp; English.
XX
CC The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AA93889 to AA94574 represent specifically claimed ribozymes, and
CC AA94575 to AA95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 776 ATTTTAGTAGAGATCG 792
DB 17 ATGTTCTGTAGAGATCG 1
RESULT 2363
AA22733
ID AAA22733 standard; RNA; 17 BP.
XX
AC AAA22733;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5959.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodioma;
KW tubercous sclerosis; pot-wine stains; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
```

```
XX WO9950403-A2.
PN
XX 07-OCT-1999.
XX
PD 24-MAR-1999; 99WO-US006507.
XX
PF 27-MAR-1998; 98US-0079678P.
XX
PR (RIBO-) RIBOZYME PHARM INC.
XX
PA Payco PA, Roberts E, Jarvis T, Coesholt C, Mcswigen JA;
XX
PI WPI; 1999-59115/50.
XX
DR Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 239; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
CC and AA17168 to AA17560 and AA17623 to AA17684 represent their
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
CC AA21596 to AA22475 and AA223263 to AA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
CC AA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (AMD), inflammation, and arthritis as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodioma of tubercous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 8 C; 3 G; 0 T; 5 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 536 TCCTGCTCAGCCTCCC 552
DB 1 UUCUGGUCACGCCUCC 17
RESULT 2364
AA22844
ID AAA22844 standard; RNA; 17 BP.
XX
AC AAA22844;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6070.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
```

KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS MO9950403-A2.
PN 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
PR (RIBO-) RIBOZYME PHARM INC.
PA (RIBO-) RIBOZYME PHARM INC.
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
DR Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 246; 305pp; English.
PS The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
CC AA21596 to AA21688 represent their corresponding target sequences;
CC AA21689 to AA22475 and AA22263 to AA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
CC AA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT, they
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 0 C; 4 G; 0 T; 9 U; 0 Other;
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. NO. 1.9e+03;
Matches 7; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 772 TTGATTTTACTAGAG 788
DB 1 UUGAUUUUUGAGAG 17
RESULT 2365
AAA22852
ID AAA22852 standard; RNA; 17 BP.
XX AAA22852;
AC
XX 19-JUN-2000 (first entry)
DT
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6078.
DE
XX Human, aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KW

KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antiporiatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX Homo sapiens.
OS MO9950403-A2.
PN 07-OCT-1999.
PD 24-MAR-1999; 99MO-US006507.
XX 27-MAR-1998; 98US-0079678P.
PR (RIBO-) RIBOZYME PHARM INC.
PA (RIBO-) RIBOZYME PHARM INC.
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
DR Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX Claim 54; Page 246; 305pp; English.
PS The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC AA11767 and AA11761 to AA17622 represent ribozyme sequences for ARNT,
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
CC and AA19155 to AA19222 represent their corresponding target sequences;
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
CC AA21596 to AA21688 represent their corresponding target sequences;
CC AA21689 to AA22475 and AA22263 to AA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
CC AA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT, they
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. NO. 1.9e+03;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 810 AGGTTGATCTTGATCTC 826
DB 1 AGGAUGAUUUCGACUUC 17
RESULT 2366
AAA22693
ID AAA22693 standard; RNA; 17 BP.
XX AAA22693;
AC
XX

DT 19-JUN-2000 (first entry)
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5919.
DE
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2; angiogenesis;
KW Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 236; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 0 C; 0 G; 0 T; 13 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 11.8%; Pred. No. 1.9e+03;
Matches 2; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
OY 429 TTTATTTATTTT 445
DB 1 UUUUUUUUUUUUU 17
RESULT 2367

AAA22688
ID AAA22688 standard; RNA; 17 BP.
XX
XX AAA22688;
AC
XX
XX 19-JUN-2000 (first entry)
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5914.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT, Tie-2; angiogenesis;
KW Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 54; Page 236; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 11.8%; Pred. No. 1.9e+03;
Matches 2; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
OY 428 TTTATTTATTTT 444

CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 0 A; 8 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.9e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 685 CTCTGCTCCCGGCTTC 701
Db 1 CCCCCCUCGCGGUUC 17

RESULT 2370
AAA22730
ID AAA22730 standard; RNA; 17 BP.

AC AAA22730;
XX
DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5956.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
tuberos sclerosis; pot-wine stain; Sturge Weber syndrome;
Klippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 238; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to
XX AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA2422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberos sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.9e+03;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1002 AAGCATTCCTCGTCT 1018
Db 1 AAGCGAUUCUUCUGGCU 17

RESULT 2371
AAA22842
ID AAA22842 standard; RNA; 17 BP.

AC AAA22842;

XX 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6068.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
tuberos sclerosis; pot-wine stain; Sturge Weber syndrome;
Klippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 245; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to
XX AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
XX sequences for integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are

CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.

XX SQ Sequence 17 BP; 7 A; 5 C; 0 G; 0 T; 5 U; 0 Other;
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 778 TTTTGTAGAGATGGGG 794
DB 17 TTTTGTAGAGATGAG 1

RESULT 2374
AAA22687
ID AAA22687 standard; RNA; 17 BP.

AC AAA22687;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5913.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX MO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwigen JA;

XX WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 236; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.

XX SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 11.8%; Pred. No. 1.9e+03;
Matches 2; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY 427 TTTTATTTTATTTT 443
DB 1 UUGUUAUUUUUUUU 17

RESULT 2375

ID AAA22822 standard; RNA; 17 BP.

AC AAA22822;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6048.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX MO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwigen JA;

XX PI

DR WPI, 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 244; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA11675 to
CC AA11167 and AA117561 to AA117622 represent ribozyme sequences for ARNT,
CC and AA117168 to AA117560 and AA117623 to AA117684 represent their
CC corresponding target sequences; AA117685 to AA118385 and AA119087 to
CC AA119154 represent ribozyme sequences for Tie-2, and AA118386 to AA119086
CC and AA119155 to AA119222 represent their corresponding target sequences;
CC AA119223 to AA120361 and AA121501 to AA121595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA120362 to AA121500 and
CC AA121596 to AA121688 represent their corresponding target sequences;
CC AA121689 to AA122475 and AA123263 to AA123342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA122476 to AA123262, AA123343 to
CC AA12422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

XX Query Match 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 64.7%; Pred. No. 1.9e+03;

XX Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 968 TCTGGCTCACTGCAAC 984

Db 1 UUUUGAGUCACUGCAAC 17

RESULT 2376

AAA22964/C

AAA22964 standard; RNA; 17 BP.

AC AAA22964;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6190.

XX Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

XX WO9950403-A2.

PD 07-OCT-1999.

PP 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX WPI, 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.

XX Claim 54; Page 253; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA11675 to
CC AA117167 and AA117561 to AA117622 represent ribozyme sequences for ARNT,
CC and AA117168 to AA117560 and AA117623 to AA117684 represent their
CC corresponding target sequences; AA117685 to AA118385 and AA119087 to
CC AA119154 represent ribozyme sequences for Tie-2, and AA118386 to AA119086
CC and AA119155 to AA119222 represent their corresponding target sequences;
CC AA119223 to AA120361 and AA121501 to AA121595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AA120362 to AA121500 and
CC AA121596 to AA121688 represent their corresponding target sequences;
CC AA121689 to AA122475 and AA123263 to AA123342 represent ribozyme sequence
CC for integrin subunit beta 3, and AA122476 to AA123262, AA123343 to
CC AA12422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

XX Query Match 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 355 CTGAGCTCAAGCACTCC 371

Db 17 CTGGGCTCAAGCAATCC 1

RESULT 2377

AAA22974/C

AAA22974 standard; RNA; 17 BP.

AC AAA22974;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6200.

XX Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

XX WO9950403-A2.

```

PD 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
PF
XX
XX 27-MAR-1998; 98US-0079678P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 254; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA2422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNNT.
CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
XX Sequence 17 BP; 13 A; 1 C; 0 G; 0 T; 3 U; 0 Other;
SQ
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 767 TTTTGTGATTTTAG 783
DB 17 TTTTGTGATTTTAG 1

```

```

XX OS Homo sapiens.
XX
XX MO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
PF
XX
XX 27-MAR-1998; 98US-0079678P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 239; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA18385 and AAA19087 to
CC corresponding target sequences; AAA17685 to AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA3422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNNT.
CC Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioblastoma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
XX Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
SQ
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.9e+03;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1004 GCGATTCCTGCTCA 1020
DB 1 GCGAUCUUCUGGCUCA 17

```

KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angioidfibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
OS Homo sapiens.
XX MO9950403-A2.
PN 07-OCT-1999.
XX PD
XX 24-MAR-1999; 99WO-US006507.
XX PF
XX 27-MAR-1998; 98US-0079678P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI WPI; 1999-591315/50.
DR
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS
XX Claim 54; Page 239; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT, they are
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidfibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 3 C; 5 G; 0 T; 7 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.9e+03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 298 GCGTGGCTAATTTTGT 314
DB 1 GCGCGGCTAATUUUUU 17
XX
RESULT 2380
AAA22754
ID AAA22754 standard; RNA; 17 BP.
XX
XX AAA22754;
AC
XX
DT 19-JUN-2000 (first entry)
XX
DB Integrin subunit beta 3 substrate sequence SEQ ID NO:5980.

XX Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW opthalmologic; antiinflammatory; antiarthritis; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angioidfibroma;
KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX MO9950403-A2.
PN 07-OCT-1999.
XX PD
XX 24-MAR-1999; 99WO-US006507.
XX PF
XX 27-MAR-1998; 98US-0079678P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI WPI; 1999-591315/50.
DR
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
PS
XX Claim 54; Page 240; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC sequences for integrin alpha 6 subunit, and AAA23263 to AAA23342 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidfibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
XX

QY 208 AGGCTGCTCGAAGTCT 224
DB 1 AGGCTGCTCGAAGTCT 17
XX
RESULT 2381
AAA22732
ID AAA22732 standard; RNA; 17 BP.
XX

XX	AAA22732;
DT	19-JUN-2000 (first entry)
DE	Integrin subunit beta 3 substrate sequence SEQ ID NO:5958.
KW	Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
KM	integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM	hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KM	ophthalmologic; antiinflammatory; antiarthritic; antipoxviral; ARMD;
KM	dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM	age related macular degeneration; inflammation; neovascular glaucoma;
KM	myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KM	tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KM	Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
OS	Homo sapiens.
PN	MO9950403-A2.
XX	
XX	07-OCT-1999.
PD	
PF	24-MAR-1999; 99WO-US006507.
XX	
PR	27-MAR-1998; 98US-0079678P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PJ	Pavco PA, Roberta E, Jarvis T, Coeshott C, Mcswigen JA;
DR	WPI, 1999-591315/50.
PT	Novel ribozymes for modulating the synthesis, expression and/or stability
PT	of an mRNA encoding an angiogenic factors.
PS	Claim 54; Page 239; 305pp; English.
XX	
CC	The present invention describes enzymatic nucleic acid molecules with RNA
CC	cleaving activity, which specifically cleave RNA encoded by an aryl
CC	hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC	gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA1675 to
CC	AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC	and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC	corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC	AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC	and AAA19155 to AAA19222 represent their corresponding target sequences;
CC	AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC	sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC	AAA21596 to AAA21688 represent their corresponding target sequences;
CC	AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC	for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC	AAA23422 represent their corresponding target sequences. The ribozymes of
CC	the invention are used for modulating the synthesis, expression and/or
CC	stability of an mRNA encoding angiogenic factor, especially ARNT,
CC	integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC	especially used to treat cancer, diabetic retinopathy, age related
CC	macular degeneration (ARMD), inflammation, and arthritis, as well as
CC	neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC	angiofibroma of tuberous scleriosis, pot-wine stains, Sturge Weber
CC	sndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC	and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC	integrin subunit alpha-6, or integrin subunit beta-3
XX	
SQ	Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
Query Match	1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	58.8%; Pred. No. 1.9e+03;
Matches 10; Conservative	5; Mismatches 2; Indels 0; Gaps 0
0Y	1005 CGATTCTCGTGTCTAG 1021 :: :: T CGAUTCUCUUGGUCAG 17

Query Match	1.4%	Score 13.8	DB 1	Length 17
Beet Local Similarity	70.6%	Fred. NO. 1.9e+03		
Matches 12	Conservative 3	Mismatches 2	Indels 0	Gaps 0

Qy 679 TGCACCTCTGCTCC 695
 Db 1 UGCACCTCCGCTUCC 17

RESULT 2383
 AAA22752
 ID AAA22752 standard; RNA; 17 BP.

AC AAA22752;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5978.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trennau-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

PN W09950403-A2.

PD 07-OCT-1999.

PF 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Payco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 240; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
 AA11767 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 and AA11768 to AA17560 and AA17623 to AA17684 represent their
 corresponding target sequences; AA17685 to AA18385 and AA19087 to
 AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 and AA19155 to AA19222 represent their corresponding target sequences;
 AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 AA21596 to AA21688 represent their corresponding target sequences;
 AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
 for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 AA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT.
 Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 syndrome, Kippel-Trennau-Weber syndrome, Osler-Weber-Rendu syndrome,
 and other syndromes and diseases related to the levels of ARNT, Tie-2,
 integrin subunit alpha-6, or integrin subunit beta-3.

Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 52.9%; Pred. No. 1.9e+03;
 Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1091 CGGGCTTCCACCATTT 1107
 Db 1 CGCGGUTCCACCAUUD 17

RESULT 2384

AAA22843
 ID AAA22843 standard; RNA; 17 BP.

AC AAA22843;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6069.

Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 age related macular degeneration; inflammation; neovascular glaucoma;
 myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
 Kippel-Trennau-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

PN W09950403-A2.

PD 07-OCT-1999.

PF 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Payco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 246; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to
 AA11767 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 and AA11768 to AA17560 and AA17623 to AA17684 represent their
 corresponding target sequences; AA17685 to AA18385 and AA19087 to
 AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086
 and AA19155 to AA19222 represent their corresponding target sequences;
 AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 AA21596 to AA21688 represent their corresponding target sequences;
 AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
 for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 AA23422 represent their corresponding target sequences. The ribozymes of
 the invention are used for modulating the synthesis, expression and/or
 stability of an mRNA encoding angiogenic factor, especially ARNT.
 Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 especially used to treat cancer, diabetic retinopathy, age related
 macular degeneration (ARMD), inflammation, and arthritis, as well as
 neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,

CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 4 A; 0 C; 3 G; 0 T; 10 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 35.3%; Pred. No. 1.9e+03;
 Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
 QY 771 TTGTATTTTGTAGTACA 787
 DB 1 UUUUGAUUUUUGAUGA 17
 RESULT 2385
 AAA22824
 ID AAA22824 standard; RNA; 17 BP.
 AC AAA22824;
 XX
 DT 19-JUN-2000 (first entry)
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:6050.
 XX
 KM Human; aryl hydrocarbon nuclear transport; ARNT; Tie-2; angiogenesis;
 KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KM hammerhead ribozyme; angiogenic factor; cytotactic; antidiabetic;
 KM ophthalmologic; antiinflammatory; antiarthritic; antipoxviral; ARMD;
 KM dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KM age related macular degeneration; inflammation; neovascular glaucoma;
 KM myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KM tuberous sclerosis; pot-wine stains; Sturge Weber syndrome;
 KM Kippel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 OS Homo sapiens.
 XX
 PN MO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
 XX
 DR WPI; 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 PS
 PS Claim 54; Page 244; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA24422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or

CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 0 A; 8 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.9e+03;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 684 CCTGCGCTCCCGGCTT 700
 DB 1 CCUCCGCUUCCCGGCUU 17
 RESULT 2386
 AAV91399
 ID AAV91399 standard; RNA; 17 BP.
 AC AAV91399;
 XX
 DT 18-FEB-1999 (first entry)
 DE Human C-raf target site nucleotide position 2899.
 XX
 KM Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KM target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KM screening; identification; synthesis; deprotection; purification; cancer;
 KM inflammation; psoriasis; non-hepatic ascites; infection; genetic difc;
 KM resenosis; rheumatoid arthritis; ss.
 KM
 OS Homo sapiens.
 XX
 PN MO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US009249.
 XX
 PR 09-MAY-1997; 97US-0046059P.
 PR 09-JUN-1997; 97US-0049003P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswigen JA, Karpistky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX
 DR WPI; 1999-009494/01.
 XX
 PT Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer.
 PT resenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 PS
 PS Claim 177; Page 154; 259pp; English.
 XX
 CC A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising

CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene

XX Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 11.8%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 2; Conservative 13; Mismatches 2; Indels 0; Gaps 0;
QY 596 TTTTATTTTATTTTAA 612
Db 1 UUUUAAUUUGUUUUUA 17

RESULT 2387

AAK18370
ID AAK18370 standard; DNA; 17 BP.

XX AAX18370;

DT 11-MAY-1999 (first entry)

DE RT-PCR primer of the invention SEQ ID 11.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

PN JP11032765-A.

PD 09-FEB-1999.

PF 18-JUL-1997; 97JP-00208312.

PR 18-JUL-1997; 97JP-00208312.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.

PS Disclosure; Page 11; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)/n-beta
CC -N3'; or (X)m5'-(gamma)/k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
sequences

XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 431 TTTTATTTTATTTTAA 447
Db 1 TTTTATTTTATTTTAA 17

RESULT 2388

AAZ36739
ID AAZ36739 standard; DNA; 17 BP.

XX AAZ36739;

DT 13-MAR-2000 (first entry)

DE Anchored oligo(DT) primer ATISA used for modified differential display.

XX Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

OS Synthetic.

PN WO955913-A2.

PD 04-NOV-1999.

PF 27-APR-1999; 99WO-US009119.

PR 27-APR-1998; 98US-008331P.

PR 27-AUG-1998; 98US-0098070P.

PR 04-FEB-1999; 99US-0118624P.

XX (KIMM-) KIMMEL CANCER CENT SIDNEY.

XX McClelland M, Welch J, Trenkle T;

DR WPI; 2000-086388/07.
XX Measuring expression of low abundance reduced complexity target nucleic acid molecules.

PS Example 3; Page 91; 187pp; English.

XX AAZ36739-41 represent oligo(DT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery

XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

QY 766 ATTTTGTGATTTTAA 782

Db 1 ATTTTATTTTATTTTA 17

RESULT 2389

AA25450 ID AAA25450 standard; DNA; 17 BP.

AC AAA25450;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.

XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KM gene expression modification; cancer; phosphorothioate; endonuclease;

XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

PN MO9954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99MO-US008547.

PR 20-APR-1998; 98US-0082404P.

PR 23-JUN-1998; 98US-00103636.

PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;

PI Matulic-Adamic J;

DR WPI; 2000-013248/01.

PT New nucleic acids that interact, and optionally cleave, target sequences,

PT used to treat cancer.

PS Claim 77; Page 79, 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphorodithioate

CC link, having endonuclease activity. (A), and more generally any catalytic

CC nucleic acid (A') that modulates expression of the oestrogen receptor

CC gene, are used to treat cancer (particularly of breast or endometrium), or

CC in vivo or by transforming cells ex vivo and implanting treated cells, or

CC for other conditions associated with levels of oestrogen receptor.

CC Because of the high selectivity for targeted RNA, (A) can also be used to

CC correlate inhibition of gene expression with alterations in phenotype,

CC particularly for identification of therapeutic targets, and as research

CC reagents (for RNA, in the same way that restriction endonucleases are

CC used with DNA). The combination of modifications in (A) improves

CC resistance to nucleases, binding affinity and/or activity. AAA23503 to

CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.

CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme

CC sequences, and AAA26107 to AAA26218 represent their corresponding target

CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and

CC antisense oligonucleotides used in the exemplification of the present

CC invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 444

DB 1 TTTTATTTTATTTT 17

RESULT 2390

AAA25600 ID AAA25600 standard; DNA; 17 BP.

AC AAA25600;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2098.

XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KM gene expression modification; cancer; phosphorothioate; endonuclease;

XX anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

PN MO9954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99MO-US008547.

PR 20-APR-1998; 98US-0082404P.

PR 23-JUN-1998; 98US-00103636.

PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;

PI Matulic-Adamic J;

DR WPI; 2000-013248/01.

PT New nucleic acids that interact, and optionally cleave, target sequences,

PT used to treat cancer.

PS Claim 77; Page 84, 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphorodithioate

CC link, having endonuclease activity. (A), and more generally any catalytic

CC nucleic acid (A') that modulates expression of the oestrogen receptor

CC gene, are used to treat cancer (particularly of breast or endometrium), or

CC in vivo or by transforming cells ex vivo and implanting treated cells, or

CC for other conditions associated with levels of oestrogen receptor.

CC Because of the high selectivity for targeted RNA, (A) can also be used to

CC correlate inhibition of gene expression with alterations in phenotype,

CC particularly for identification of therapeutic targets, and as research

CC reagents (for RNA, in the same way that restriction endonucleases are

CC used with DNA). The combination of modifications in (A) improves

CC resistance to nucleases, binding affinity and/or activity. AAA23503 to

CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.

CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme

CC sequences, and AAA26107 to AAA26218 represent their corresponding target

CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and

CC antisense oligonucleotides used in the exemplification of the present

CC invention

XX Sequence 17 BP; 3 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 AATTTTGTGATTTT 781

DB 1 AATCTTTGTATTTT 17

```
RESULT 2391
AAA25178
ID AAA25178 standard; DNA; 17 BP.
XX
XX AAA25178;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1676.
DE
XX
XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
XX Claim 77; Page 71; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodi(thioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA24748 to AAA25992 represent their corresponding target sequences.
XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 86.2%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 591 CTAATTTTATTTTAT 607
DB 1 CTGATTTTGTTTTAT 17
XX
XX RESULT 2392
XX AAA25603
```

```
ID AAA25603 standard; DNA; 17 BP.
XX
XX AAA25603;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2101.
DE
XX
XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
XX Claim 77; Page 84; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodi(thioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA24748 to AAA25992 represent their corresponding target sequences.
XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 771 TTTGATTTTATAGTGA 787
DB 1 TTTGATTTTACTTGA 17
XX
XX RESULT 2393
XX AAA25444
XX ID AAA25444 standard; DNA; 17 BP.
XX
```

AC AAA25444;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1942.
XX
KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 162 ATTTGATTTT 178
DB 1 ATTAGTTTTTTT 17

RESULT 2394
AAA25445
ID AAA25445 standard; DNA; 17 BP.
XX
AC AAA25445;
XX

DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943.
XX
KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswigen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 429 TTTATTTTATTTT 445
DB 1 TTTAGTTTTTTT 17

RESULT 2395
AAA98232
ID AAA98232 standard; DNA; 17 BP.
XX
AC AAA98232;
XX
DT 30-JAN-2001 (first entry)
XX

DE Human retrovirus HERV LTR PCR primer #31.
 XX Cell-specific expression; tissue-specific expression; gene therapy; LTR;
 KM U3-R segment; long terminal repeat; retroviral expression vector;
 KM PCR primer; ss.
 XX Human endogenous retrovirus.
 OS
 XX WO200053789-A2.
 PN
 XX 14-SEP-2000.
 PD
 XX 09-MAR-2000; 2000MO-EP002064.
 PF
 XX 10-MAR-1999; 99DE-01010650.
 PR
 XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
 PA
 XX Leib-Moesch C, Schoen U, Baust C;
 PI
 XX WPI; 2000-587442/55.
 DR
 XX Retroviral expression vector, useful in gene therapy, contains a promoter
 PT from a human endogenous retrovirus to provide cell-specific expression.
 PS
 XX Disclosure; Page 27; 67pp; German.
 XX
 XX This invention describes a novel retroviral expression vector (A)
 CC containing DNA sequences (1) for packaging vector RNA and for cell-
 CC specific expression of proteins or peptides encoding by heterologous DNA
 CC (11). The sequences controlling cell-specific expression contain a cell-
 CC specifically regulatable promoter region (p) from a human endogenous
 CC retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and
 CC RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)
 CC eukaryotic cells containing (A) in integrated form; (d) viruses
 CC containing a retroviral expression vector RNA derived from (A); (e) a
 CC method for producing the viruses of (d); (f) a method for incorporating
 CC protein-encoding nucleic acid sequences into a eukaryotic cell by
 CC infection with the viruses of (d); and (g) a retroviral vector system
 CC containing (A) and a packaging cell line, that contains at least one
 CC (recombinant) retrovirus construct that encodes for the packaging
 CC proteins of (A). (A) are used for cell- or tissue-specific expression of
 CC foreign genes for gene therapy and to produce viruses for introducing
 CC (11) into the chromosomal DNA of eukaryotic cells, preferably mammalian
 CC and specifically human. (A) retain the advantages of usual retroviral
 CC promoters with all the signal structures required for transcription in a
 CC small region within the U3-R segment, but without their disadvantages
 CC (excessive strength and limited cell specificity). Since (A) are derived
 CC from endogenous (harmless) viral sequences, they do not introduce any new
 CC viral sequences into the genome and recombination will not create new
 CC types of retrovirus. The promoters provide cell or tissue specific
 CC expression, according to which HERV they are derived from
 CC
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTT 444
 |||||
 Db 1 TTTTATTTTATTTT 17
 RESULT 2396
 ID AAA50197 standard; DNA; 17 BP.
 AC AAA50197;
 XX
 XX 07-NOV-2000 (first entry)
 DT
 XX 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.

XX
 KM Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..19
 FT /*tag= a
 FT /note= "2'-methoxyethoxy modified thymidine"
 FT modified_base 1..17
 FT /*tag= b
 FT /note= "phosphorothioate internucleoside linkages"
 XX
 PN WO200047593-A1.
 PD
 XX 17-AUG-2000.
 PD
 XX 11-FEB-2000; 2000MO-US003543.
 PF
 XX 12-FEB-1999; 99US-00250075.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Manoharan M, Maier MA;
 PI
 XX WPI; 2000-558188/51.
 DR
 XX Preparation of mixed backbone oligomeric compounds useful as e.g. primers
 PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
 PT linkages to phosphodiester internucleoside linkages.
 PS
 XX Example 12; Page 34; 49pp; English.
 XX
 XX The present sequence is that of a phosphorothioate oligonucleotide
 CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
 CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound
 CC produced according to the methods of the invention. The invention
 CC provides compounds and methods for the preparation of mixed backbone
 CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
 CC linkages in addition to phosphorothioate and/or phosphoramidate
 CC internucleoside linkages. The methods also include incorporation of
 CC boranophosphate internucleoside linkages. The methods utilize H-
 CC boranophosphate intermediates that are coupled together forming contiguous
 CC regions of 1 or more H-phosphonate internucleoside linkages. Each
 CC contiguous region is subsequently oxidized to phosphodiester,
 CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
 CC linkages prior to further elongation. Mixed backbone oligomeric compounds
 CC are prepared in this manner by oxidizing adjacent regions with different
 CC reagents. Oligomeric compounds of the invention are prepared using novel
 CC oxidation steps that oxidize a region of 1 or more H-phosphonate
 CC internucleoside linkages without degrading existing linkages that have
 CC been previously oxidized. The oligonucleotides obtained are useful as
 CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
 CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
 CC and as antiviral agents
 CC
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 428 TTTTATTTTATTTT 444
 |||||
 Db 1 TTTTATTTTATTTT 17
 RESULT 2397
 ID AAF05509 standard; DNA; 17 BP.
 AC AAF05509;
 XX
 XX

DT 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #2728.
 DE
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KM interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blact L, Zwick M, Pavco P, Mcswigen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 18; Page 118; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 CC
 SQ Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 U; 0 Other;
 XX
 QY
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 164 TTTGATTTTTTTTAG 180
 1 TTTGATTTTTTTCTGG 17
 XX
 RESULT 2398
 AAF05510
 ID AAF05510 standard; DNA; 17 BP.
 AC AAF05510;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #2729.
 XX
 KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KM interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX

XX Blact L, Zwick M, Pavco P, Mcswigen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 18; Page 118; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 CC
 SQ Sequence 17 BP; 1 A; 1 C; 3 G; 12 T; 0 U; 0 Other;
 XX
 QY
 Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 165 TTTGATTTTTTTTACT 181
 1 TTTGATTTTTTTCTGGT 17
 XX
 RESULT 2399
 AAF06381
 ID AAF06381 standard; DNA; 17 BP.
 AC AAF06381;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #3178.
 XX
 KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KM interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blact L, Zwick M, Pavco P, Mcswigen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 128; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and

```
CC Interferon alpha
XX
SQ Sequence 17 BP; 2 A; 0 C; 1 G; 0 T; 14 U; 0 Other;

Query Match      1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 11.8%; Pred. No. 1.9e+03;
Matches 2; Conservative 13; Mismatches 2; Indels 0; Gaps 0;

QY      603 TTTATTTTAAATTTT 619
      :::::|:::|
Db      1 UUUUUUUUAUUUUUG 17

RESULT 2400
AAF05469
ID AAF05469 standard; DNA; 17 BP.
XX
AC AAF05469;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2688.
XX
KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KM Interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PR 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcawiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 18; Page 117; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EARS/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the C/EBP displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 2 A; 2 C; 0 G; 13 T; 0 U; 0 Other;

Query Match      1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      595 TTTTATTTTATTTT 611
      |||||
Db      1 TCTTATTTTCATTTT 17

RESULT 2401
ABK00892
ID ABK00892 standard; RNA; 17 BP.
XX
AC ABK00892;
```

```
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #162.
XX
KM Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KM DNAzyme; inozyme; G-cleaver; amidezyme; zinzyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced ataxia; Huntington's disease;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PR 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
XX
PR 28-FEB-2000; 2000US-0185516P.
XX
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcawiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 80; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA motif) or
CC possessing an NCH motif, a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberyze (cleaving RNA with an NGN tripler), a zinzyme (cleaving RNA
CC with a YGf motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
```

CC chemotherapy-induced neuropathy; amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia; Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

XX Sequence 17 BP; 0 A; 11 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.9e+03;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 242 CTCGCTCTCGGCTCC 258
 1 CUCGCGCCGCGCCUCC 17

RESULT 2402

ID ABRK00891 standard; RNA; 17 BP.

AC ABRK00891;

DT 12-MAR-2002 (first entry)

DE Human NOGO Inozyme #161.

XX Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; Inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
 OS Synthetic.

PN WO200159103-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.

PI Blact L, Meswigen J, Chowrira BM,

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

XX Claim 88; Page 80; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulate expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an inozyme of the invention

XX Sequence 17 BP; 0 A; 11 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 1.9e+03;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 241 CTCGCTCTCGGCTCC 257
 1 CUCGCGCCGCGCCUCC 17

RESULT 2403

ID ABRK00891 standard; RNA; 17 BP.

AC ABRK00891;

DT 12-MAR-2002 (first entry)

DE Human NOGO Hammerhead Ribozyme #89.

XX Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; Inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
 OS Synthetic.

PN WO200159103-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 67; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 CC
 XX
 SQ Sequence 17 BP; 1 A; 9 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 1.44; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 1.9e+03;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Oy 1009 TCTGCTGTCAGCCTC 1025
 Db 1 UCUCUCUCUCAGCCGC 17
 RESULT 2404
 ABK00237/c
 ID ABK00237 standard; RNA; 17 BP.
 XX
 AC ABK00237;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Hammerhead Ribozyme #237.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyyme; zinzyme; lymphocytic leukemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001MO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 CC Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 CC constructs, which down regulate expression of a CD20 gene or neurite
 CC growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 CC central nervous system injury.
 XX
 PS Claim 88; Page 69; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 CC
 XX
 SQ Sequence 17 BP; 14 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TTTTATTTTATTTT 444
 |||||
 17 TTTCTCTATTTT 1

DB

RESULT 2405
 ABL46735
 ID ABL46735 standard; RNA; 17 BP.
 XX
 AC ABL46735;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID NCH ribozyme substrate oligonucleotide #189.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswigen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX
 PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 PS Claim 4; Page 66; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 4 A; 10 C; 2 G; 0 T; 1 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.9e+03;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 371 CACCTGCTCAGCTCC 387
 |||||
 1 CACGACCCAGCCTCC 17

DB

RESULT 2406
 ABA82505
 ID ABA82505 standard; DNA; 17 BP.
 XX
 AC ABA82505;
 XX
 PD

DT 25-JAN-2002 (first entry)
 XX
 DE Zmax1 gene region physical map preparation STS marker #464.
 XX
 KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
 KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
 KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
 KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200177327-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 21-JUN-2000; 2000WO-US016951.
 XX
 PR 05-APR-2000; 2000US-00543771.
 XX
 PR 05-APR-2000; 2000US-00544398.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Carulli JP, Little RD, Recker RR, Johnson ML;
 XX WPI; 2001-657171/75.
 DR
 XX
 PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
 PT modulating bone mass for the treatment of e.g. osteoporosis.
 XX
 PS Disclosure; Page 36; 443pp; English.
 XX
 CC The present invention describes the human Zmax1 gene and the high bone
 CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
 CC genes have osteopathic activities. The genes can be used in gene therapy,
 CC antisense therapy and in the production of vaccines. They can be used in
 CC the diagnosis and treatment of bone disorders including osteoporosis,
 CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
 CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 996 GGGCTCAAGCGATTCTC 1012
 |||||
 1 GCGCTCAAGCAATTCTC 17

DB

RESULT 2407
 ABA82230/c
 ID ABA82230 standard; DNA; 17 BP.
 XX
 AC ABA82230;
 XX
 DT 25-JAN-2002 (first entry)
 XX
 DE Zmax1 gene region physical map preparation STS marker #189.
 XX
 KW Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
 KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
 KW antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
 KW sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200177327-A1.
 XX
 PD 18-OCT-2001.

XX 21-JUN-2000; 2000MO-US016951.
PF 05-APR-2000; 2000US-00543771.
XX 05-APR-2000; 2000US-00544398.
PR (GENO-) GENOME THERAPEUTICS CORP.
XX Carulli JP, Little RD, Recker RR, Johnson ML;
XX WPI; 2001-657171/75.
XX New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT modulating bone mass for the treatment of e.g. osteoporosis.
XX Disclosure; Page 34; 443pp; English.
XX The present invention describes the human Zmax1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
CC genes have osteopathic activities. The genes can be used in gene therapy,
CC antisense therapy and in the production of vaccines. They can be used in
CC the diagnosis and treatment of bone disorders including osteoporosis,
CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 994 CCGGGCTCAAGCGATTC 1010
DB 17 CTGGGTTCAAGCGATTC 1
RESULT 2408
ABN08871/c
ID ABN08871 standard; DNA; 17 BP.
XX
AC ABN08871;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8863.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
AC WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-000424253.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 8863; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and vaccine production. The hGDMLP-1
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 197 CCATGTTGTCAGGCTG 213
DB 17 CCATCTGTATCAGGCTG 1
RESULT 2409
ABN09432/c
ID ABN09432 standard; DNA; 17 BP.
XX
AC ABN09432;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9424.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
AC WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 200GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
XX
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 9424; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP-
CC 1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 346 GCTGTCTCTCTGAGTC 362
DB 17 GCTGTCTCTCTGAGTC 1
XX
RESULT 2410
ABN09435/c
ID ABN09435 standard; DNA; 17 BP.
XX
AC ABN09435;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9427.
XX
XX Human; genome-derived myosin-like protein 1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; 88.
XX

OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0235359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 9427; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP-
CC 1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 343 CAGCTGTCTCTGAG 359
DB 17 CAGCTGTCTCTGAG 1
XX
RESULT 2411
ABN06554/c
ID ABN06554 standard; DNA; 17 BP.

XX AC ABN06554;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6546.
 XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 XX KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 XX KM skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX PN WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 30-JAN-2001; 2001WO-US000670.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PA (ABOM-) ABOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX DR WPI; 2002-179446/23.
 XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 XX PT or as specific biomolecule capture probes for surface-enhanced laser
 XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX PS Disclosure; SEQ ID NO 6546; 214pp; English.
 XX CC The present invention describes a human genome-derived myosin-like
 XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 XX CC nucleic acids can be used as probes to detect, characterise and quantify
 XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
 XX CC protein variants having desired phenotypic improvements, and for
 XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 XX CC -1 proteins, as standards in assays used to determine the concentration
 XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 XX CC capture probes for surface-enhanced laser desorption/ionisation, as
 XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 XX CC production, and in vaccines or for replacement therapy. The
 XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 XX CC disorder associated with the expression of hGDMLP-1, in particular heart
 XX CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 XX CC The present sequence represents an oligomer used in the screening of the
 XX CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 XX CC The sequence data for this patent did not form part of the printed
 XX CC specification, but was obtained in electronic format directly from WIFO
 XX CC at ftp.wipo.int/pub/published_pct_sequence
 XX SQ Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 369 TCACCTGCTCAGCCT 385
 Db 17 TCACCTGCCGCCAGCCT 1
 RESULT 2412
 ID ABN06555/c
 ID ABN06555 standard; DNA; 17 BP.
 XX AC ABN06555;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6547.
 XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 XX KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 XX KM skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX PN WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 30-JAN-2001; 2001WO-US000670.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PA (ABOM-) ABOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX DR WPI; 2002-179446/23.
 XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 XX PT or as specific biomolecule capture probes for surface-enhanced laser
 XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX PS Disclosure; SEQ ID NO 6547; 214pp; English.
 XX CC The present invention describes a human genome-derived myosin-like
 XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 XX CC nucleic acids can be used as probes to detect, characterise and quantify
 XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
 XX CC protein variants having desired phenotypic improvements, and for
 XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 XX CC -1 proteins, as standards in assays used to determine the concentration
 XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 XX CC capture probes for surface-enhanced laser desorption/ionisation, as
 XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 XX CC production, and in vaccines or for replacement therapy. The
 XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPL-1, in particular heart
CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pot_sequence

XX SQ Sequence 17 BP; 2 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 368 GTCCACCTGCTCAGCC 384

DB 17 GTCCACCTGCTCAGCC 1

RESULT 2413

ABV79240/c

XX ID ABV79240 standard; DNA; 17 BP.

XX AC ABV79240;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPPL scanning oligonucleotide SEQ ID 486.

XX KW Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

XX KM male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX PT WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPL.

XX PS Example 2; Page 127; 718pp; English.

XX CC The present invention relates to human testis expressed Patched like

XX CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL

XX CC has two isoforms, with a few single base pair differences between the

XX CC two. One of the single base pair changes introduces a premature stop

XX CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

XX CC shares an overall structure organisation with the Patched protein. The

XX CC shared structural features strongly imply that HTPL plays a role similar

XX CC to that of Patched, and is a potential tumour suppressor. HTPL is

XX CC important in regulating male germ cell development, and the HTPL gene was

XX CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention

XX SQ Sequence 17 BP; 1 A; 2 C; 11 G; 3 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1047 CACCTGCCACCCAGCC 1063

DB 17 CACCTGCCACCCAGCC 1

RESULT 2414

ABK23302

XX ID ABK23302 standard; DNA; 17 BP.

XX AC ABK23302;

XX DT 09-APR-2002 (first entry)

XX DE Human Zmax1 cDNA reverse PCR primer #232.

XX KW Human; mouse; Zmax1; HBW; high bone mass gene; lipid regulation; stroke;

XX KM lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;

XX KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;

XX KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;

XX KW bone development disorder; antihypertensive; cardiovascular;

XX KW osteopathic; cerebroprotective.

XX OS Homo sapiens.

XX PN WO200192891-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016946.

XX PR 26-MAY-2000; 2000US-00578900.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.

XX PI Carulli JP, Little RD, Recker RR, Johnson ML,

XX PT WPI; 2002-097784/13.

XX PT Identifying molecules involved in lipid regulation, useful for

XX PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises

XX PT identifying a molecule that binds to high bone mass gene or its

XX PT corresponding wild type gene.

XX PS Disclosure; Page 41; 409pp; English.

XX CC The invention relates to a method for identifying a molecule involved in

XX CC lipid regulation comprising identifying a molecule that binds to or

XX CC inhibits binding of a molecule to high bone mass (HBM) or its wild type

XX CC gene, Zmax1. Compounds identified by the method are useful for treating,

XX CC diagnosing, preventing or screening for normal and abnormal lipid-

XX CC associated conditions, including arteriosclerosis, cardiovascular

XX CC disease, stroke, and osteoporosis. The compounds may also be used in the

XX CC treatment or prevention of diabetic atherosclerosis, neurovascular

XX CC conditions caused by plaque build-up, poor circulation due to plaque

XX CC build-up and associated poor wound healing. The methods may be used in

XX CC gene therapy, pharmaceutical development, and diagnostic assays for bone

CC development disorders. Molecules identified by comparison of Zmax1 and
 CC HBM systems can be used as surrogate markers in pharmaceutical
 CC development, in diagnosis of human or animal bone disease, and in the
 CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention

XX Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 CGCGCTCAAGCATTTCTC 17

RESULT 2415

ABK23027/c

ID ABK23027 standard; DNA; 17 BP.

XX ABK23027;

XX 09-APR-2002 (first entry)

DE Human Zmax1 cDNA forward PCR primer #95.

XX Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
 XX lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
 XX osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
 XX neurovascular condition; wound healing; gene therapy; PCR primer; probe;
 XX bone development disorder; antiarteriosclerotic; cardiovascular;
 XX osteopathic; cerebroprotective.

OS Homo sapiens.

XX WO200192891-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016946.

XX 26-MAY-2000; 2000US-00578990.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX (UTCR-) UNIV CREIGHTON SCHOOL MEDICINE.

XX Carulli JP, Little RD, Recker RR, Johnson ML;

XX WPI; 2002-097784/13.

XX Identifying molecules involved in lipid regulation, useful for
 XX diagnosing, treating or preventing e.g., arteriosclerosis, comprises
 XX identifying a molecule that binds to high bone mass gene or its
 XX corresponding wild type gene.

XX Disclosure; Page 39; 409pp; English.

XX The invention relates to a method for identifying a molecule involved in
 XX lipid regulation comprising identifying a molecule that binds to or
 XX inhibits binding of a molecule to high bone mass (HBM) or its wild type
 XX gene, Zmax1. Compounds identified by the method are useful for treating,
 XX diagnosing, preventing or screening for normal and abnormal lipid-
 XX associated conditions, including arteriosclerosis, cardiovascular
 XX disease, stroke, and osteoporosis. The compounds may also be used in the
 XX treatment or prevention of diabetic atherosclerosis, neurovascular
 XX conditions caused by plaque build-up, poor circulation due to plaque
 XX build-up and associated poor wound healing. The methods may be used in
 XX gene therapy, pharmaceutical development, and diagnostic assays for bone
 XX development disorders. Molecules identified by comparison of Zmax1 and
 XX HBM systems can be used as surrogate markers in pharmaceutical
 XX development, in diagnosis of human or animal bone disease, and in the

CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention

XX Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 17 CTGGCTTCAAGCATTTCTC 1

RESULT 2416

ABK23027/c

ID ABK23027 standard; DNA; 17 BP.

XX ABK23027;

XX 24-DEC-2002 (first entry)

XX Human PAPP-Ea associated 17-mer SEQ ID 851.
 XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
 XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 XX dysgenetic pregnancy; primer; ss.

OS Homo sapiens.

XX US2002102252-A1.

XX 01-AUG-2002.

XX 06-APR-2001; 2001US-00827998.

XX 26-MAY-2000; 2000US-0207456P.

XX (GUY/) GU Y.

XX (SHAN/) SHANNON M E.

XX Gu Y, Shannon ME;

XX WPI; 2002-697817/75.

XX New isolated nucleic acid encoding an isoform of human pregnancy
 XX associated plasma protein E, for preventing or aborting pregnancy.

XX Example 2; Page 187; 353pp; English.

XX This invention describes a novel isolated nucleic acid that encodes one
 XX of three new isoforms of human pregnancy associated plasma protein E,
 XX hPAPP-E. The products of the invention have abortive and contraceptive
 XX activity and can be used for gene therapy or in a vaccine. The nucleic
 XX acid, polypeptide encoded by it, or antibody to the polypeptide can be
 XX used in pharmaceutical compositions or vaccines for preventing or
 XX aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 XX dysgenetic pregnancies. The nucleic acids are used as probes to assess
 XX the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 XX antibodies can be used to assess the expression levels of PAPP-E isoform
 XX proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 XX antenatally. This sequence represents an oligomer used in scanning the
 XX human PAPP-E genes described in the disclosure of the invention

XX Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 890 CGCCGGGCTTATTTTA 906

DB 17 CGCAGGCTTATCTTA 1

RESULT 2417
ID ABE56068/c
ID ABE56068 standard; RNA; 17 BP.

AC ABE56068;
XX
XX
XX 02-JUL-2002 (first entry)
XX
XX
XX Human CLCA1 gene enzymatic nucleic acid #439.
DE
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX acetylcysteine.
XX
XX Homo sapiens.
XX
XX MO200211674-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US024970.
XX
XX 09-AUG-2000; 2000US-0224383P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (SYNT) SYNTAX USA LLC.
XX (THOM/) THOMPSON J.
XX
XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;
XX Grube A;
XX
XX WPI; 2002-217145/27.
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
XX channel calcium activated gene, useful for treating Chronic obstructive
XX pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX Claim 4; Page 60; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
by cleaving RNA derived from the genes. The nucleic acid sequences are
useful as pharmaceutical agents for treating conditions such as chronic
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
fibrosis, obstructive bowel syndrome and any other diseases or conditions
that are related to or will respond to the levels of CLCA1 in a cell or
tissue. The sequences are useful for reducing CLCA1 activity in a cell,
hence, are useful for treatment of a patient having a condition
associated with the level of CLCA1, where the invention further comprises
the use of one or more therapies under conditions suitable for the
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
examine genetic drift and mutations within diseased cells or to detect
the presence of CLCA1 RNA in a cell. This sequence represents an
enzymatic nucleic acid molecule of the invention

Sequence 17 BP; 4 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 520 CTGAGATCAAGATCCT 536
DB 17 CTGAGATCAAGATCT 1

RESULT 2418
ID ACN01141
ID ACN01141 standard; RNA; 17 BP.
XX
XX ACN01141;
XX
XX 22-APR-2004 (first entry)
XX
XX
XX MNV Hammerhead Ribozyme substrate SEQ ID NO 1131.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
XX virus; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 23; SEQ ID NO 1131; 495pp; English.

The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (MNV). The nucleic acid molecules are useful for
treating a condition related to MNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention

Sequence 17 BP; 4 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.9e+03;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1109 GTCAGGCTGTCTCAA 1125
DB 1 GTCAGGCTGTCTCAA 17

RESULT 2419
ID ACN14418/c
ID ACN14418 standard; RNA; 17 BP.
XX
XX ACN14418;
XX
XX 22-APR-2004 (first entry)
XX
XX

XX 19-OCT-2001; 2001MO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (MNV), useful for treating a condition related to MNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 4918; 495bp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 XX treating a condition related to MNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention

SO Sequence 17 BP; 7 A; 4 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 TCGCCAGTTGATCTTG 821
 DB 17 TCGCCAGTTGTTCTTG 1

RESULT 2422
 ACN01975/c
 ID ACN01975 standard; RNA; 17 BP.
 XX
 XX ACN01975;
 XX
 XX 22-APR-2004 (first entry)
 XX
 XX MNV Inozyme substrate SEQ ID NO 1965.
 XX
 XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 XX encephalitis; myocarditis; meningitis; infection; hepatitis;
 XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 XX Amberzyme; Zinzyne; ss.
 XX
 XX West Nile Virus.
 XX
 XX MO200268637-A2.
 XX
 XX 06-SEP-2002.
 XX
 XX 19-OCT-2001; 2001MO-US048350.
 XX
 XX 20-OCT-2000; 2000US-0242411P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (MNV), useful for treating a condition related to MNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 1965; 495bp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 XX treating a condition related to MNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention

SO Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 806 CGCCAGTTGATCTTGA 822
 DB 17 CGCCAGTTGTTCTTGA 1

RESULT 2423
 ABR34829/c
 ID ABR34829 standard; DNA; 17 BP.
 XX
 XX ABR34829;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 XX Tumour suppression related human fukutin oligo SEQ ID NO 466.
 XX
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 XX schizophrenia; protein chip; gene therapy; tumour suppression;
 XX human fukutin; ds.
 XX
 XX Homo sapiens.
 XX
 XX WO2003025175-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002MO-IB004208.
 XX
 XX 17-SEP-2001; 2001FR-00011978.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Teleman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumour and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.

PS Disclosure; Page 89; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 5 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

QY Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 479 AGTCAGTGTGTGATC 495
17 AGTCAGTGTGTGATC 1

RESULT 2424
ABT39507
ID ABT39507 standard; DNA; 17 BP.
XX
AC ABT39507;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 5144.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOL-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 635; 720pp; French.

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

QY Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 837 GATCTGCTGCGCCGCGC 853
1 GATCTGCTGCGCCCTTGGC 17

RESULT 2425
ABT35178/c
ID ABT35178 standard; DNA; 17 BP.
XX
AC ABT35178;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 815.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOL-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 128; 720pp; French.

CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
DB 17 AGGCGAGTGTGTGATC 1

RESULT 2426

ABT8397/c
ID ABT8397 standard; DNA; 17 BP.

XX AC ABT8397;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 4034.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004208.

XX PR 17-SEP-2001; 2001FR-00011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.

XX PS Disclosure; Page 505; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that

CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 479 AGTGCAGTGTGTGATC 495
DB 17 NATGCAGTGTGTGATC 1

RESULT 2427

ABT40193/c
ID ABT40193 standard; DNA; 17 BP.

XX AC ABT40193;

XX DT 13-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 5830.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004208.

XX PR 17-SEP-2001; 2001FR-00011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.

XX PS Disclosure; Page 715; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic

CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 653 AGTGCAGTGGCGCATC 669
 DB 17 AGTGCAGTGGCGCATC 1

RESULT 2428
 ABT35657/c
 ID ABT35657 standard; DNA; 17 BP.
 XX
 AC ABT35657;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 1294.
 XX
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; protein chip; gene therapy; tumour suppression;
 KM human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 184; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX
 SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 479 AGTGCAGTGGTGTGATC 495
 DB 17 AGTGCAGTGGCGCATC 1

RESULT 2429
 ABT36213
 ID ABT36213 standard; DNA; 17 BP.
 XX
 AC ABT36213;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 1850.
 XX
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; protein chip; gene therapy; tumour suppression;
 KM human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 249; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,

polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention

Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 492 GATCAGCTGCTGCTGCA 508
1 GATCATGCTCTGCTGCA 17

Db 1 GATCATGCTCTGCTGCA 17

RESULT 2430
ABT37096
ID ABT37096 standard; DNA; 17 BP.
AC ABT37096;
XX
XX
DT 12-JUN-2003 (first entry)
XX
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 2733.
XX
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression;
XX
XX
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
XX
PN WO2003025175-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313353/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated with tumours and cell degeneration, also related polypeptides, antibodies and transfected cells.
XX
XX
PS Disclosure; Page 352; 720pp; French.
XX
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acid of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for

preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention

Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 837 GATCGCTGCTGCTGCGC 853
1 GATCCGCGCTGCTGCGC 17

Db 1 GATCCGCGCTGCTGCGC 17

RESULT 2431
ABT38743/C
ID ABT38743 standard; DNA; 17 BP.
AC ABT38743;
XX
XX
DT 12-JUN-2003 (first entry)
XX
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4380.
XX
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression;
XX
XX
KW human fukutin; ds.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025175-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX
DR WPI; 2003-313353/30.
XX
XX
PT New isolated nucleic acid, useful for treating viral diseases associated with tumours and cell degeneration, also related polypeptides, antibodies and transfected cells.
XX
XX
PS Disclosure; Page 546; 720pp; French.
XX
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acid of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell